

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4278
- Ceres seq_id 1580122
- Location of start within SEQ ID NO 4275: at 28 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Eukaryotic protein kinase domain
- Location within SEQ ID NO 4278: from 1 to 86 aa.

(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

related to:

Clone IDs:

342142

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 4279
- Ceres seq_id 1580127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4280
- Ceres seq_id 1580128
- Location of start within SEQ ID NO 4279: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Sperm histone P2
- Location within SEQ ID NO 4280: from 43 to 101 aa.

(Dp) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4281
- Ceres seq_id 1580129
- Location of start within SEQ ID NO 4279: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..874
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atcactaaca aaacacacat caaaaacgat tttacaagaa aaaaatatca gaaaaaatgt	60
cagagaccaa caagaatgcc ttccaagccg gtcaggccgc tggcaaagct gaggagaaga	120
gcaatgttct gctggacaag gccaaaggatg ctgctgctgc agctggagct tccgcgcaac	180
aggcgggaaa gagtatatcg gatgcggcag tgggagggtgc tccatctggt cctgaagctg	240
gccctcgaac aatgaaattc cttgacaatt tccatgtgca aacaaagaga gagcatgctt	300
tgttgggaga taacgagaat ggtgagaacg atgaggaagg cggtgagggt gcaaacccaa	360
aatggatcac cattaaaGca gctctgctGc tactgttagg agctgccatt gcagctgcat	420
ttgctgatcc tttagtcgac actgttaaca acttctccgc agccacaggg attccgtctt	480
tcttcatttc cttcatcgct ttgccttttg ccaccaattc aagtgaagcc gtgtctgcc	540
tcattcttcg atcccgaac aagatcagaa ccgcctcttt aactttctcc gagctatgcg	600
gtggagtgc aatgaacaac attctgtgtc tctcggtgtt cttagcaatc gtctacgttc	660
gaggactgac atggaacttc tcatacagaag tgttggtgat tctcatcggt tgtctggtga	720
tgggcgggtt cgcgagtttc cgcacaactt atcctctttg gacatgtttc atagcttact	780
tgctttaccc attctccttg ggtctggtct atattcttga ttactgggtt ggctggctcg	840
agatatcact ctctgttcaa agagtttggt ctac	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Glu Thr Lys Asn Ala Phe Gln Ala Gly Gln Ala Ala Gly	
1 5 10 15	
Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala	
20 25 30	
Ala Ala Ala Ala Gly Ala Ser Ala Gln Gln Ala Gly Lys Ser Ile Ser	
35 40 45	
Asp Ala Ala Val Gly Gly Ala Pro Ser Gly Pro Glu Ala Gly Pro Arg	
50 55 60	
Thr Met Lys Phe Leu Asp Asn Phe His Val Gln Thr Lys Arg Glu His	
65 70 75 80	
Ala Leu Leu Gly Asp Asn Glu Asn Gly Glu Asn Asp Glu Glu Gly Gly	
85 90 95	
Glu Val Ala Asn Pro Lys Trp Ile Thr Ile Lys Ala Ala Leu Leu Leu	
100 105 110	
Leu Leu Gly Ala Ala Ile Ala Ala Phe Ala Asp Pro Leu Val Asp	
115 120 125	
Thr Val Asn Asn Phe Ser Ala Ala Thr Gly Ile Pro Ser Phe Phe Ile	
130 135 140	
Ser Phe Ile Ala Leu Pro Leu Ala Thr Asn Ser Ser Glu Ala Val Ser	
145 150 155 160	
Ala Ile Ile Phe Ala Ser Arg Lys Lys Ile Arg Thr Ala Ser Leu Thr	
165 170 175	

Phe Ser Glu Leu Cys Gly Gly Val Thr Met Asn Asn Ile Leu Cys Leu
180 185 190
Ser Val Phe Leu Ala Ile Val Tyr Val Arg Gly Leu Thr Trp Asn Phe
195 200 205
Ser Ser Glu Val Leu Val Ile Leu Ile Val Cys Leu Val Met Gly Gly
210 215 220
Phe Ala Ser Phe Arg Thr Thr Tyr Pro Leu Trp Thr Cys Phe Ile Ala
225 230 235 240
Tyr Leu Leu Tyr Pro Phe Ser Leu Gly Leu Val Tyr Ile Leu Asp Tyr
245 250 255
Trp Phe Gly Trp Ser
260

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Phe Leu Asp Asn Phe His Val Gln Thr Lys Arg Glu His Ala
1 5 10 15
Leu Leu Gly Asp Asn Glu Asn Gly Glu Asn Asp Glu Glu Gly Gly Glu
20 25 30
Val Ala Asn Pro Lys Trp Ile Thr Lys Ala Ala Leu Leu Leu
35 40 45
Leu Gly Ala Ala Ile Ala Ala Ala Phe Ala Asp Pro Leu Val Asp Thr
50 55 60
Val Asn Asn Phe Ser Ala Ala Thr Gly Ile Pro Ser Phe Phe Ile Ser
65 70 75 80
Phe Ile Ala Leu Pro Leu Ala Thr Asn Ser Ser Glu Ala Val Ser Ala
85 90 95
Ile Ile Phe Ala Ser Arg Lys Lys Ile Arg Thr Ala Ser Leu Thr Phe
100 105 110
Ser Glu Leu Cys Gly Gly Val Thr Met Asn Asn Ile Leu Cys Leu Ser
115 120 125
Val Phe Leu Ala Ile Val Tyr Val Arg Gly Leu Thr Trp Asn Phe Ser
130 135 140
Ser Glu Val Leu Val Ile Leu Ile Val Cys Leu Val Met Gly Gly Phe
145 150 155 160
Ala Ser Phe Arg Thr Tyr Pro Leu Trp Thr Cys Phe Ile Ala Tyr
165 170 175
Leu Leu Tyr Pro Phe Ser Leu Gly Leu Val Tyr Ile Leu Asp Tyr Trp
180 185 190
Phe Gly Trp Ser
195

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565546

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(A1) SEQUENCE DESCRIPTION: SEQ ID: 1						
aaatttcaat	tttaagata	aaagtaaagt	aactgtgaag	ccaChgnttt	tggttctgct	60
cttaccgtta	tcccaacttc	catatccaaa	ctgaaagaca	ctgggttttg	ttttgtcggg	120
aaaaggagaa	acttcaaaaa	gatgccact	ttgaatctct	tcactaacat	accagtcgac	180
gccgtcactt	gctcagacat	cctcaaggac	gccactaagg	ccgtcgctaa	aatcatcggc	240
aaacctgaat	cctatgtgat	gatactgctt	aacagtggag	tgcccattgc	atttgccggg	300
acctaggaac	ctgctgcata	tggagaattg	atatctattg	ggggattagg	acctggcgta	360
aacgggaagc	ttagcgagac	gatatctgag	attctccaaa	ttaagctctc	catagcagc	420
tctcgctttt	atatcaaatt	ctacgattct	ccgcgacctt	tcttcgggta	caatggatca	480
actttctgaa	aagagcgcaa	ttcaaccttg	taatgatatt	tgggttagaa	ctgtttgctt	540
attcatttca	aaagctgtaa	ttctgaacca	taatttataa	ttttacctcc	ctcaaaagc	

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..54
(D) OTHER INFORMATION: / Ceres Seq. ID 1565547

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..54
(D) OTHER INFORMATION: / Ceres Seq. ID 1565548

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..35
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(D) OTHER INFORMATION: / Ceres Seq. ID 1565549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Gln Leu Ser Glu Lys Arg Arg Ile Gln Pro Cys Asn Asp Ile  
1 5 10 15  
Trp Val Arg Thr Val Cys Leu Phe Ile Ser Lys Ala Val Ile Leu Asn  
20 25 30  
His Asn Leu  
35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1285

(D) OTHER INFORMATION: / Ceres Seq. ID 1565556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

gcagacgaat gtttttggtt tcgagaattt gctgaaatct attcaacgta tacagaggct 60  
ggagctgggg aagaaaagga ttgtctatgg agggagacgt cggaataggt ttggtatgcc 120  
agaatactat ggatgggaag gcgagtaatg gaaatggttt agagaagact gtaccttctt 180  
gttgccctaa ggctatggca tgtgtacctg aggatgatgc taagtgtcac tccactgttg 240  
tttctgggtg gttttcggaa cctcaccctc gctctgggaa aaaaggcggc aaagcagtct 300  
atttcaacaa cctatgtgg ccaggagaag cacactcact gaaagttgag aaagttctgt 360  
tcaaagacaa gtcggatttt caggaagtc tagtgttcga gtcagccacg tacggaaagg 420  
tgcttggtct agatggtatc gtacagctga ccgaaaaaga tgaatgtgca tatcaggaga 480  
tgatagccca tctgccttta tgctctatat cttcccctaa aaatgttctt gttgttggtg 540  
gaggtgatgg ttgtgttctt cgagagattt ctgcccatag ttctgttgag gttattgata 600  
tctgtgagat agacaaagatg gttatagatg tgtctaagaa gttcttcccc gagttagcgg 660  
ttgggtttga cgatcctcgt gttcaacttc acattggtga tgctgctgag ttctctcgtg 720  
aatcccctga agggaagtat gatgccatca ttgttgattc ttcagatccc gtaggtcctg 780  
ctcttgcgct tgttgagaag cttttcttcg agacactggc tagagcggtg aagcctgggg 840  
gagttctttg taacatggca gaaagtatgt ggctccatac tcatcttatt gaagatatga 900  
tctccatttg ccgtcaaaca ttcaaaagtg ttcactatgc gtggagcagc gtccccacat 960  
atccaagcgg cgtgatttgt ttctgtctgt gctctactga aggaccagct gttgacttca 1020  
agaacccaat caaccctatt gagaaactag acggtgcgat gaccataaa agagaattga 1080  
agttctataa ctctgatatg cacagagccg catttgcttt gccacattc Ctgcggagag 1140  
aagtagcttc acttctggct tcttgacttc tgtttggctc taccatatcc ctcatatcaa 1200  
actttgtaga actcttgaag aggaataata aatcattgaa ggctttgtat ctctaagttt 1260  
actcctttat aaaaagactt atatt

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1565557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Gly Asp Val Gly Ile Gly Leu Val Cys Gln Asn Thr Met Asp  
1 5 10 15  
Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro Ser Cys  
20 25 30  
Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys Cys His  
35 40 45  
Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly

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50 55 60  
Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly  
65 70 75 80  
Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser  
85 90 95  
Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val  
100 105 110  
Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala  
115 120 125  
Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro  
130 135 140  
Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu  
145 150 155 160  
Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp  
165 170 175  
Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val  
180 185 190  
Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala Ala Glu  
195 200 205  
Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp  
210 215 220  
Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe  
225 230 235 240  
Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn  
245 250 255  
Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile  
260 265 270  
Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser  
275 280 285  
Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr  
290 295 300  
Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys  
305 310 315 320  
Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser  
325 330 335  
Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu  
340 345 350  
Val Ala Ser Leu Leu Ala Ser  
355

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..345
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro  
1 5 10 15  
Ser Cys Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys  
20 25 30  
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg  
35 40 45  
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp  
50 55 60  
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp  
65 70 75 80

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1565559

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Cys | Val | Pro | Glu | Asp | Asp | Ala | Lys | Cys | His | Ser | Thr | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Trp | Phe | Ser | Glu | Pro | His | Pro | Arg | Ser | Gly | Lys | Lys | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ala | Val | Tyr | Phe | Asn | Asn | Pro | Met | Trp | Pro | Gly | Glu | Ala | His | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Val | Glu | Lys | Val | Leu | Phe | Lys | Asp | Lys | Ser | Asp | Phe | Gln | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Val | Phe | Glu | Ser | Ala | Thr | Tyr | Gly | Lys | Val | Leu | Val | Leu | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ile | Val | Gln | Leu | Thr | Glu | Lys | Asp | Glu | Cys | Ala | Tyr | Gln | Glu | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | His | Leu | Pro | Leu | Cys | Ser | Ile | Ser | Ser | Pro | Lys | Asn | Val | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Val | Gly | Gly | Gly | Asp | Gly | Gly | Val | Leu | Arg | Glu | Ile | Ser | Arg | His |

115 120 125  
Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp Lys Met Val Ile  
130 135 140  
Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val Gly Phe Asp Asp  
145 150 155 160  
Pro Arg Val Gln Leu His Ile Gly Asp Ala Ala Glu Phe Leu Arg Lys  
165 170 175  
Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp Ser Ser Asp Pro  
180 185 190  
Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe Phe Glu Thr Leu  
195 200 205  
Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn Met Ala Glu Ser  
210 215 220  
Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile Ser Ile Cys Arg  
225 230 235 240  
Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser Val Pro Thr Tyr  
245 250 255  
Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr Glu Gly Pro Ala  
260 265 270  
Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys Leu Asp Gly Ala  
275 280 285  
Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser Asp Met His Arg  
290 295 300  
Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu Val Ala Ser Leu  
305 310 315 320  
Leu Ala Ser

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| aacacctagg | ttcttgtttc | ctaacaaagg | ctctactttt  | tcttttagtta | actactatgg  | 60   |
| ctcatttcct | cgagacacag | gaacccctcg | tattctccgg  | gaagaaacga  | aacgatcgcg  | 120  |
| atgacaacga | cggtagcgcc | ttgggtgcga | agaaatcagc  | actggcggtg  | tgtgatgccg  | 180  |
| accctgcagc | ggccatagcg | aatatccgac | atgagtttgg  | ggagcacggg  | ggagtaaaca  | 240  |
| tgtccatcga | agcctccgcc | accttcaccg | tcatggaacc  | ggataccatg  | aggcggatgt  | 300  |
| tcaccggaga | actgggaccg | gacaacgact | tctacgtata  | cagccgacac  | ttcaacccca  | 360  |
| ccgtgctcaa | cctcagccgt | cagatggctg | ctctcgaagg  | cacccaagct  | gcctactgta  | 420  |
| cctctagcgg | tatgtcggcg | atatcgtcag | tgatgctgca  | actgtgcagc  | agcggaggac  | 480  |
| acgtggtcgc | ggcaagcacg | ctctacggag | gaacacacgc  | tttgctctct  | catttcttgc  | 540  |
| cacggacatg | taacataacc | acctccttcg | ttgacataac  | ggaccatggc  | gcggtggcaa  | 600  |
| acgcgatcgt | tgagggtagg | acacaggttc | tctactttga  | gtcgggtggc  | aaccgcagcg  | 660  |
| tgactgtggc | tgacatacct | gaactgagcc | gtatggcaca  | cgagaagggc  | gtgacggtgg  | 720  |
| tggttgacaa | cacattcgcc | cccatggtgc | tgtctccggc  | caagcttgga  | gcagatgtgg  | 780  |
| tggttcacag | tatctccaag | ttcatcagtg | gtggggctga  | catcatcgca  | ggggccgtgt  | 840  |
| gtgggagtga | gaagctggtg | gaaagagatg | atggatcttc  | gtggcggatc  | tctgatgctt  | 900  |
| ctaggtccca | ccatgaacgc | caaggtggct | ttcgagctct  | cagagcgaat  | ccctcacttg  | 960  |
| ggcctacgca | tgagagagca | cagccacaga | gcccgaagtgt | atgctgagag  | aatgagggat  | 1020 |
| ttggggatga | aagtcatata | tccagggctc | gagacccacc  | cgcagcacia  | gctcttcaaa  | 1080 |
| ggtatggtga | atagagacta | tggatacgga | ggattgctgt  | cgatagacat  | ggagacagag  | 1140 |
| gagaaagcca | acaagctcat | ggcatatctc | cagaacgcca  | ctcagtttgg  | cttcattggcc | 1200 |
| gtcagtttgg | gttactacga | gacactcatg | tcttgctccg  | ggagcagcac  | cagcagcgag  | 1260 |
| cttgaccctt | cgcagaagga | agctgcaggc | atctctcctg  | gtcttgtaag  | aatatcgggtg | 1320 |

gggtatgtgg gtacattgga gcagaagtgg acacaattcg agaagcattc ctcagaatgt 1380  
aaaatgtctt cttctatata tgatgggttt ctttcccca aataccaaca attcatcatc 1440  
tgcggtatat gtatgatgtg gccaatgttc agtctcttat ttgtc

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | His | Phe | Leu | Glu | Thr | Gln | Glu | Pro | Leu | Val | Phe | Ser | Gly | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Arg | Asn | Asp | Arg | Asp | Asp | Asn | Asp | Gly | Asp | Ala | Leu | Val | Ala | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ser | Ala | Leu | Ala | Val | Cys | Asp | Ala | Asp | Pro | Ala | Ala | Ile | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ile | Arg | His | Glu | Phe | Gly | Glu | His | Gly | Gly | Val | Asn | Met | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ala | Ser | Ala | Thr | Phe | Thr | Val | Met | Glu | Pro | Asp | Thr | Met | Arg | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Phe | Thr | Gly | Glu | Leu | Gly | Pro | Asp | Asn | Asp | Phe | Tyr | Val | Tyr | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | His | Phe | Asn | Pro | Thr | Val | Leu | Asn | Leu | Ser | Arg | Gln | Met | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Gly | Thr | Gln | Ala | Ala | Tyr | Cys | Thr | Ser | Ser | Gly | Met | Ser | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Ser | Val | Met | Leu | Gln | Leu | Cys | Ser | Ser | Gly | Gly | His | Val | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Ser | Thr | Leu | Tyr | Gly | Gly | Thr | His | Ala | Leu | Leu | Ser | His | Phe |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Pro | Arg | Thr | Cys | Asn | Ile | Thr | Thr | Ser | Phe | Val | Asp | Ile | Thr | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| His | Gly | Ala | Val | Ala | Asn | Ala | Ile | Val | Glu | Gly | Arg | Thr | Gln | Val | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Tyr | Phe | Glu | Ser | Val | Ala | Asn | Pro | Thr | Leu | Thr | Val | Ala | Asp | Ile | Pro |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Glu | Leu | Ser | Arg | Met | Ala | His | Glu | Lys | Gly | Val | Thr | Val | Val | Val | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Thr | Phe | Ala | Pro | Met | Val | Leu | Ser | Pro | Ala | Lys | Leu | Gly | Ala | Asp |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Val | Val | His | Ser | Ile | Ser | Lys | Phe | Ile | Ser | Gly | Gly | Ala | Asp | Ile |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ile | Ala | Gly | Ala | Val | Cys | Gly | Ser | Glu | Lys | Leu | Val | Glu | Arg | Asp | Asp |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Gly | Ser | Ser | Trp | Arg | Ile | Ser | Asp | Ala | Ser | Arg | Ser | His | His | Glu | Arg |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Gln | Gly | Gly | Phe | Arg | Ala | Leu | Arg | Ala | Asn | Pro | Ser | Leu | Gly | Pro | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| His | Glu | Arg | Ala | Gln | Pro | Gln | Ser | Pro | Ser | Val | Cys |     |     |     |     |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Pro | Asp | Thr | Met | Arg | Arg | Met | Phe | Thr | Gly | Glu | Leu | Gly | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asn | Asp | Phe | Tyr | Val | Tyr | Ser | Arg | His | Phe | Asn | Pro | Thr | Val | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Ser | Arg | Gln | Met | Ala | Ala | Leu | Glu | Gly | Thr | Gln | Ala | Ala | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Thr | Ser | Ser | Gly | Met | Ser | Ala | Ile | Ser | Ser | Val | Met | Leu | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Ser | Ser | Gly | Gly | His | Val | Val | Ala | Ala | Ser | Thr | Leu | Tyr | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | His | Ala | Leu | Leu | Ser | His | Phe | Leu | Pro | Arg | Thr | Cys | Asn | Ile | Thr |



|                                                                 |    |  |     |  |     |
|-----------------------------------------------------------------|----|--|-----|--|-----|
|                                                                 | 85 |  | 90  |  | 95  |
| Thr Ser Phe Val Asp Ile Thr Asp His Gly Ala Val Ala Asn Ala Ile |    |  |     |  |     |
| 100                                                             |    |  | 105 |  | 110 |
| Val Glu Gly Arg Thr Gln Val Leu Tyr Phe Glu Ser Val Ala Asn Pro |    |  |     |  |     |
| 115                                                             |    |  | 120 |  | 125 |
| Thr Leu Thr Val Ala Asp Ile Pro Glu Leu Ser Arg Met Ala His Glu |    |  |     |  |     |
| 130                                                             |    |  | 135 |  | 140 |
| Lys Gly Val Thr Val Val Val Asp Asn Thr Phe Ala Pro Met Val Leu |    |  |     |  |     |
| 145                                                             |    |  | 150 |  | 155 |
| Ser Pro Ala Lys Leu Gly Ala Asp Val Val Val His Ser Ile Ser Lys |    |  |     |  |     |
| 165                                                             |    |  | 170 |  | 175 |
| Phe Ile Ser Gly Gly Ala Asp Ile Ile Ala Gly Ala Val Cys Gly Ser |    |  |     |  |     |
| 180                                                             |    |  | 185 |  | 190 |
| Glu Lys Leu Val Glu Arg Asp Asp Gly Ser Ser Trp Arg Ile Ser Asp |    |  |     |  |     |
| 195                                                             |    |  | 200 |  | 205 |
| Ala Ser Arg Ser His His Glu Arg Gln Gly Gly Phe Arg Ala Leu Arg |    |  |     |  |     |
| 210                                                             |    |  | 215 |  | 220 |
| Ala Asn Pro Ser Leu Gly Pro Thr His Glu Arg Ala Gln Pro Gln Ser |    |  |     |  |     |
| 225                                                             |    |  | 230 |  | 235 |
| Pro Ser Val Cys                                                 |    |  |     |  | 240 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..751
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaggagaag gaacattcac tctcacgcgc ttcaactttc tccagaaaca agaaaatttc  | 60  |
| acagcaaaat ttttctcgag aaaatccgaa gaagacaaaa tggcggatca gctaaccgat  | 120 |
| gaccagatct ccgagttcaa ggaagctttt agcctattcg acaaagacgg agatggttgt  | 180 |
| atcaccacaa aggagcttgg gactgtgatg agatcacttg ggcagaaccc gacagaagcc  | 240 |
| gagctccagg atatgatcaa tgaagtggat gcagacggga acgggacaat agatttccct  | 300 |
| gagttcctga acctaattggc acgtaagatg aaagacactg attcagagga agagcttaag | 360 |
| gaagccttca gggtttttga caaggaccag aacggtttca tctcggcggc tgagcttcgt  | 420 |
| cacgtgatga caaatcttgg ggagaagttg acggatgagg aagtcgatga gatgatccga  | 480 |
| gaggctgatg tcgatggtga tggtcagatc aactatgaag agttcgtcaa agtcgatgat  | 540 |
| gcaaagtgag attcttctta tccctcgaaa tcctaagcat gtttttcttt tacatcttta  | 600 |
| aaactgagaa aagtaattta ttgaacaaaa agaaacagag agatttgctt ccttgtttgt  | 660 |
| tttgttggtc Agtgattttt tggtaacggt gcttcttctt tgcccttttg ttttgttatt  | 720 |
| gtccgtgacg ttgcaactca tcatttgctt t                                 |     |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Lys Gly Glu Gly Thr Phe Thr Leu Thr Arg Phe Asn Phe Leu Gln Lys |    |
| 1                                                               | 5  |
|                                                                 | 10 |
|                                                                 | 15 |
| Gln Glu Asn Phe Thr Ala Lys Phe Phe Ser Arg Lys Ser Glu Glu Asp |    |

20 25 30  
Lys Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ser Glu Phe Lys Glu  
35 40 45  
Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys  
50 55 60  
Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala  
65 70 75 80  
Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr  
85 90 95  
Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp  
100 105 110  
Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys  
115 120 125  
Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr  
130 135 140  
Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg  
145 150 155 160  
Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val  
165 170 175  
Lys Val Met Met Ala Lys  
180

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ser Glu Phe Lys Glu Ala  
1 5 10 15  
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu  
20 25 30  
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu  
35 40 45  
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile  
50 55 60  
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr  
65 70 75 80  
Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp  
85 90 95  
Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn  
100 105 110  
Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu  
115 120 125  
Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys  
130 135 140  
Val Met Met Ala Lys  
145

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1565579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met
1 5 10 15
Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu
20 25 30
Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu
35 40 45
Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe
50 55 60
Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys
65 70 75 80
Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Val Asp
85 90 95
Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Val Met Met Ala
100 105 110
Lys
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1602 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1602

(D) OTHER INFORMATION: / Ceres Seq. ID 1565612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
agctactact gttgaagcga ttctcactaa aaccctcgaa cacatcgctt ttatctcttt 60
ctctagatct actcgctatg gctactatca ccgttgtaa ggctagacag atcttcgaca 120
gtcgtggtaa tcccaccgtt gaggtggata tccacacgtc aaatgggtgtt aaggttacag 180
cagctgttcc aagtggagct tccactggta tctatgaggc tcttgagctg agggatggag 240
gatctgacta ccttggaag ggtgtatcta aggctgttg caatgtgaac aacatcatcg 300
ggccagcact tattggaaag gacccaactc agcagactgc tattgacaac ttcatgggtcc 360
atgaacttga cggaaaccaa aacgagtggtt ggtggtgcaa gcaaaagctt ggagccaatg 420
cgattcttgc tgtgtctctt gctgtctgca aagctggggc tgtgtgcagc ggcattcctc 480
tatacaagca cattgccaac cttgctggta accccaagat tgtgctacca gttcctgcct 540
tcaacgtcat caatggtgga tcccatgccg gaaacaagct tgctatgcag gagtttatga 600
tcttccctgt tggagctgct tctttcaagg gagccatgaa gatgggtgtg gaagtttacc 660
accacttgaa gtctgtgatt aagaagaagt acggccagga tgccacaaat gttggtgatg 720
aaggtgggtt tgcaccaaac attcaggaga acaaggaggg tcttgaattg ctcaagactg 780
ctatcgagaa ggctggatac actggaaagg ttgtcattgg aatggatgtt gccgcttcag 840
agttctactc agaagacaag acctacgact tgaacttcaa agaagagaac aacaatggct 900
ctcagaagat ttctggtgat gctctaaagg acctgtacaa gtctttgtc gctgagtacc 960
caatcgtgtc cattgaggac ccatttgacc aagatgactg ggagcactat gctaagatga 1020
ccactgagtg tggaaaccgag gttcagaTtt gtcggtgatg atttgttggt cactaaccct 1080
aagagagttg ctaaggcaat cgccgagaag tcttgcaatg ctcttctttt gaaggttaac 1140
caaatcggat ctgtaaccga gagtatcgag gcagtttaaga tgtcgaagaa agcaggttg 1200
ggagtgatga ccagccacag aagtggtgaa accgaggaca cattcattgc tgacttagcc 1260
gttggtctgt ctactggaca aatcaaaacc ggtgctcctt gcagatccga gcgtcttgcc 1320
aagtacaacc agcttttgcg tattgaggag gaggttggat cagaggcaat ttacgctgga 1380
gtcaacttcc gcaaacctgt agaacctac taaatggagc ttttagaagc aaagtggctc 1440
tctttgtgac gaggagaaga tgacctgagt ttgatcattt gctttaatta aataaaacgt 1500
tctgtttttg tttcttcttt gtttggtttc ttacgtcttt tgttgaacct ttttgggaa 1560
aagttactca tttttgtaag ggaaacatga gaatgctctg cc
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

```

 (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..351
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565613
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

|         |         |         |         |         |         |         |         |         |        |        |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|--------|--------|---------|---------|---------|---------|---------|
| Leu 1   | Leu     | Leu     | Leu     | Lys 5   | Arg     | Phe     | Ser     | Leu     | Lys 10 | Pro    | Ser     | Asn     | Thr     | Ser 15  | Pro     |
| Leu     | Ser     | Leu     | Ser     | Leu     | Asp     | Leu     | Leu     | Ala 25  | Met    | Ala    | Thr     | Ile     | Thr     | Val 30  | Val     |
| Lys     | Ala     | Arg     | Gln     | Ile     | Phe     | Asp     | Ser 40  | Arg     | Gly    | Asn    | Pro     | Thr 45  | Val     | Glu     | Val     |
| Asp     | Ile     | His     | Thr     | Ser     | Asn     | Gly 55  | Val     | Lys     | Val    | Thr    | Ala 60  | Ala     | Val     | Pro     | Ser     |
| Gly 65  | Ala     | Ser     | Thr     | Gly     | Ile 70  | Tyr     | Glu     | Ala     | Leu    | Glu 75 | Leu     | Arg     | Asp     | Gly     | Gly 80  |
| Ser     | Asp     | Tyr     | Leu     | Gly 85  | Lys     | Gly     | Val     | Ser     | Lys 90 | Ala    | Val     | Gly     | Asn     | Val 95  | Asn     |
| Asn     | Ile     | Ile     | Gly 100 | Pro     | Ala     | Leu     | Ile     | Gly 105 | Lys    | Asp    | Pro     | Thr     | Gln 110 | Gln     | Thr     |
| Ala     | Ile     | Asp 115 | Asn     | Phe     | Met     | Val     | His 120 | Glu     | Leu    | Asp    | Gly     | Thr 125 | Gln     | Asn     | Glu     |
| Trp     | Gly 130 | Trp     | Cys     | Lys     | Gln     | Lys 135 | Leu     | Gly     | Ala    | Asn    | Ala 140 | Ile     | Leu     | Ala     | Val     |
| Ser 145 | Leu     | Ala     | Val     | Cys     | Lys 150 | Ala     | Gly     | Ala     | Val    | Val    | Ser 155 | Gly     | Ile     | Pro     | Leu 160 |
| Tyr     | Lys     | His     | Ile     | Ala 165 | Asn     | Leu     | Ala     | Gly     | Asn    | Pro    | Lys     | Ile     | Val     | Leu 175 | Pro     |
| Val     | Pro     | Ala     | Phe 180 | Asn     | Val     | Ile     | Asn     | Gly 185 | Gly    | Ser    | His     | Ala     | Gly 190 | Asn     | Lys     |
| Leu     | Ala     | Met 195 | Gln     | Glu     | Phe     | Met     | Ile 200 | Leu     | Pro    | Val    | Gly     | Ala 205 | Ala     | Ser     | Phe     |
| Lys     | Gly 210 | Ala     | Met     | Lys     | Met     | Gly 215 | Val     | Glu     | Val    | Tyr    | His     | His     | Leu     | Lys     | Ser     |
| Val 225 | Ile     | Lys     | Lys     | Lys     | Tyr 230 | Gly     | Gln     | Asp     | Ala    | Thr    | Asn     | Val     | Gly     | Asp     | Glu 240 |
| Gly     | Gly     | Phe     | Ala     | Pro 245 | Asn     | Ile     | Gln     | Glu     | Asn    | Lys    | Glu     | Gly     | Leu     | Glu 255 | Leu     |
| Leu     | Lys     | Thr     | Ala 260 | Ile     | Glu     | Lys     | Ala     | Gly 265 | Tyr    | Thr    | Gly     | Lys     | Val     | Val     | Ile     |
| Gly     | Met     | Asp 275 | Val     | Ala     | Ala     | Ser     | Glu 280 | Phe     | Tyr    | Ser    | Glu     | Asp     | Lys     | Thr     | Tyr     |
| Asp     | Leu     | Asn     | Phe     | Lys     | Glu     | Glu 295 | Asn     | Asn     | Asn    | Gly    | Ser     | Gln     | Lys     | Ile     | Ser     |
| Gly 305 | Asp     | Ala     | Leu     | Lys     | Asp 310 | Leu     | Tyr     | Lys     | Ser    | Phe    | Val     | Ala     | Glu     | Tyr     | Pro 320 |
| Ile     | Val     | Ser     | Ile     | Glu 325 | Asp     | Pro     | Phe     | Asp     | Gln    | Asp    | Asp     | Trp     | Glu     | His     | Tyr     |
| Ala     | Lys     | Met     | Thr     | Glu 340 | Cys     | Gly     | Thr     | Glu     | Val    | Gln    | Ile     | Cys     | Arg     |         |         |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1565614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Thr Ile Thr Val Val Lys Ala Arg Gln Ile Phe Asp Ser Arg  
1 5 10 15  
Gly Asn Pro Thr Val Glu Val Asp Ile His Thr Ser Asn Gly Val Lys  
20 25 30  
Val Thr Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala  
35 40 45  
Leu Glu Leu Arg Asp Gly Gly Ser Asp Tyr Leu Gly Lys Gly Val Ser  
50 55 60  
Lys Ala Val Gly Asn Val Asn Asn Ile Ile Gly Pro Ala Leu Ile Gly  
65 70 75 80  
Lys Asp Pro Thr Gln Gln Thr Ala Ile Asp Asn Phe Met Val His Glu  
85 90 95  
Leu Asp Gly Thr Gln Asn Glu Trp Gly Trp Cys Lys Gln Lys Leu Gly  
100 105 110  
Ala Asn Ala Ile Leu Ala Val Ser Leu Ala Val Cys Lys Ala Gly Ala  
115 120 125  
Val Val Ser Gly Ile Pro Leu Tyr Lys His Ile Ala Asn Leu Ala Gly  
130 135 140  
Asn Pro Lys Ile Val Leu Pro Val Pro Ala Phe Asn Val Ile Asn Gly  
145 150 155 160  
Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu Phe Met Ile Leu  
165 170 175  
Pro Val Gly Ala Ala Ser Phe Lys Gly Ala Met Lys Met Gly Val Glu  
180 185 190  
Val Tyr His His Leu Lys Ser Val Ile Lys Lys Lys Tyr Gly Gln Asp  
195 200 205  
Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro Asn Ile Gln Glu  
210 215 220  
Asn Lys Glu Gly Leu Glu Leu Leu Lys Thr Ala Ile Glu Lys Ala Gly  
225 230 235 240  
Tyr Thr Gly Lys Val Val Ile Gly Met Asp Val Ala Ala Ser Glu Phe  
245 250 255  
Tyr Ser Glu Asp Lys Thr Tyr Asp Leu Asn Phe Lys Glu Glu Asn Asn  
260 265 270  
Asn Gly Ser Gln Lys Ile Ser Gly Asp Ala Leu Lys Asp Leu Tyr Lys  
275 280 285  
Ser Phe Val Ala Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Phe Asp  
290 295 300  
Gln Asp Asp Trp Glu His Tyr Ala Lys Met Thr Thr Glu Cys Gly Thr  
305 310 315 320  
Glu Val Gln Ile Cys Arg  
325

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1565615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Val His Glu Leu Asp Gly Thr Gln Asn Glu Trp Gly Trp Cys Lys  
1 5 10 15

Gln Lys Leu Gly Ala Asn Ala Ile Leu Ala Val Ser Leu Ala Val Cys  
20 25 30  
Lys Ala Gly Ala Val Val Ser Gly Ile Pro Leu Tyr Lys His Ile Ala  
35 40 45  
Asn Leu Ala Gly Asn Pro Lys Ile Val Leu Pro Val Pro Ala Phe Asn  
50 55 60  
Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu  
65 70 75 80  
Phe Met Ile Leu Pro Val Gly Ala Ala Ser Phe Lys Gly Ala Met Lys  
85 90 95  
Met Gly Val Glu Val Tyr His His Leu Lys Ser Val Ile Lys Lys Lys  
100 105 110  
Tyr Gly Gln Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro  
115 120 125  
Asn Ile Gln Glu Asn Lys Glu Gly Leu Glu Leu Leu Lys Thr Ala Ile  
130 135 140  
Glu Lys Ala Gly Tyr Thr Gly Lys Val Val Ile Gly Met Asp Val Ala  
145 150 155 160  
Ala Ser Glu Phe Tyr Ser Glu Asp Lys Thr Tyr Asp Leu Asn Phe Lys  
165 170 175  
Glu Glu Asn Asn Asn Gly Ser Gln Lys Ile Ser Gly Asp Ala Leu Lys  
180 185 190  
Asp Leu Tyr Lys Ser Phe Val Ala Glu Tyr Pro Ile Val Ser Ile Glu  
195 200 205  
Asp Pro Phe Asp Gln Asp Asp Trp Glu His Tyr Ala Lys Met Thr Thr  
210 215 220  
Glu Cys Gly Thr Glu Val Gln Ile Cys Arg  
225 230

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| ataaaaatca  | ttatccaaaa  | aagtgcgaacc | tctttcgccg | tagaaaacat | tccgtaacc  | 60   |
| atgctccgaa  | gaatcaacttg | ttctttcttca | cttgcttcac | cctctctctt | cctccgcttc | 120  |
| tttcgccaac  | tccctcgctc  | ttactcctca  | ccgaccacca | tcgccgtctc | aggccgcaac | 180  |
| attcgccgac  | tatcaactcc  | aaccactctt  | cgttgcattt | gttcacactc | ttcatctgaa | 240  |
| atcatctccg  | agcatcctcc  | gttcgtcagg  | gtttacaaag | acggtcgtat | cgaacgtctt | 300  |
| tccggcaccg  | aaacagtcct  | ggcttctcta  | aaccacgaa  | acgacgtcgt | ttcaaaagac | 360  |
| gttgctact   | caccggggca  | taacctctcc  | gttcgtctct | ttctccctca | caaataca   | 420  |
| caactcgccg  | ccgtaacaa   | actccctcta  | cttatctact | tccacggcgg | agcttgata  | 480  |
| aacgaatccc  | ctttctcccc  | aatctaccac  | aatttctctc | cggaggtagt | taaatccgct | 540  |
| aactgcctcg  | ccgtctcggt  | tcaataccgc  | cgtgcaccgg | aagatccggt | tccggctgcg | 600  |
| tatgaagata  | catggctctg  | tattcaatgg  | atcttctcac | attccgatgg | atctggtgaa | 660  |
| gaagattgga  | ttaacaaata  | cgctgatttc  | gaaaaagttt | ttctcgccgg | agatagtgcc | 720  |
| ggtggttaata | tatctcatca  | catggctatg  | agagctggta | aagagaagct | taagcctaga | 780  |
| atcaaaggga  | ctgtgattgt  | gcattccagc  | atttggggga | aagatccggt | cgatgagcac | 840  |
| gatgtgcaag  | atagagagat  | cagagacgga  | gttgacagaa | tttgggagaa | aattgtgagt | 900  |
| ccgaatagtg  | ttgatggagc  | ggatgatccg  | tggtttaatg | tggttggatc | cgggtcggat | 960  |
| ttttccggga  | tgggatgtga  | gaagggtttt  | gttgaggtgg | ctgggaaaga | tgtgttttgg | 1020 |
| cggcaaggat  | tagCttacgc  | ggagaagcta  | aagaagagtg | ggtggaaagg | agaggtggag | 1080 |
| gtgattgagg  | aagaagatga  | agaacattgc  | ttccatctct | taaatccaag | ttctgaaaat | 1140 |
| gctcccagct  | tcatgaagag  | acttgtggag  | tttatcaact | gttaacattg | ttctttgtgt | 1200 |
| gacacgaata  | aattttgatg  | taacctttga  | atttgatttg | gttagataat | tatggttaag | 1260 |

gaattaaata caggaataac tctgttctga ct

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1565617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Ile | Ile | Ile | Gln | Lys | Ser | Ala | Thr | Ser | Phe | Ala | Val | Glu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Pro | Val | Thr | Met | Leu | Arg | Arg | Ile | Thr | Cys | Ser | Ser | Ser | Leu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Ser | Leu | Phe | Leu | Arg | Phe | Phe | Arg | Gln | Leu | Pro | Arg | Ser | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Pro | Thr | Thr | Ile | Ala | Val | Ser | Gly | Arg | Asn | Ile | Arg | Arg | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Pro | Thr | Thr | Leu | Arg | Cys | Ile | Cys | Ser | His | Ser | Ser | Ser | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Ile | Ser | Glu | His | Pro | Pro | Phe | Val | Arg | Val | Tyr | Lys | Asp | Gly | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Glu | Arg | Leu | Ser | Gly | Thr | Glu | Thr | Val | Pro | Ala | Ser | Leu | Asn | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Asn | Asp | Val | Val | Ser | Lys | Asp | Val | Val | Tyr | Ser | Pro | Gly | His | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Val | Arg | Leu | Phe | Leu | Pro | His | Lys | Ser | Thr | Gln | Leu | Ala | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Gly | Asn | Lys | Leu | Pro | Leu | Leu | Ile | Tyr | Phe | His | Gly | Gly | Ala | Trp | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Glu | Ser | Pro | Phe | Ser | Pro | Ile | Tyr | His | Asn | Phe | Leu | Thr | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Lys | Ser | Ala | Asn | Cys | Leu | Ala | Val | Ser | Val | Gln | Tyr | Arg | Arg | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Pro | Glu | Asp | Pro | Val | Pro | Ala | Ala | Tyr | Glu | Asp | Thr | Trp | Ser | Ala | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Trp | Ile | Phe | Ser | His | Ser | Asp | Gly | Ser | Gly | Glu | Glu | Asp | Trp | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Lys | Tyr | Ala | Asp | Phe | Glu | Lys | Val | Phe | Leu | Ala | Gly | Asp | Ser | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Gly | Asn | Ile | Ser | His | His | Met | Ala | Met | Arg | Ala | Gly | Lys | Glu | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Lys | Pro | Arg | Ile | Lys | Gly | Thr | Val | Ile | Val | His | Pro | Ala | Ile | Trp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Gly | Lys | Asp | Pro | Val | Asp | Glu | His | Asp | Val | Gln | Asp | Arg | Glu | Ile | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Gly | Val | Ala | Glu | Ile | Trp | Glu | Lys | Ile | Val | Ser | Pro | Asn | Ser | Val |
|     | 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Asp | Gly | Ala | Asp | Asp | Pro | Trp | Phe | Asn | Val | Val | Gly | Ser | Gly | Ser | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Ser | Gly | Met | Gly | Cys | Glu | Lys | Val | Leu | Val | Glu | Val | Ala | Gly | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Val | Phe | Trp | Arg | Gln | Gly | Leu | Ala | Tyr | Ala | Glu | Lys | Leu | Lys | Lys |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Ser | Gly | Trp | Lys | Gly | Glu | Val | Glu | Val | Ile | Glu | Glu | Glu | Asp | Glu | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| His | Cys | Phe | His | Leu | Leu | Asn | Pro | Ser | Ser | Glu | Asn | Ala | Pro | Ser | Phe |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:26:

(A) LENGTH: 374 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1565618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

[illegible]



370

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atcttaatta tactgatctt tatcggtgac tagatttaag aaacaaaata ataagatggt  | 60   |
| tagggcaa atagtgagca tggttctctt gatgcatgcc atcggtgggt ttccttttca    | 120  |
| tgcgagggga ttaagtatga cttactacat gatgagctgt cctttcgctg aacagattgt  | 180  |
| gaagaacagt gttaacaatg ctcttcaagc cgatcccaact ttagccgctg gtcttatccg | 240  |
| tatgttggtc cagcactgtt tcatcgaggg atgtgatgcg tcaattctgc tagattcaac  | 300  |
| gaaagacaac actgcggaag aggattcgcc tgcgaatctg agtctacgtg gctacgagat  | 360  |
| catcgatgat gcaaaggaga aaatcgagaa tagatgtcca ggagttgtat catgcgcaga  | 420  |
| tatagttgcc atggctgcta gagatgctgt cttttgggct ggtggtccat attatgacat  | 480  |
| accgaaagga aggtttgatg gtaaaagatc aaagatagaa gatacaagaa atctaccttc  | 540  |
| accttttctt aatgcctctc aactcattca aacttttggc caacgtgggt tcaactccaca | 600  |
| agatgttggt gctctctctg gagcacatac cctaggagtt gcacgatgct cctccttcaa  | 660  |
| ggctagactt accgtcccag actcttcatt agactcgact tttgcaaaca ctctctctaa  | 720  |
| aacatgcagc gcgggtgaca atgcagagca accctttgat gCtaacgcgca acgatttcga | 780  |
| caatgcttac ttcaatgcgc ttcagatgaa atcaggagtc ctcttttcag accaaacttt  | 840  |
| attcaacaca ccaaggacca ggaatcttgt taacggctat gcacttaacc aagccaagtt  | 900  |
| cttctttgat ttccaacagg ccatgcgcaa gatgagcaat cttgatgtta aacttggtc   | 960  |
| tcaaggtgaa gtccgtcaaa attgtcggag tattaattag gctagaccac atctacttac  | 1020 |
| gatttttgta tttataataa gttctctact cttgttatat gaagaatcat gaatcttcta  | 1080 |
| ggctactatg taaaaattgt gtactctcgt aatatgcagt tgtatactta ttgcttgtgt  | 1140 |
| ggttcagata tccatcaaaa agtaatatat tttggttgc                         |      |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Arg Ala Asn Ile Val Ser Met Val Leu Leu Met His Ala Ile |  |
| 1 5 10 15                                                       |  |
| Val Gly Phe Pro Phe His Ala Arg Gly Leu Ser Met Thr Tyr Tyr Met |  |
| 20 25 30                                                        |  |
| Met Ser Cys Pro Phe Ala Glu Gln Ile Val Lys Asn Ser Val Asn Asn |  |
| 35 40 45                                                        |  |
| Ala Leu Gln Ala Asp Pro Thr Leu Ala Ala Gly Leu Ile Arg Met Leu |  |
| 50 55 60                                                        |  |
| Phe His Asp Cys Phe Ile Glu Gly Cys Asp Ala Ser Ile Leu Leu Asp |  |
| 65 70 75 80                                                     |  |
| Ser Thr Lys Asp Asn Thr Ala Glu Lys Asp Ser Pro Ala Asn Leu Ser |  |
| 85 90 95                                                        |  |
| Leu Arg Gly Tyr Glu Ile Ile Asp Asp Ala Lys Glu Lys Ile Glu Asn |  |
| 100 105 110                                                     |  |
| Arg Cys Pro Gly Val Val Ser Cys Ala Asp Ile Val Ala Met Ala Ala |  |
| 115 120 125                                                     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | Ala | Val | Phe | Trp | Ala | Gly | Gly | Pro | Tyr | Tyr | Asp | Ile | Pro | Lys |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Arg | Phe | Asp | Gly | Lys | Arg | Ser | Lys | Ile | Glu | Asp | Thr | Arg | Asn | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Ser | Pro | Phe | Leu | Asn | Ala | Ser | Gln | Leu | Ile | Gln | Thr | Phe | Gly | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Gly | Phe | Thr | Pro | Gln | Asp | Val | Val | Ala | Leu | Ser | Gly | Ala | His | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Val | Ala | Arg | Cys | Ser | Ser | Phe | Lys | Ala | Arg | Leu | Thr | Val | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Ser | Ser | Leu | Asp | Ser | Thr | Phe | Ala | Asn | Thr | Leu | Ser | Lys | Thr | Cys |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ala | Gly | Asp | Asn | Ala | Glu | Gln | Pro | Phe | Asp | Ala | Thr | Arg | Asn | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Asp | Asn | Ala | Tyr | Phe | Asn | Ala | Leu | Gln | Met | Lys | Ser | Gly | Val | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Ser | Asp | Gln | Thr | Leu | Phe | Asn | Thr | Pro | Arg | Thr | Arg | Asn | Leu | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Gly | Tyr | Ala | Leu | Asn | Gln | Ala | Lys | Phe | Phe | Phe | Asp | Phe | Gln | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Met | Arg | Lys | Met | Ser | Asn | Leu | Asp | Val | Lys | Leu | Gly | Ser | Gln | Gly |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Val | Arg | Gln | Asn | Cys | Arg | Ser | Ile | Asn |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1565635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Leu | Met | His | Ala | Ile | Val | Gly | Phe | Pro | Phe | His | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Ser | Met | Thr | Tyr | Tyr | Met | Met | Ser | Cys | Pro | Phe | Ala | Glu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Val | Lys | Asn | Ser | Val | Asn | Asn | Ala | Leu | Gln | Ala | Asp | Pro | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Gly | Leu | Ile | Arg | Met | Leu | Phe | His | Asp | Cys | Phe | Ile | Glu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Cys | Asp | Ala | Ser | Ile | Leu | Leu | Asp | Ser | Thr | Lys | Asp | Asn | Thr | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asp | Ser | Pro | Ala | Asn | Leu | Ser | Leu | Arg | Gly | Tyr | Glu | Ile | Ile | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ala | Lys | Glu | Lys | Ile | Glu | Asn | Arg | Cys | Pro | Gly | Val | Val | Ser | Cys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Asp | Ile | Val | Ala | Met | Ala | Ala | Arg | Asp | Ala | Val | Phe | Thr | Ala | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Pro | Tyr | Tyr | Asp | Ile | Pro | Lys | Gly | Arg | Phe | Asp | Gly | Lys | Arg | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ile | Glu | Asp | Thr | Arg | Asn | Leu | Pro | Ser | Pro | Phe | Leu | Asn | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Leu | Ile | Gln | Thr | Phe | Gly | Gln | Arg | Gly | Phe | Thr | Pro | Gln | Asp | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ala | Leu | Ser | Gly | Ala | His | Thr | Leu | Gly | Val | Ala | Arg | Cys | Ser | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Lys | Ala | Arg | Leu | Thr | Val | Pro | Asp | Ser | Ser | Leu | Asp | Ser | Thr | Phe |

195 200 205  
Ala Asn Thr Leu Ser Lys Thr Cys Ser Ala Gly Asp Asn Ala Glu Gln  
210 215 220  
Pro Phe Asp Ala Thr Arg Asn Asp Phe Asp Asn Ala Tyr Phe Asn Ala  
225 230 235 240  
Leu Gln Met Lys Ser Gly Val Leu Phe Ser Asp Gln Thr Leu Phe Asn  
245 250 255  
Thr Pro Arg Thr Arg Asn Leu Val Asn Gly Tyr Ala Leu Asn Gln Ala  
260 265 270  
Lys Phe Phe Asp Phe Gln Gln Ala Met Arg Lys Met Ser Asn Leu  
275 280 285  
Asp Val Lys Leu Gly Ser Gln Gly Glu Val Arg Gln Asn Cys Arg Ser  
290 295 300  
Ile Asn  
305

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1565636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met His Ala Ile Val Gly Phe Pro Phe His Ala Arg Gly Leu Ser Met  
1 5 10 15  
Thr Tyr Tyr Met Met Ser Cys Pro Phe Ala Glu Gln Ile Val Lys Asn  
20 25 30  
Ser Val Asn Asn Ala Leu Gln Ala Asp Pro Thr Leu Ala Ala Gly Leu  
35 40 45  
Ile Arg Met Leu Phe His Asp Cys Phe Ile Glu Gly Cys Asp Ala Ser  
50 55 60  
Ile Leu Leu Asp Ser Thr Lys Asp Asn Thr Ala Glu Lys Asp Ser Pro  
65 70 75 80  
Ala Asn Leu Ser Leu Arg Gly Tyr Glu Ile Ile Asp Asp Ala Lys Glu  
85 90 95  
Lys Ile Glu Asn Arg Cys Pro Gly Val Val Ser Cys Ala Asp Ile Val  
100 105 110  
Ala Met Ala Ala Arg Asp Ala Val Phe Trp Ala Gly Gly Pro Tyr Tyr  
115 120 125  
Asp Ile Pro Lys Gly Arg Phe Asp Gly Lys Arg Ser Lys Ile Glu Asp  
130 135 140  
Thr Arg Asn Leu Pro Ser Pro Phe Leu Asn Ala Ser Gln Leu Ile Gln  
145 150 155 160  
Thr Phe Gly Gln Arg Gly Phe Thr Pro Gln Asp Val Val Ala Leu Ser  
165 170 175  
Gly Ala His Thr Leu Gly Val Ala Arg Cys Ser Ser Phe Lys Ala Arg  
180 185 190  
Leu Thr Val Pro Asp Ser Ser Leu Asp Ser Thr Phe Ala Asn Thr Leu  
195 200 205  
Ser Lys Thr Cys Ser Ala Gly Asp Asn Ala Glu Gln Pro Phe Asp Ala  
210 215 220  
Thr Arg Asn Asp Phe Asp Asn Ala Tyr Phe Asn Ala Leu Gln Met Lys  
225 230 235 240  
Ser Gly Val Leu Phe Ser Asp Gln Thr Leu Phe Asn Thr Pro Arg Thr  
245 250 255  
Arg Asn Leu Val Asn Gly Tyr Ala Leu Asn Gln Ala Lys Phe Phe Phe  
260 265 270

Asp Phe Gln Gln Ala Met Arg Lys Met Ser Asn Leu Asp Val Lys Leu  
275 280 285  
Gly Ser Gln Gly Glu Val Arg Gln Asn Cys Arg Ser Ile Asn  
290 295 300

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

gaaatctcct atccattctt ctccgtctgc caaaatcccc acttcacgaa tcgcaaaaga 60  
tcaagggttta ttgatctatt gcgaaattag gggtttgtgaa ttcgaatcgg agattaataa 120  
tagattttgt gatggagtgt tcatcacgca tagaagaatc ttgatttcga tctcgatgaa 180  
attaggagtc gagggatttt atttataatt aagatgggtga atattaaaag ccctttacgg 240  
ctattcatag aggattctat taaggaatta attaggggtt tcaggagaca aaggatcaaa 300  
tggagaaatg catttcttct tggttctata atgactacca ttgttgttct gcttcataca 360  
ccaacgtttt cagtcttctc tgatgaagaa gaaaccgagt cttcttcgcc tatttacttg 420  
aatggttctc tgcatttgaa tatccatatt gttagtagtg aagcaaaagt tgaaaatttt 480  
catactotta gaacaagaac tcctattgtg caattgaatg cttctgaagc aagtgaagct 540  
gttatttcga gaaaaaggcg aaaaaggaaa aaaagaaaga agacaaaaga tgatctgatt 600  
ctcactgata ctctccagc accacgacat gttctatctt cctcagagag acgtgctctt 660  
tccttgccac cgaagaaagc tcttacttat gcaaaactgg agattcagcg tgccccggag 720  
gtcataaatg acacagatct atttgctcca ttgtttagaa acctctctgt tttcaaaagg 780  
agctatgagc ttatggaact gatactaaag gtctacatat atCctgacgg agacaaaccc 840  
atcttccacg aaccgcattt gaacggtata tatgcttcag aagggttggtt tatgaagcta 900  
atggagtcac acacacagtt tgtcaciaaag aaccctgaga aggctcactt gttctacatg 960  
ccatatagtg tgaaacagct tcagaaaagt atctttgttc ctggatcaca taacatcaaa 1020  
cctttatoga tctttcttag aGactacgtc aacatgctct ccatcaaata ccccttctgg 1080  
aaccgcactc atgggtcaga tcatttcctt gtcgcttgcc acgattgggt atcgaaaatg 1140  
tttctatggt aaagaccaat gggtttactt ccctcatttt tatgttatga tctctatttc 1200

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Val Asn Ile Lys Ser Pro Leu Arg Leu Phe Ile Glu Asp Ser Ile  
1 5 10 15  
Lys Glu Leu Ile Arg Gly Phe Arg Arg Gln Arg Ile Lys Trp Arg Asn  
20 25 30  
Ala Phe Leu Leu Gly Ser Ile Met Thr Thr Ile Val Val Leu Leu His  
35 40 45  
Thr Pro Thr Phe Ser Val Phe Ser Asp Glu Glu Glu Thr Glu Ser Ser  
50 55 60  
Ser Pro Ile Tyr Leu Asn Gly Ser Leu His Leu Asn Ile His Ile Val  
65 70 75 80  
Ser Ser Glu Ala Lys Val Glu Asn Phe His Thr Leu Arg Thr Arg Thr  
85 90 95

Pro Ile Val Gln Leu Asn Ala Ser Glu Ala Ser Glu Ala Val Ile Ser  
100 105 110  
Arg Lys Arg Arg Lys Arg Lys Lys Arg Lys Lys Thr Lys Asp Asp Leu  
115 120 125  
Ile Leu Thr Asp Pro Pro Pro Ala Pro Arg His Val Leu Ser Ser Ser  
130 135 140  
Glu Arg Arg Ala Leu Ser Leu Pro Pro Lys Lys Ala Leu Thr Tyr Ala  
145 150 155 160  
Lys Leu Glu Ile Gln Arg Ala Pro Glu Val Ile Asn Asp Thr Asp Leu  
165 170 175  
Phe Ala Pro Leu Phe Arg Asn Leu Ser Val Phe Lys Arg Ser Tyr Glu  
180 185 190  
Leu Met Glu Leu Ile Leu Lys Val Tyr Ile Tyr Pro Asp Gly Asp Lys  
195 200 205  
Pro Ile Phe His Glu Pro His Leu Asn Gly Ile Tyr Ala Ser Glu Gly  
210 215 220  
Trp Phe Met Lys Leu Met Glu Ser Asn Thr Gln Phe Val Thr Lys Asn  
225 230 235 240  
Pro Glu Lys Ala His Leu Phe Tyr Met Pro Tyr Ser Val Lys Gln Leu  
245 250 255  
Gln Lys Ser Ile Phe Val Pro Gly Ser His Asn Ile Lys Pro Leu Ser  
260 265 270  
Ile Phe Leu Arg Asp Tyr Val Asn Met Leu Ser Ile Lys Tyr Pro Phe  
275 280 285  
Trp Asn Arg Thr His Gly Ser Asp His Phe Leu Val Ala Cys His Asp  
290 295 300  
Trp Val Ser Lys Met Phe Leu Cys  
305 310

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..273
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Thr Thr Ile Val Val Leu Leu His Thr Pro Thr Phe Ser Val Phe  
1 5 10 15  
Ser Asp Glu Glu Glu Thr Glu Ser Ser Ser Pro Ile Tyr Leu Asn Gly  
20 25 30  
Ser Leu His Leu Asn Ile His Ile Val Ser Ser Glu Ala Lys Val Glu  
35 40 45  
Asn Phe His Thr Leu Arg Thr Arg Thr Pro Ile Val Gln Leu Asn Ala  
50 55 60  
Ser Glu Ala Ser Glu Ala Val Ile Ser Arg Lys Arg Arg Lys Arg Lys  
65 70 75 80  
Lys Arg Lys Lys Thr Lys Asp Asp Leu Ile Leu Thr Asp Pro Pro Pro  
85 90 95  
Ala Pro Arg His Val Leu Ser Ser Ser Glu Arg Arg Ala Leu Ser Leu  
100 105 110  
Pro Pro Lys Lys Ala Leu Thr Tyr Ala Lys Leu Glu Ile Gln Arg Ala  
115 120 125  
Pro Glu Val Ile Asn Asp Thr Asp Leu Phe Ala Pro Leu Phe Arg Asn  
130 135 140  
Leu Ser Val Phe Lys Arg Ser Tyr Glu Leu Met Glu Leu Ile Leu Lys  
145 150 155 160  
Val Tyr Ile Tyr Pro Asp Gly Asp Lys Pro Ile Phe His Glu Pro His

165 170 175  
Leu Asn Gly Ile Tyr Ala Ser Glu Gly Trp Phe Met Lys Leu Met Glu  
180 185 190  
Ser Asn Thr Gln Phe Val Thr Lys Asn Pro Glu Lys Ala His Leu Phe  
195 200 205  
Tyr Met Pro Tyr Ser Val Lys Gln Leu Gln Lys Ser Ile Phe Val Pro  
210 215 220  
Gly Ser His Asn Ile Lys Pro Leu Ser Ile Phe Leu Arg Asp Tyr Val  
225 230 235 240  
Asn Met Leu Ser Ile Lys Tyr Pro Phe Trp Asn Arg Thr His Gly Ser  
245 250 255  
Asp His Phe Leu Val Ala Cys His Asp Trp Val Ser Lys Met Phe Leu  
260 265 270  
Cys

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

aaccaaaaga atcacgacat tgaatcttct ttcatttctc tcctcaagac atagtagcat 60  
aagamaatga agatatcatc actaggatgg gtcttagtcc ttatcttcat ctctattacc 120  
attgtttcga gtgcaccagc acctaaacct cctaaacctc agcctgcacc agcacctaca 180  
cctcctaaac ctaagcccac accagcacct acacctccta aacctagcc caaaccagca 240  
cctacacctc ctaaacctaa gccacacca gcacctacac ctctaaacc taagcctgca 300  
ccagcaccag caccagcacc aacaccagca ccgaaacctc aacctgcacc taaaccagca 360  
ccaggtggag aagttgagga cgaaacogag tttagctacg agacgaaagg aaacaagggg 420  
ccagcgaat ggggaacact acatgcagag tggaaaatgt gtggaatagg caaatgcaa 480  
tctctattg atcttcggga caaaaatgtg gtagttagta ataaatttgg attgcttcgt 540  
agccagtatc tgccttctaa taccaccatt aagaacagag gtcattgat catgttgaaa 600  
ttcaaaggag gcaataaagg tattggtgtc actatccgtg gtactagata tcaacttcaa 660  
caacttcatt ggcactctcc ttccgaacat acaatcaatg gcaaaagggt tgcgctagag 720  
gaacacttgg ttcatgagag taaagatava cGctacgtg ttgtcgcttt cttatacaat 780  
ctcggagcat ctgacccttt tctcttttgc ttggaaaaac aattgaagaa gataactgat 840  
acacatgcgt ccgaggaaca tgtcggaatc attgatccca aaaaactcag ttttgaatca 900  
aaacattatt atagatatcc cggatcactt actgctcctc catgtttctga aaatgttatt 960  
tggtccggtt ccaaagagat tcgcaactgt tcaagtaaac aagtgaagct tctccgtgtg 1020  
gctgtacacg atgcttcaga ttcaaagtc aggcgcgttc aagcagtcaa taagcgcaag 1080  
gtatatattt acaaaccaaa ggtaagtta atgaagaaat actgtaatat aagttcttac 1140  
tagtaatctt taattcttta tatatgtaca ttatgaattg tacactaaaa tgatgttttt 1200  
agggataaac tgatgacttg gttttgttat t

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..358
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Lys Ile Ser Ser Leu Gly Trp Val Leu Val Leu Ile Phe Ile Ser

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1 5 10 15
Ile Thr Ile Val Ser Ser Ala Pro Ala Pro Lys Pro Pro Lys Pro Lys
20 25 30
Pro Ala Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Thr Pro Ala Pro
35 40 45
Thr Pro Pro Lys Pro Lys Pro Lys Pro Ala Pro Thr Pro Pro Lys Pro
50 55 60
Lys Pro Thr Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Ala Pro Ala
65 70 75 80
Pro Ala Pro Ala Pro Thr Pro Ala Pro Lys Pro Lys Pro Ala Pro Lys
85 90 95
Pro Ala Pro Gly Gly Glu Val Glu Asp Glu Thr Glu Phe Ser Tyr Glu
100 105 110
Thr Lys Gly Asn Lys Gly Pro Ala Lys Trp Gly Thr Leu His Ala Glu
115 120 125
Trp Lys Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg
130 135 140
Asp Lys Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln
145 150 155 160
Tyr Leu Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met
165 170 175
Leu Lys Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly
180 185 190
Thr Arg Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His
195 200 205
Thr Ile Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu
210 215 220
Ser Lys Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly
225 230 235 240
Ala Ser Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile
245 250 255
Thr Asp Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys
260 265 270
Lys Leu Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu
275 280 285
Thr Ala Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu
290 295 300
Ile Arg Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val
305 310 315 320
His Asp Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys
325 330 335
Arg Lys Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr
340 345 350
Cys Asn Ile Ser Ser Tyr
355

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(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

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Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp Lys
1 5 10 15
Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu
20 25 30

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Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu Lys  
35 40 45  
Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr Arg  
50 55 60  
Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr Ile  
65 70 75 80  
Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser Lys  
85 90 95  
Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser  
100 105 110  
Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp  
115 120 125  
Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys Lys Leu  
130 135 140  
Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala  
145 150 155 160  
Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu Ile Arg  
165 170 175  
Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val His Asp  
180 185 190  
Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys Arg Lys  
195 200 205  
Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr Cys Asn  
210 215 220  
Ile Ser Ser Tyr  
225

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1565649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Gln Ser Pro Ile Asp Leu Arg Asp Lys Asn Val Val Val Ser Asn  
1 5 10 15  
Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu Pro Ser Asn Thr Thr Ile  
20 25 30  
Lys Asn Arg Gly His Asp Ile Met Leu Lys Phe Lys Gly Gly Asn Lys  
35 40 45  
Gly Ile Gly Val Thr Ile Arg Gly Thr Arg Tyr Gln Leu Gln Gln Leu  
50 55 60  
His Trp His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Ala  
65 70 75 80  
Leu Glu Glu His Leu Val His Glu Ser Lys Asp Xaa Arg Tyr Ala Val  
85 90 95  
Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser Asp Pro Phe Leu Phe Ser  
100 105 110  
Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp Thr His Ala Ser Glu Glu  
115 120 125  
His Val Gly Ile Ile Asp Pro Lys Lys Leu Ser Phe Glu Ser Lys His  
130 135 140  
Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala Pro Pro Cys Ser Glu Asn  
145 150 155 160  
Val Ile Trp Ser Val Ser Lys Glu Ile Arg Thr Val Ser Ser Lys Gln  
165 170 175  
Val Lys Leu Leu Arg Val Ala Val His Asp Ala Ser Asp Ser Asn Ala



180 185 190  
Arg Pro Leu Gln Ala Val Asn Lys Arg Lys Val Tyr Leu Tyr Lys Pro  
195 200 205  
Lys Val Lys Leu Met Lys Lys Tyr Cys Asn Ile Ser Ser Tyr  
210 215 220

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..943
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

aatttctttc gacgaaactt catttctcaa tttcttttga ttttgatcgc ttcgaagaac 60  
gaatcaattt aggcctgcc aacacaaacc ctagaatacg acaacgcacg acgacgaaga 120  
agtcaagaa gactactact ataaacgacg aagatcatta cttcaatctt caatcgagct 180  
tttaaatttt cagatcgtag aagaaaatcg aacttttgat tctaaaagcg atgagaccga 240  
ttcaatcgcc tccaggaggt tccgttcogt tgaaaagccg tccccgtcgc cgtcctgatc 300  
ttaccttacc gcttctctcaa cgcgagtgtt ctctcgtgtt acctcttcct ctcccaccta 360  
cttcggtggg ttccggtggc tctagtggat ctgcgcgcgtc ttctgggtggg tcggcgtctt 420  
caacgaacac taacagctcc atagaagcga agaactattc ggatttagtg agaggtaacc 480  
gtatcggaag cggagSaggt ggaacggtat acaaagtgat tcaccgtccg agttctcgtc 540  
tatatgcact taagggtgata tacggtaacc acgaggagac tgtgagacgt cagatctgta 600  
gagagatcga gattttacga gatgtgaatc atccaaacat ttcacaacgt ttggaagata 660  
ccaccagcac tgactaaact acacctcgag catttcaacg tgagcgacaa ccattctctgc 720  
ggaaaaatcc caagtggcgg tctccttcag acotttgaac catctgcctt cgctcacaac 780  
atctgtcttt gtggaactcc ccttaaggct tgttaatttg gtttaatctt ggcggaagaa 840  
taaaaattat gttgaatatg ttatgatgat gtgttcatta tcaccgcaa accaagttta 900  
ttgtttcttt gttatgaatt taatttaatg gcaagaattg gtt

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Pro Ile Gln Ser Pro Pro Gly Val Ser Val Pro Val Lys Ser  
1 5 10 15  
Arg Pro Arg Arg Arg Pro Asp Leu Thr Leu Pro Leu Pro Gln Arg Asp  
20 25 30  
Val Ser Leu Ala Val Pro Leu Pro Leu Pro Pro Thr Ser Gly Gly Ser  
35 40 45  
Gly Gly Ser Ser Gly Ser Ala Pro Ser Ser Gly Gly Ser Ala Ser Ser  
50 55 60  
Thr Asn Thr Asn Ser Ser Ile Glu Ala Lys Asn Tyr Ser Asp Leu Val  
65 70 75 80  
Arg Gly Asn Arg Ile Gly Ser Gly Xaa Gly Gly Thr Val Tyr Lys Val  
85 90 95  
Ile His Arg Pro Ser Ser Arg Leu Tyr Ala Leu Lys Val Ile Tyr Gly  
100 105 110  
Asn His Glu Glu Thr Val Arg Arg Gln Ile Cys Arg Glu Ile Glu Ile  
115 120 125

Leu Arg Asp Val Asn His Pro Asn Ile Ser Gln Arg Leu Glu Asp Thr  
130 135 140  
Thr Ser Thr Asp  
145

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

aattccatt cgtgtttttt cggattgcga gaatcctacg ttattttcttc acttttcatg 60  
atcccgagga catcttagac cccaaatggt Gbktcgtcga tgttcttttg aaactgggtc 120  
ctctatactt gttcggatca gaaacacagt ctctctcagc aacagagtcc attttgcaga 180  
tagttcctga ggcaatggct gctacttcat ctaacgtcct ttgcaatgct agcgagtcag 240  
atctttgtct tgatgattcc gctgcatttc tacttaaatt tgtagccatt gcttcgattc 300  
tcttagctgg agctgctggg gtaactatac cactcattgg caggaaccgt cgtttccttc 360  
aaactgatgg taatctcttt gtgactgcta aagcttttgc agctgggtg attctcgcca 420  
cgtgttttgt tcatatgttg gcgggtggca cggaagcttt gaagaaccg tgcttaccgg 480  
atttcccttg gtctaagttt cctttcccgg gattctttgc gatgattgct gctttgatca 540  
ctctgtttgt ggatttcagt gggactcagt actatgaacg gaagcaagag agggaagcta 600  
gtgagtcctg tgaaccgttt ggccgtgaac aatcaccggg tattgttgtt cccatgattg 660  
gagaaggaac gaatgatggg aaagtgtttg gtgaagaaga cagtgggtggg attcacattg 720  
ttggcattca tgctcatgct gctcatcata gacatagtca tctcctggt catgattcat 780  
gtgaaggaca cagtaaaatc gacattggtc atgctcatgc tcatgggcac gggcatggac 840  
acggacatgg acacgtacac gggggtttgg atgctgttaa tggagctagg catatcgttg 900  
tttctcaggt tctggagctt ggaattgtgt cacattccat aatcatcggt ctatcccttg 960  
gagtatctca gtctccttgc acaatccggc ctctaatacg agcactatcc ttccaccaat 1020  
tctttgaagg atttgcgctc ggtggatgca tctcccaagc gcaattcagg aacaaatcag 1080  
cgaccataat ggcttgtttt ttgcacctca caaccocgat agggatcggg attggaaccg 1140  
cagtggcgtc gtctttcaat tctcacagtg tccgagcatt ggtaactgaa ggtatcttgg 1200  
actcgctctc agccggaatt cttgtgtaca tggctttagt ggatctcata gctgctgatt 1260  
tcttgagtac aaaaatgagg tgtaacttta ggcttcaaat tgtatcttat gtaatgttgt 1320  
tcttaggagc tggactcatg tcttctcttg ccatttgggc ttaattagag tataagattc 1380  
cac

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..453
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Phe Pro Phe Val Phe Phe Arg Ile Ala Arg Ile Leu Arg Tyr Phe Phe  
1 5 10 15  
Thr Phe His Asp Pro Glu Asp Ile Leu Asp Pro Lys Cys Xaa Xaa Val  
20 25 30  
Asp Val Leu Trp Lys Leu Val Pro Leu Tyr Leu Phe Gly Ser Glu Thr  
35 40 45  
Gln Ser Leu Ser Ala Thr Glu Ser Ile Leu Gln Ile Val Pro Glu Ala  
50 55 60  
Met Ala Ala Thr Ser Ser Asn Val Leu Cys Asn Ala Ser Glu Ser Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Leu | Cys | Leu | Asp | Asp | Ser | Ala | Ala | Phe | Leu | Leu | Lys | Phe | Val | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Ala | Ser | Ile | Leu | Leu | Ala | Gly | Ala | Ala | Gly | Val | Thr | Ile | Pro | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Gly | Arg | Asn | Arg | Arg | Phe | Leu | Gln | Thr | Asp | Gly | Asn | Leu | Phe | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ala | Lys | Ala | Phe | Ala | Ala | Gly | Val | Ile | Leu | Ala | Thr | Cys | Phe | Val |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Met | Leu | Ala | Gly | Gly | Thr | Glu | Ala | Leu | Lys | Asn | Pro | Cys | Leu | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Phe | Pro | Trp | Ser | Lys | Phe | Pro | Phe | Pro | Gly | Phe | Phe | Ala | Met | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Ala | Leu | Ile | Thr | Leu | Phe | Val | Asp | Phe | Met | Gly | Thr | Gln | Tyr | Tyr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Arg | Lys | Gln | Glu | Arg | Glu | Ala | Ser | Glu | Ser | Val | Glu | Pro | Phe | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Glu | Gln | Ser | Pro | Gly | Ile | Val | Val | Pro | Met | Ile | Gly | Glu | Gly | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Asp | Gly | Lys | Val | Phe | Gly | Glu | Glu | Asp | Ser | Gly | Gly | Ile | His | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Gly | Ile | His | Ala | His | Ala | Ala | His | His | Arg | His | Ser | His | Pro | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |
| His | Asp | Ser | Cys | Glu | Gly | His | Ser | Lys | Ile | Asp | Ile | Gly | His | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     | 270 |     |     |
| Ala | His | Gly | His | Gly | His | Gly | His | Gly | His | Gly | His | Val | His | Gly |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Leu | Asp | Ala | Val | Asn | Gly | Ala | Arg | His | Ile | Val | Val | Ser | Gln | Val |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Glu | Leu | Gly | Ile | Val | Ser | His | Ser | Ile | Ile | Ile | Gly | Leu | Ser | Leu |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Val | Ser | Gln | Ser | Pro | Cys | Thr | Ile | Arg | Pro | Leu | Ile | Ala | Ala | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |
| Phe | His | Gln | Phe | Phe | Glu | Gly | Phe | Ala | Leu | Gly | Gly | Cys | Ile | Ser |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |
| Ala | Gln | Phe | Arg | Asn | Lys | Ser | Ala | Thr | Ile | Met | Ala | Cys | Phe | Phe |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |
| Leu | Thr | Thr | Pro | Ile | Gly | Ile | Gly | Ile | Gly | Thr | Ala | Val | Ala | Ser |
|     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Phe | Asn | Ser | His | Ser | Val | Gly | Ala | Leu | Val | Thr | Glu | Gly | Ile | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Ser | Leu | Ser | Ala | Gly | Ile | Leu | Val | Tyr | Met | Ala | Leu | Val | Asp | Leu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |
| Ala | Ala | Asp | Phe | Leu | Ser | Thr | Lys | Met | Arg | Cys | Asn | Phe | Arg | Leu |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |
| Ile | Val | Ser | Tyr | Val | Met | Leu | Phe | Leu | Gly | Ala | Gly | Leu | Met | Ser |
|     |     | 435 |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| Leu | Ala | Ile | Trp | Ala |     |     |     |     |     |     |     |     |     |     |
|     |     | 450 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

{A} NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1565661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Leu Ala Gly Gly Thr Glu Ala Leu Lys Asn Pro Cys Leu Pro Asp  
1 5 10 15  
Phe Pro Trp Ser Lys Phe Pro Phe Pro Gly Phe Phe Ala Met Ile Ala  
20 25 30  
Ala Leu Ile Thr Leu Phe Val Asp Phe Met Gly Thr Gln Tyr Tyr Glu  
35 40 45  
Arg Lys Gln Glu Arg Glu Ala Ser Glu Ser Val Glu Pro Phe Gly Arg  
50 55 60  
Glu Gln Ser Pro Gly Ile Val Val Pro Met Ile Gly Glu Gly Thr Asn  
65 70 75 80  
Asp Gly Lys Val Phe Gly Glu Glu Asp Ser Gly Gly Ile His Ile Val  
85 90 95  
Gly Ile His Ala His Ala Ala His His Arg His Ser His Pro Pro Gly  
100 105 110  
His Asp Ser Cys Glu Gly His Ser Lys Ile Asp Ile Gly His Ala His  
115 120 125  
Ala His Gly His Gly His Gly His Gly His Gly His Val His Gly Gly  
130 135 140  
Leu Asp Ala Val Asn Gly Ala Arg His Ile Val Val Ser Gln Val Leu  
145 150 155 160  
Glu Leu Gly Ile Val Ser His Ser Ile Ile Ile Gly Leu Ser Leu Gly  
165 170 175  
Val Ser Gln Ser Pro Cys Thr Ile Arg Pro Leu Ile Ala Ala Leu Ser  
180 185 190  
Phe His Gln Phe Phe Glu Gly Phe Ala Leu Gly Gly Cys Ile Ser Gln  
195 200 205  
Ala Gln Phe Arg Asn Lys Ser Ala Thr Ile Met Ala Cys Phe Phe Ala  
210 215 220  
Leu Thr Thr Pro Ile Gly Ile Gly Thr Ala Val Ala Ser Ser  
225 230 235 240  
Phe Asn Ser His Ser Val Gly Ala Leu Val Thr Glu Gly Ile Leu Asp  
245 250 255  
Ser Leu Ser Ala Gly Ile Leu Val Tyr Met Ala Leu Val Asp Leu Ile  
260 265 270  
Ala Ala Asp Phe Leu Ser Thr Lys Met Arg Cys Asn Phe Arg Leu Gln  
275 280 285  
Ile Val Ser Tyr Val Met Leu Phe Leu Gly Ala Gly Leu Met Ser Ser  
290 295 300  
Leu Ala Ile Trp Ala  
305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1728
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ctcgcacaca cttctctctc tctctctctg cctccttttcg gattcaaatac tcagatctag 60  
ctcaaccatg gcgttgctcg tcgagaagac ctcaagtggc cgtgaataca aggtcaaaga 120  
catgtctcaa gccgatttcg gtcgtctcga actcgagctc gccgaagttg agatgcctgg 180  
actcatggct tgctcgaccg aattcggacc ttctcagcca ttcaaaggcg ctagaatacac 240  
cggatctctt cacatgacca tccaaaccgc cgtactcatc gaaaccctaa ctgctctcgg 300  
tgctgaagtc agatgggtgtt cctgcaacat cttctccact caagaccacg ccgccgcagc 360  
catcgctcgt gactccgccg ctgttttcgc ctggaaaggt gagactcttc aggagtactg 420  
gtggtgtacc gacgtgctc tagattgggg tccagtggtt ggtcctgata tgAttgttga 480

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| tgatggtggt | gacgctactc  | ttttgattca | tgagggtggt | aaagctgagg | agatctttga | 540  |
| gaagactggt | caagttcctg  | atcctacttc | tactgataac | cctgagtttc | agatcgtggt | 600  |
| gtctattatc | aaggaaggtc  | ttcaagttga | tcctaagaag | taccacaaga | tgaaggagag | 660  |
| acttggtggt | gtctctgagg  | aaactaccac | tggtgttaag | aggctttacc | agatgcagca | 720  |
| aaatggaact | cttttgttcc  | ctgccattaa | cgttaacgac | tctgtcacca | agagcaagtt | 780  |
| cgacaacttg | tatggttgcc  | gtcactcact | ccctgatggt | ctcatgaggg | ccactgatgt | 840  |
| catgatcgct | ggaaaggttg  | ctgttatctg | tggatatggt | gatgttgga  | agggttgtgc | 900  |
| tgctgccatg | aagactgctg  | gtgctagagt | cattgtgact | gagattgatc | ccatctgtgc | 960  |
| ccttcaagct | ttgatggaag  | gacttcaggt | tcttaccctt | gaggatggtg | tctcagaagc | 1020 |
| tgatatcttt | gtcaccacca  | cggtaacaa  | agacatcatc | atggtcgacc | acatgaggaa | 1080 |
| gatgaagaac | aacgctattg  | tgtgcaacat | tggtcacttt | gacaatgaga | ttgacatgct | 1140 |
| tggacttgag | acttaccctg  | gtgtgaagcg | tatcaccatc | aagccacaga | ctgacaggtg | 1200 |
| gggtgttccc | gagaccaagg  | ctggaatcat | tgtcttggtc | gagggtcgtc | tgatgaactt | 1260 |
| gggttggtgc | actggtcacc  | caagtttcgt | gatgtcttgc | tctttcacca | accaggtgat | 1320 |
| tgcccagctc | gagctctgga  | acgagaaagc | aagcggaaag | tacgagaaga | aggtgtacgt | 1380 |
| tcttcccaag | catttggtatg | agaaggttgc | attacttcac | ttgggcaagc | ttggagccag | 1440 |
| gcttacaag  | ctgtcaaagg  | accNaTctg  | actacgtcag | cattccaatt | gagggaccat | 1500 |
| acaagcctcc | tactacagg   | tactgagaga | gagagagagt | cgacaaagcg | gttcagggtc | 1560 |
| ggatctactt | gtggttttgt  | gttgggttgt | ggtggaagag | tggaacagtt | tgagatattg | 1620 |
| gtcttctgat | gaagttgacc  | aaatatcagt | attaataagg | gttattggct | tttgaaggtt | 1680 |
| gtgcttgttt | tctccatttt  | tcatgaaact | taaattagtt | tttggttt   |            |      |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1565663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | His | Thr | Leu | Leu | Ser | Leu | Ser | Leu | Cys | Leu | Leu | Ser | Asp | Ser | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Ser | Ser | Ser | Thr | Met | Ala | Leu | Val | Glu | Lys | Thr | Ser | Ser |     |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Arg | Glu | Tyr | Lys | Val | Lys | Asp | Met | Ser | Gln | Ala | Asp | Phe | Gly | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | Leu | Glu | Leu | Ala | Glu | Val | Glu | Met | Pro | Gly | Leu | Met | Ala | Cys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Thr | Glu | Phe | Gly | Pro | Ser | Gln | Pro | Phe | Lys | Gly | Ala | Arg | Ile | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ser | Leu | His | Met | Thr | Ile | Gln | Thr | Ala | Val | Leu | Ile | Glu | Thr | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Ala | Leu | Gly | Ala | Glu | Val | Arg | Trp | Cys | Ser | Cys | Asn | Ile | Phe | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Gln | Asp | His | Ala | Ala | Ala | Ala | Ile | Ala | Arg | Asp | Ser | Ala | Ala | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ala | Trp | Lys | Gly | Glu | Thr | Leu | Gln | Glu | Tyr | Trp | Trp | Cys | Thr | Glu |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Arg | Ala | Leu | Asp | Trp | Gly | Pro | Gly | Gly | Gly | Pro | Asp | Leu | Ile | Val | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Gly | Gly | Asp | Ala | Thr | Leu | Leu | Ile | His | Glu | Gly | Val | Lys | Ala | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ile | Phe | Glu | Lys | Thr | Gly | Gln | Val | Pro | Asp | Pro | Thr | Ser | Thr | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Pro | Glu | Phe | Gln | Ile | Val | Leu | Ser | Ile | Ile | Lys | Glu | Gly | Leu | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Asp | Pro | Lys | Lys | Tyr | His | Lys | Met | Lys | Glu | Arg | Leu | Val | Gly | Val |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |

```

Ser Glu Glu Thr Thr Thr Gly Val Lys Arg Leu Tyr Gln Met Gln Gln
225 230 235 240
Asn Gly Thr Leu Leu Phe Pro Ala Ile Asn Val Asn Asp Ser Val Thr
 245 250 255
Lys Ser Lys Phe Asp Asn Leu Tyr Gly Cys Arg His Ser Leu Pro Asp
 260 265 270
Gly Leu Met Arg Ala Thr Asp Val Met Ile Ala Gly Lys Val Ala Val
 275 280 285
Ile Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Ala Ala Met Lys
290 295 300
Thr Ala Gly Ala Arg Val Ile Val Thr Glu Ile Asp Pro Ile Cys Ala
305 310 315 320
Leu Gln Ala Leu Met Glu Gly Leu Gln Val Leu Thr Leu Glu Asp Val
 325 330 335
Val Ser Glu Ala Asp Ile Phe Val Thr Thr Thr Gly Asn Lys Asp Ile
 340 345 350
Ile Met Val Asp His Met Arg Lys Met Lys Asn Asn Ala Ile Val Cys
355 360 365
Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met Leu Gly Leu Glu Thr
370 375 380
Tyr Pro Gly Val Lys Arg Ile Thr Ile Lys Pro Gln Thr Asp Arg Trp
385 390 395 400
Val Phe Pro Glu Thr Lys Ala Gly Ile Ile Val Leu Ala Glu Gly Arg
 405 410 415
Leu Met Asn Leu Gly Cys Ala Thr Gly His Pro Ser Phe Val Met Ser
 420 425 430
Cys Ser Phe Thr Asn Gln Val Ile Ala Gln Leu Glu Leu Trp Asn Glu
435 440 445
Lys Ala Ser Gly Lys Tyr Glu Lys Lys Val Tyr Val Leu Pro Lys His
450 455 460
Leu Asp Glu Lys Val Ala Leu Leu His Leu Gly Lys Leu Gly Ala Arg
465 470 475 480
Leu Thr Lys Leu Ser Lys Asp Xaa Ile
 485

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..467

(D) OTHER INFORMATION: / Ceres Seq. ID 1565664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Met Ala Leu Leu Val Glu Lys Thr Ser Ser Gly Arg Glu Tyr Lys Val
1 5 10 15
Lys Asp Met Ser Gln Ala Asp Phe Gly Arg Leu Glu Leu Glu Leu Ala
 20 25 30
Glu Val Glu Met Pro Gly Leu Met Ala Cys Arg Thr Glu Phe Gly Pro
35 40 45
Ser Gln Pro Phe Lys Gly Ala Arg Ile Thr Gly Ser Leu His Met Thr
50 55 60
Ile Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu
65 70 75 80
Val Arg Trp Cys Ser Cys Asn Ile Phe Ser Thr Gln Asp His Ala Ala
85 90 95
Ala Ala Ile Ala Arg Asp Ser Ala Ala Val Phe Ala Trp Lys Gly Glu
100 105 110
Thr Leu Gln Glu Tyr Trp Trp Cys Thr Glu Arg Ala Leu Asp Trp Gly

```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Pro Gly Gly Gly Pro Asp Leu Ile Val Asp Asp Gly Gly Asp Ala Thr |     |     |
| 130                                                             | 135 | 140 |
| Leu Leu Ile His Glu Gly Val Lys Ala Glu Glu Ile Phe Glu Lys Thr |     |     |
| 145                                                             | 150 | 155 |
| Gly Gln Val Pro Asp Pro Thr Ser Thr Asp Asn Pro Glu Phe Gln Ile |     |     |
| 165                                                             | 170 | 175 |
| Val Leu Ser Ile Ile Lys Glu Gly Leu Gln Val Asp Pro Lys Lys Tyr |     |     |
| 180                                                             | 185 | 190 |
| His Lys Met Lys Glu Arg Leu Val Gly Val Ser Glu Glu Thr Thr Thr |     |     |
| 195                                                             | 200 | 205 |
| Gly Val Lys Arg Leu Tyr Gln Met Gln Gln Asn Gly Thr Leu Leu Phe |     |     |
| 210                                                             | 215 | 220 |
| Pro Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn |     |     |
| 225                                                             | 230 | 235 |
| Leu Tyr Gly Cys Arg His Ser Leu Pro Asp Gly Leu Met Arg Ala Thr |     |     |
| 245                                                             | 250 | 255 |
| Asp Val Met Ile Ala Gly Lys Val Ala Val Ile Cys Gly Tyr Gly Asp |     |     |
| 260                                                             | 265 | 270 |
| Val Gly Lys Gly Cys Ala Ala Ala Met Lys Thr Ala Gly Ala Arg Val |     |     |
| 275                                                             | 280 | 285 |
| Ile Val Thr Glu Ile Asp Pro Ile Cys Ala Leu Gln Ala Leu Met Glu |     |     |
| 290                                                             | 295 | 300 |
| Gly Leu Gln Val Leu Thr Leu Glu Asp Val Val Ser Glu Ala Asp Ile |     |     |
| 305                                                             | 310 | 315 |
| Phe Val Thr Thr Thr Gly Asn Lys Asp Ile Ile Met Val Asp His Met |     |     |
| 325                                                             | 330 | 335 |
| Arg Lys Met Lys Asn Asn Ala Ile Val Cys Asn Ile Gly His Phe Asp |     |     |
| 340                                                             | 345 | 350 |
| Asn Glu Ile Asp Met Leu Gly Leu Glu Thr Tyr Pro Gly Val Lys Arg |     |     |
| 355                                                             | 360 | 365 |
| Ile Thr Ile Lys Pro Gln Thr Asp Arg Trp Val Phe Pro Glu Thr Lys |     |     |
| 370                                                             | 375 | 380 |
| Ala Gly Ile Ile Val Leu Ala Glu Gly Arg Leu Met Asn Leu Gly Cys |     |     |
| 385                                                             | 390 | 395 |
| Ala Thr Gly His Pro Ser Phe Val Met Ser Cys Ser Phe Thr Asn Gln |     |     |
| 405                                                             | 410 | 415 |
| Val Ile Ala Gln Leu Glu Leu Trp Asn Glu Lys Ala Ser Gly Lys Tyr |     |     |
| 420                                                             | 425 | 430 |
| Glu Lys Lys Val Tyr Val Leu Pro Lys His Leu Asp Glu Lys Val Ala |     |     |
| 435                                                             | 440 | 445 |
| Leu Leu His Leu Gly Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Lys |     |     |
| 450                                                             | 455 | 460 |
| Asp Xaa Ile                                                     |     |     |
| 465                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1565665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Ser Gln Ala Asp Phe Gly Arg Leu Glu Leu Glu Leu Ala Glu Val |    |    |
| 1                                                               | 5  | 10 |
| Glu Met Pro Gly Leu Met Ala Cys Arg Thr Glu Phe Gly Pro Ser Gln |    |    |
| 20                                                              | 25 | 30 |

SEQUENCE INFORMATION



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Phe | Lys | Gly | Ala | Arg | Ile | Thr | Gly | Ser | Leu | His | Met | Thr | Ile | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Val | Leu | Ile | Glu | Thr | Leu | Thr | Ala | Leu | Gly | Ala | Glu | Val | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Cys | Ser | Cys | Asn | Ile | Phe | Ser | Thr | Gln | Asp | His | Ala | Ala | Ala | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ala | Arg | Asp | Ser | Ala | Ala | Val | Phe | Ala | Trp | Lys | Gly | Glu | Thr | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Glu | Tyr | Trp | Trp | Cys | Thr | Glu | Arg | Ala | Leu | Asp | Trp | Gly | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Pro | Asp | Leu | Ile | Val | Asp | Asp | Gly | Gly | Asp | Ala | Thr | Leu | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | His | Glu | Gly | Val | Lys | Ala | Glu | Glu | Ile | Phe | Glu | Lys | Thr | Gly | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Pro | Asp | Pro | Thr | Ser | Thr | Asp | Asn | Pro | Glu | Phe | Gln | Ile | Val | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ile | Ile | Lys | Glu | Gly | Leu | Gln | Val | Asp | Pro | Lys | Lys | Tyr | His | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Lys | Glu | Arg | Leu | Val | Gly | Val | Ser | Glu | Glu | Thr | Thr | Thr | Gly | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Arg | Leu | Tyr | Gln | Met | Gln | Gln | Asn | Gly | Thr | Leu | Leu | Phe | Pro | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Asn | Val | Asn | Asp | Ser | Val | Thr | Lys | Ser | Lys | Phe | Asp | Asn | Leu | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Cys | Arg | His | Ser | Leu | Pro | Asp | Gly | Leu | Met | Arg | Ala | Thr | Asp | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Ile | Ala | Gly | Lys | Val | Ala | Val | Ile | Cys | Gly | Tyr | Gly | Asp | Val | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Gly | Cys | Ala | Ala | Ala | Met | Lys | Thr | Ala | Gly | Ala | Arg | Val | Ile | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Glu | Ile | Asp | Pro | Ile | Cys | Ala | Leu | Gln | Ala | Leu | Met | Glu | Gly | Leu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Gln | Val | Leu | Thr | Leu | Glu | Asp | Val | Val | Ser | Glu | Ala | Asp | Ile | Phe | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Thr | Thr | Gly | Asn | Lys | Asp | Ile | Ile | Met | Val | Asp | His | Met | Arg | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Met | Lys | Asn | Asn | Ala | Ile | Val | Cys | Asn | Ile | Gly | His | Phe | Asp | Asn | Glu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ile | Asp | Met | Leu | Gly | Leu | Glu | Thr | Tyr | Pro | Gly | Val | Lys | Arg | Ile | Thr |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Lys | Pro | Gln | Thr | Asp | Arg | Trp | Val | Phe | Pro | Glu | Thr | Lys | Ala | Gly |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Ile | Val | Leu | Ala | Glu | Gly | Arg | Leu | Met | Asn | Leu | Gly | Cys | Ala | Thr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | His | Pro | Ser | Phe | Val | Met | Ser | Cys | Ser | Phe | Thr | Asn | Gln | Val | Ile |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Gln | Leu | Glu | Leu | Trp | Asn | Glu | Lys | Ala | Ser | Gly | Lys | Tyr | Glu | Lys |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Val | Tyr | Val | Leu | Pro | Lys | His | Leu | Asp | Glu | Lys | Val | Ala | Leu | Leu |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| His | Leu | Gly | Lys | Leu | Gly | Ala | Arg | Leu | Thr | Lys | Leu | Ser | Lys | Asp | Xaa |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:48:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1415 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1415

(D) OTHER INFORMATION: / Ceres Seq. ID 1565666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| gtgtttgtgt  | atgtgtggaa  | aattaatttc  | ttctcccgac  | gaatcccaaa | agtttgttga  | 60   |
| aatttgccctc | caagaaatct  | gcaattagaa  | atttcatttc  | gccgtcatcg | tcttcttctt  | 120  |
| ctgattctga  | ttaattccag  | atgtcttctc  | gagtccttac  | gagattaggt | cattttcgcc  | 180  |
| togactcgaa  | ctctgtctcg  | cagcttccgt  | gagagagtca  | tggacacgcc | accgacttct  | 240  |
| cgtatcgcat  | cttttggtca  | gacggagatt  | aactgggaca  | aacttgacaa | aaggagggtc  | 300  |
| tacattaatg  | gagctggcct  | cttcactggt  | gttacagtag  | ctctgtatcc | tgtatccggt  | 360  |
| gtgaaaacaa  | ggcttcaagt  | tgcttctaaa  | gagattgctg  | agagaagtgc | cttttctgta  | 420  |
| gttaaaggaa  | ttttaaagaa  | tgatgggtgt  | cctggctctg  | accgagggtt | tgggtactgtc | 480  |
| attacagggtg | ctgtacctgc  | aagaatcata  | tttctaactg  | ctcttgagac | cactaagatt  | 540  |
| tctgctttta  | agttgggttg  | accttggag   | ttaagtgaac  | ctacacaagc | cgccattgca  | 600  |
| aatggaattg  | ctggcatgac  | agcatctctt  | ttctcacagg  | ctgtgtttgt | cccaattgat  | 660  |
| gttggttagcc | aaaagttgat  | ggtacaagga  | tactcaggtc  | atgctacata | tactgggtgt  | 720  |
| atcgatgttg  | ccacaaaaat  | cattaagtca  | tatgggtgtg  | ggggattata | cagaggggtt  | 780  |
| gggtctgtctg | ttatgaocct  | ttctccttca  | agtgcgcgtt  | ggtgggctag | ctatggatca  | 840  |
| agccaacgtg  | ttatctggag  | attcttaggt  | tatgggtggtg | actcggatgc | aactactgct  | 900  |
| cctagtaagt  | caaaaattgt  | tatgggtccag | gctgctggag  | gaattattgc | tgggtgcaaca | 960  |
| gcattcctcaa | ttacaacacc  | attagacaca  | atcaaaacgc  | gactgcaggt | catgggacat  | 1020 |
| caagaaaata  | gaccttcagc  | gaaacaagt   | gtgaaaaaac  | tgctagcaga | agatggctgg  | 1080 |
| aaaggattct  | ataggggttt  | gggcccaga   | ttcttttagca | tgctggcttg | gggaacctcg  | 1140 |
| atgatattga  | cttaacgaata | cttaaagcgt  | ctgtgtgcaa  | tagaagatta | gaaagcttca  | 1200 |
| ctactgttcg  | ttgggttttc  | tcttctact   | aactcgagta  | gacggcatca | ccttgattca  | 1260 |
| aatctcggt   | attgggagct  | tccatgttga  | caattggacc  | attctttcaa | ctttgaagtc  | 1320 |
| tgagtccgt   | tattgtaatc  | attctttcaa  | cttaatttgc  | gtattggagt | gtattcttac  | 1380 |

agcagaagAa aktoGtagct tacgttcttc tgctt

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1565667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Pro | Pro | Thr | Ser | Arg | Ile | Ala | Ser | Phe | Gly | Gln | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Trp | Asp | Lys | Leu | Asp | Lys | Arg | Arg | Phe | Tyr | Ile | Asn | Gly | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Phe | Thr | Gly | Val | Thr | Val | Ala | Leu | Tyr | Pro | Val | Ser | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Thr | Arg | Leu | Gln | Val | Ala | Ser | Lys | Glu | Ile | Ala | Glu | Arg | Ser | Ala |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | Ser | Val | Val | Lys | Gly | Ile | Leu | Lys | Asn | Asp | Gly | Val | Pro | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Arg | Gly | Phe | Gly | Thr | Val | Ile | Thr | Gly | Ala | Val | Pro | Ala | Arg | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Phe | Leu | Thr | Ala | Leu | Glu | Thr | Thr | Lys | Ile | Ser | Ala | Phe | Lys | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ala | Pro | Leu | Glu | Leu | Ser | Glu | Pro | Thr | Gln | Ala | Ala | Ile | Ala | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ile | Ala | Gly | Met | Thr | Ala | Ser | Leu | Phe | Ser | Gln | Ala | Val | Phe | Val |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Pro | Ile | Asp | Val | Val | Ser | Gln | Lys | Leu | Met | Val | Gln | Gly | Tyr | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

His Ala Thr Tyr Thr Gly Gly Ile Asp Val Ala Thr Lys Ile Ile Lys  
165 170 175  
Ser Tyr Gly Val Arg Gly Leu Tyr Arg Gly Phe Gly Leu Ser Val Met  
180 185 190  
Thr Tyr Ser Pro Ser Ser Ala Ala Trp Trp Ala Ser Tyr Gly Ser Ser  
195 200 205  
Gln Arg Val Ile Trp Arg Phe Leu Gly Tyr Gly Gly Asp Ser Asp Ala  
210 215 220  
Thr Thr Ala Pro Ser Lys Ser Lys Ile Val Met Val Gln Ala Ala Gly  
225 230 235 240  
Gly Ile Ile Ala Gly Ala Thr Ala Ser Ser Ile Thr Thr Pro Leu Asp  
245 250 255  
Thr Ile Lys Thr Arg Leu Gln Val Met Gly His Gln Glu Asn Arg Pro  
260 265 270  
Ser Ala Lys Gln Val Val Lys Lys Leu Leu Ala Glu Asp Gly Trp Lys  
275 280 285  
Gly Phe Tyr Arg Gly Leu Gly Pro Arg Phe Phe Ser Met Ser Ala Trp  
290 295 300  
Gly Thr Ser Met Ile Leu Thr Tyr Glu Tyr Leu Lys Arg Leu Cys Ala  
305 310 315 320  
Ile Glu Asp

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Thr Ala Ser Leu Phe Ser Gln Ala Val Phe Val Pro Ile Asp Val  
1 5 10 15  
Val Ser Gln Lys Leu Met Val Gln Gly Tyr Ser Gly His Ala Thr Tyr  
20 25 30  
Thr Gly Gly Ile Asp Val Ala Thr Lys Ile Ile Lys Ser Tyr Gly Val  
35 40 45  
Arg Gly Leu Tyr Arg Gly Phe Gly Leu Ser Val Met Thr Tyr Ser Pro  
50 55 60  
Ser Ser Ala Ala Trp Trp Ala Ser Tyr Gly Ser Ser Gln Arg Val Ile  
65 70 75 80  
Trp Arg Phe Leu Gly Tyr Gly Gly Asp Ser Asp Ala Thr Thr Ala Pro  
85 90 95  
Ser Lys Ser Lys Ile Val Met Val Gln Ala Ala Gly Gly Ile Ile Ala  
100 105 110  
Gly Ala Thr Ala Ser Ser Ile Thr Thr Pro Leu Asp Thr Ile Lys Thr  
115 120 125  
Arg Leu Gln Val Met Gly His Gln Glu Asn Arg Pro Ser Ala Lys Gln  
130 135 140  
Val Val Lys Lys Leu Leu Ala Glu Asp Gly Trp Lys Gly Phe Tyr Arg  
145 150 155 160  
Gly Leu Gly Pro Arg Phe Phe Ser Met Ser Ala Trp Gly Thr Ser Met  
165 170 175  
Ile Leu Thr Tyr Glu Tyr Leu Lys Arg Leu Cys Ala Ile Glu Asp  
180 185 190

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids

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- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..170  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565669  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Val Gln Gly Tyr Ser Gly His Ala Thr Tyr Thr Gly Gly Ile Asp  
1 5 10 15  
Val Ala Thr Lys Ile Ile Lys Ser Tyr Gly Val Arg Gly Leu Tyr Arg  
20 25 30  
Gly Phe Gly Leu Ser Val Met Thr Tyr Ser Pro Ser Ser Ala Ala Trp  
35 40 45  
Trp Ala Ser Tyr Gly Ser Ser Gln Arg Val Ile Trp Arg Phe Leu Gly  
50 55 60  
Tyr Gly Gly Asp Ser Asp Ala Thr Thr Ala Pro Ser Lys Ser Lys Ile  
65 70 75 80  
Val Met Val Gln Ala Ala Gly Gly Ile Ile Ala Gly Ala Thr Ala Ser  
85 90 95  
Ser Ile Thr Thr Pro Leu Asp Thr Ile Lys Thr Arg Leu Gln Val Met  
100 105 110  
Gly His Gln Glu Asn Arg Pro Ser Ala Lys Gln Val Val Lys Lys Leu  
115 120 125  
Leu Ala Glu Asp Gly Trp Lys Gly Phe Tyr Arg Gly Leu Gly Pro Arg  
130 135 140  
Phe Phe Ser Met Ser Ala Trp Gly Thr Ser Met Ile Leu Thr Tyr Glu  
145 150 155 160  
Tyr Leu Lys Arg Leu Cys Ala Ile Glu Asp  
165 170

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1213  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565672  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

gaccattttt acacacagcc aatcagagcc ttgtttcatt gtctcttgct gaggcgataa 60  
tatttagatc tgctcaccat ttctccgcca tcgccgacgg aagaagaaag atgggagaca 120  
acaaccctaa ccgatcagaa gcagaacgct ttctcggaat cgcggagaag cttctcgagt 180  
cacgagatct aaacggttca aaagagtttg caatcttagc tcaagagaca gagccactcc 240  
tcgaaggcac cgatcaaata ctcgcccgtc tcgatgtctt actctcatca gcaccagaga 300  
atcgtatcaa aaaccaacca aactggtaca aaatccttca gatcgaagat cttaaataat 360  
catcaacaga caacgatcta atcaagaaac aataccgtcg tcttgctctt cttctccacc 420  
cagacaaaaa ccgtttccct ttgcgcgatc aagctttcag attcgtgctt gatgcatggg 480  
aagttctatc aacaccttcg aagaaatctc aattcgatgg agatttgaat ctcatcttca 540  
ctaaagtaaa tctcaacact cagaaatcga agaagaaaac aacaacgaat gagaagatgt 600  
ctacgttttg gacggcgtgt ccgtactgtt acagtcttca tgagtatcct agggtttatc 660  
aagagtattg tattagatgt caaaactgtc aaagaGcgtt tcacgctgcg agtattcctc 720  
agttgcctcc gttgatacct ggtaaagatg agtattattg ttgctggggg ttttttccga 780  
tggggtttgt tggttgtaaa ggaggagaag ccgccattgc taatggagta gatgcagcta 840  
agttccctta ttggatgcct ccggttttct catccggcgg cgttgcagct cctccaagtg 900  
gtaatggtgt tagttttgat ggatggtcag gtggagcggc gaagagagat aatgaggctg 960  
tgaggagtaa taatggtgtt ggagttaatt cagatggaac accgaagaag agaggaagag 1020  
gaaggccgaa gaagaatccg gtttagtgat ctcttttcaa actccgggtca tgattgttaa 1080

aattatggag acaaaatttt aaaggcaagt ttttttaagg caaggaagtt taggatcagc 1140  
gtttgttgtc ttagtgtaaa ctttattatg catttggtgt tattaccggt gtgtaattgt 1200  
gttatcttga ttt

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1565673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Phe Leu His Thr Ala Asn Gln Ser Leu Val Ser Ser Ser Leu Val  
1 5 10 15  
Glu Ala Ile Ile Phe Arg Ser Ala His His Phe Ser Ala Ile Ala Asp  
20 25 30  
Gly Arg Arg Lys Met Gly Asp Asn Asn Pro Asn Arg Ser Glu Ala Glu  
35 40 45  
Arg Leu Leu Gly Ile Ala Glu Lys Leu Leu Glu Ser Arg Asp Leu Asn  
50 55 60  
Gly Ser Lys Glu Phe Ala Ile Leu Ala Gln Glu Thr Glu Pro Leu Leu  
65 70 75 80  
Glu Gly Thr Asp Gln Ile Leu Ala Val Val Asp Val Leu Leu Ser Ser  
85 90 95  
Ala Pro Glu Asn Arg Ile Lys Asn Gln Pro Asn Trp Tyr Lys Ile Leu  
100 105 110  
Gln Ile Glu Asp Leu Asn Glu Ser Thr Asp Asn Asp Leu Ile Lys  
115 120 125  
Lys Gln Tyr Arg Arg Leu Ala Leu Leu Leu His Pro Asp Lys Asn Arg  
130 135 140  
Phe Pro Phe Ala Asp Gln Ala Phe Arg Phe Val Leu Asp Ala Trp Glu  
145 150 155 160  
Val Leu Ser Thr Pro Ser Lys Lys Ser Gln Phe Asp Gly Asp Leu Asn  
165 170 175  
Leu Ile Phe Thr Lys Val Asn Leu Asn Thr Gln Lys Ser Lys Lys Lys  
180 185 190  
Thr Thr Thr Asn Glu Lys Met Ser Thr Phe Trp Thr Ala Cys Pro Tyr  
195 200 205  
Cys Tyr Ser Leu His Glu Tyr Pro Arg Val Tyr Gln Glu Tyr Cys Ile  
210 215 220  
Arg Cys Gln Asn Cys Gln Arg Ala Phe His Ala Ala Ser Ile Pro Gln  
225 230 235 240  
Leu Pro Pro Leu Ile Pro Gly Lys Asp Glu Tyr Tyr Cys Cys Trp Gly  
245 250 255  
Phe Phe Pro Met Gly Phe Val Gly Gly Lys Gly Gly Glu Ala Ala Ile  
260 265 270  
Ala Asn Gly Val Asp Ala Ala Lys Phe Pro Tyr Trp Met Pro Pro Val  
275 280 285  
Phe Ser Ser Gly Gly Val Ala Ala Pro Pro Ser Gly Asn Gly Val Ser  
290 295 300  
Phe Asp Gly Trp Ser Gly Gly Ala Ala Lys Arg Asp Asn Glu Ala Val  
305 310 315 320  
Arg Ser Asn Asn Gly Val Gly Val Asn Ser Asp Gly Thr Pro Lys Lys  
325 330 335  
Arg Gly Arg Gly Arg Pro Lys Lys Asn Pro Val  
340 345

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..311
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1565674
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Gly Asp Asn Asn Pro Asn Arg Ser Glu Ala Glu Arg Leu Leu Gly  
1 5 10 15  
Ile Ala Glu Lys Leu Leu Glu Ser Arg Asp Leu Asn Gly Ser Lys Glu  
20 25 30  
Phe Ala Ile Leu Ala Gln Glu Thr Glu Pro Leu Leu Glu Gly Thr Asp  
35 40 45  
Gln Ile Leu Ala Val Val Asp Val Leu Leu Ser Ser Ala Pro Glu Asn  
50 55 60  
Arg Ile Lys Asn Gln Pro Asn Trp Tyr Lys Ile Leu Gln Ile Glu Asp  
65 70 75 80  
Leu Asn Glu Ser Ser Thr Asp Asn Asp Leu Ile Lys Lys Gln Tyr Arg  
85 90 95  
Arg Leu Ala Leu Leu Leu His Pro Asp Lys Asn Arg Phe Pro Phe Ala  
100 105 110  
Asp Gln Ala Phe Arg Phe Val Leu Asp Ala Trp Glu Val Leu Ser Thr  
115 120 125  
Pro Ser Lys Lys Ser Gln Phe Asp Gly Asp Leu Asn Leu Ile Phe Thr  
130 135 140  
Lys Val Asn Leu Asn Thr Gln Lys Ser Lys Lys Lys Thr Thr Thr Asn  
145 150 155 160  
Glu Lys Met Ser Thr Phe Trp Thr Ala Cys Pro Tyr Cys Tyr Ser Leu  
165 170 175  
His Glu Tyr Pro Arg Val Tyr Gln Glu Tyr Cys Ile Arg Cys Gln Asn  
180 185 190  
Cys Gln Arg Ala Phe His Ala Ala Ser Ile Pro Gln Leu Pro Pro Leu  
195 200 205  
Ile Pro Gly Lys Asp Glu Tyr Tyr Cys Cys Trp Gly Phe Phe Pro Met  
210 215 220  
Gly Phe Val Gly Gly Lys Gly Gly Glu Ala Ala Ile Ala Asn Gly Val  
225 230 235 240  
Asp Ala Ala Lys Phe Pro Tyr Trp Met Pro Pro Val Phe Ser Ser Gly  
245 250 255  
Gly Val Ala Ala Pro Pro Ser Gly Asn Gly Val Ser Phe Asp Gly Trp  
260 265 270  
Ser Gly Gly Ala Ala Lys Arg Asp Asn Glu Ala Val Arg Ser Asn Asn  
275 280 285  
Gly Val Gly Val Asn Ser Asp Gly Thr Pro Lys Lys Arg Gly Arg Gly  
290 295 300  
Arg Pro Lys Lys Asn Pro Val  
305 310

- (2) INFORMATION FOR SEQ ID NO:55:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 470 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..470
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1565683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|            |            |             |            |             |            |     |
|------------|------------|-------------|------------|-------------|------------|-----|
| cacttagggg | tcatagcagc | cagagagaga  | gacaagtga  | agggatctac  | caaacgaagc | 60  |
| aacaatggg  | aagttcttga | agcagaacaa  | ggccgtgatc | cttcttcaag  | gacgttacgc | 120 |
| cggaagaaa  | gccgtcatca | tcaaatcctt  | cgacgacgg  | aaccgtgatc  | gTccttacgg | 180 |
| acactgcctc | gtcgccggac | tgaagaagta  | cccagcaaaa | gtcatccgca  | aagactcagc | 240 |
| taagaagaca | gctaagaaat | ctaggggttaa | gtgtttcatc | aagcttggtta | attaccagca | 300 |
| tctgatgcct | actcggtaca | cactcgacgt  | ggcagtgtct | gtaaggacga  | tcacggttac | 360 |
| cgtcgtcgaa | ggatttgatg | atgacggttt  | tctcttctac | attatgatgc  | tgtttgtgaa | 420 |
| ctctctctct | gtctttgctg | ataaataata  | aattgttact | aatataatct  |            |     |

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Lys | Phe | Lys | Lys | Gln | Asn | Lys | Ala | Val | Ile | Leu | Leu | Gln | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Tyr | Ala | Gly | Lys | Lys | Ala | Val | Ile | Ile | Lys | Ser | Phe | Asp | Asp | Gly |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Arg | Asp | Arg | Pro | Tyr | Gly | His | Cys | Leu | Val | Ala | Gly | Leu | Lys | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Pro | Ser | Lys | Val | Ile | Arg | Lys | Asp | Ser | Ala | Lys | Lys | Thr | Ala | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Ser | Arg | Val | Lys | Cys | Phe | Ile | Lys | Leu | Val | Asn | Tyr | Gln | His | Leu |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Met | Pro | Thr | Arg | Tyr | Thr | Leu | Asp | Val | Ala | Val | Ser | Val | Arg | Thr | Ile |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Thr | Val | Thr | Val | Val | Glu | Gly | Phe | Asp | Asp | Asp | Gly | Phe | Leu | Phe | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Met | Met | Leu | Phe | Val | Asn | Ser | Leu | Ser | Val | Phe | Ala | Asp | Lys |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1881
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atagattata | gatataaccc | actgaattaa | tattacgggc | ttcaatatag | gtgcatttaa  | 60  |
| aacataacgt | tccctctctt | gtcttcttat | ttttgctctc | tgttctttag | aactgccatt  | 120 |
| aacgagagt  | gagagagac  | acacacacac | agcgagtga  | aatgtctccg | gagaagaaga  | 180 |
| gtcaaaactt | ccctccaata | acggaatgca | gagacggaga | gtacgattcg | atagccgccg  | 240 |
| atcttgacgg | gactcStgct | tctctcaaga | agctccttcc | cttacttcat | gctcgtcgct  | 300 |
| gttgaagctg | gaagcctttt | acgtggacta | atcctccttc | tctcgttacc | attcgtcatt  | 360 |
| atctcttacc | tattcgtatc | cgaatctctt | ggtatccaga | tcctcatctt | catctcattc  | 420 |
| gctgggtctc | aaatccgcga | tatcgaaact | gtctctcgcg | cagttcttcc | acgggtacgag | 480 |
| atctaacata | gagtggtttt | ttgttagtag | atcactttag | tttttttccg | atgaactatg  | 540 |
| tttaggtttt | acgcggcgga | tgtgaggaaa | gacagttttg | aggtgtttga | taagtgtaa   | 600 |
| aagaaagtgg | tagtgacggc | gaatccgatt | gtgatgggtg | aggcgtttgt | gaaggSatta  | 660 |
| tcttgagggt | gataaagttt | tgggaacaga | gattgaagtt | aaccctaaaa | ccaatagagc  | 720 |

|            |             |             |            |             |            |      |
|------------|-------------|-------------|------------|-------------|------------|------|
| cactggattt | gtgaagaagc  | ctgggtgttct | tgttggtgat | cttaagaggt  | tagccatttt | 780  |
| aaaagagttt | ggtaacgaat  | cacctgatct  | cggcctcggg | gatcgaacct  | ctgatcatga | 840  |
| tttcatgtct | ctctgcaaga  | aagggttacat | ggttcatgcg | accaagtcag  | ccacaacgat | 900  |
| tccaaaagaa | cgcttaaaga  | accgcatagt  | cttccatgat | ggcggtttag  | cgcaacgtcc | 960  |
| aactccggtt | aagccattta  | tcacataacct | atggcttcct | tttggtttca  | tcctctccat | 1020 |
| cattcgcgtc | tacttcaacc  | tccttttacc  | tgaagatttt | gtccgttaca  | cttacgagat | 1080 |
| gctcgggata | cacttaacca  | ttcgtgggtca | tcgtcctcca | cctccttccc  | ctggaactct | 1140 |
| tggcaacctc | tatgtcctta  | accaccgtac  | cgcgcttgat | cccatcatcg  | ttgctattgc | 1200 |
| tcttgagcgt | aagatctggt  | gcgtcactta  | cagtgtctct | cgtctctccc  | ttatgctttc | 1260 |
| tcctattcct | gctggtgccc  | tcacccgtga  | ccgtgccacc | gatgctgcca  | acatgagaaa | 1320 |
| acttctcgag | aaaggcgact  | tgggtgatatg | tcccgaaggc | acgacgtgca  | gagaagagta | 1380 |
| tctactgaga | tttagcgctc  | tattcgcaga  | gctaagcgac | cggattgtgc  | cagtagcgat | 1440 |
| gaactgtaaa | caaggaatgt  | tcaacgggac  | cacagttagg | ggtgtgaagt  | tttgggacct | 1500 |
| ttacttcttc | ttcatgaacc  | caagaccaag  | ctatgaagcc | actttcttgg  | atcgtttgcc | 1560 |
| tgaagaaatg | actgtcaacg  | gtgggtggcaa | gactcctata | gaggtgggcta | attacgtcca | 1620 |
| gaaagttatc | ggcgcgggtt  | tgggcttcga  | atgcaccgaa | cttactcgca  | aggataaata | 1680 |
| tcttttgctt | ggaggtaatg  | acggcaaggt  | agagtctatc | aacaacacca  | agaagtgaaa | 1740 |
| atccaaacaa | gggttttttc  | ttgttatgtc  | gtatacgaat | tttcatgtgt  | gtaattgctg | 1800 |
| gagctcttgt | catcattatg  | gtacgttttt  | gttatgtgta | atacgacgta  | tatatgtttg | 1860 |
| aataaaacta | tgtttcgggtg | g           |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Cys | Lys | Lys | Gly | Tyr | Met | Val | His | Ala | Thr | Lys | Ser | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Thr | Ile | Pro | Lys | Glu | Arg | Leu | Lys | Asn | Arg | Ile | Val | Phe | His | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Arg | Leu | Ala | Gln | Arg | Pro | Thr | Pro | Leu | Asn | Ala | Ile | Ile | Thr | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Trp | Leu | Pro | Phe | Gly | Phe | Ile | Leu | Ser | Ile | Ile | Arg | Val | Tyr | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Pro | Leu | Pro | Glu | Arg | Phe | Val | Arg | Tyr | Thr | Tyr | Glu | Met | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ile | His | Leu | Thr | Ile | Arg | Gly | His | Arg | Pro | Pro | Pro | Pro | Ser | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Thr | Leu | Gly | Asn | Leu | Tyr | Val | Leu | Asn | His | Arg | Thr | Ala | Leu | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ile | Ile | Val | Ala | Ile | Ala | Leu | Gly | Arg | Lys | Ile | Cys | Cys | Val | Thr |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Ser | Val | Ser | Arg | Leu | Ser | Leu | Met | Leu | Ser | Pro | Ile | Pro | Ala | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Leu | Thr | Arg | Asp | Arg | Ala | Thr | Asp | Ala | Ala | Asn | Met | Arg | Lys | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Glu | Lys | Gly | Asp | Leu | Val | Ile | Cys | Pro | Glu | Gly | Thr | Thr | Cys | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Glu | Tyr | Leu | Leu | Arg | Phe | Ser | Ala | Leu | Phe | Ala | Glu | Leu | Ser | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ile | Val | Pro | Val | Ala | Met | Asn | Cys | Lys | Gln | Gly | Met | Phe | Asn | Gly |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Thr | Thr | Val | Arg | Gly | Val | Lys | Phe | Trp | Asp | Pro | Tyr | Phe | Phe | Phe | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Pro | Arg | Pro | Ser | Tyr | Glu | Ala | Thr | Phe | Leu | Asp | Arg | Leu | Pro | Glu |

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(2) INFORMATION FOR SEO ID NO:59:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1565690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

(A) LENGTH: 219 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..219  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565691  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:  
Met Leu Gly Ile His Leu Thr Ile Arg Gly His Arg Pro Pro Pro Pro  
1 5 10 15  
Ser Pro Gly Thr Leu Gly Asn Leu Tyr Val Leu Asn His Arg Thr Ala  
20 25 30  
Leu Asp Pro Ile Ile Val Ala Ile Ala Leu Gly Arg Lys Ile Cys Cys  
35 40 45  
Val Thr Tyr Ser Val Ser Arg Leu Ser Leu Met Leu Ser Pro Ile Pro  
50 55 60  
Ala Val Ala Leu Thr Arg Asp Arg Ala Thr Asp Ala Ala Asn Met Arg  
65 70 75 80  
Lys Leu Leu Glu Lys Gly Asp Leu Val Ile Cys Pro Glu Gly Thr Thr  
85 90 95  
Cys Arg Glu Glu Tyr Leu Leu Arg Phe Ser Ala Leu Phe Ala Glu Leu  
100 105 110  
Ser Asp Arg Ile Val Pro Val Ala Met Asn Cys Lys Gln Gly Met Phe  
115 120 125  
Asn Gly Thr Thr Val Arg Gly Val Lys Phe Trp Asp Pro Tyr Phe Phe  
130 135 140  
Phe Met Asn Pro Arg Pro Ser Tyr Glu Ala Thr Phe Leu Asp Arg Leu  
145 150 155 160  
Pro Glu Glu Met Thr Val Asn Gly Gly Gly Lys Thr Pro Ile Glu Val  
165 170 175  
Ala Asn Tyr Val Gln Lys Val Ile Gly Ala Val Leu Gly Phe Glu Cys  
180 185 190  
Thr Glu Leu Thr Arg Lys Asp Lys Tyr Leu Leu Leu Gly Gly Asn Asp  
195 200 205  
Gly Lys Val Glu Ser Ile Asn Asn Thr Lys Lys  
210 215

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1065  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

aaagaagaaa ttggatccgc cgttgatcgt ccg gatctgg aacgaggaag atgagctctc 60  
tatcttaaag gggttagttg attacagagc taagacagga ttcaatccca aaattgattg 120  
ggatgcgttt tgtagtttcc tcggaagttc tatcgttgag agattctcca aggatcaggt 180  
tttgagtaaa atcaggaagt tgaaaaggag gtttcatgtt cactcggaga aaatcaatca 240  
agggaatgat cccaaattta ctagggtctag tgattctgaa gcctttgggt tttcttcgat 300  
gatttgggga caaggtgatg atgatggtat ggataaggag cacgaggtaa acggaaatgg 360  
tgcagcggaa aaccggacta acgagagcgg ggaggagatg ttgaaggagc acgaggagga 420  
agtggctaata actgaacttt taaatgagaa tGgggcagcc aaaacaacag agaatgggac 480  
tagtagtgga aaagagagac atgatgagga caatgatgat gatgatgagt tatgcgcggt 540  
gcaggatgca tttgaggcgg tgatgtcgca aggtttaagt ggttatcaaa agaagttgca 600  
gcttgagaag ctgatgaacc ttggaaatgg taaaagaaga gagttgagtg atgaatggaa 660

(2) INFORMATION FOR SEQ ID NO:62:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1565693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

[illegible]

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1565695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1498

(D) OTHER INFORMATION: / Ceres Seq. ID 1565723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aaattcaatg  | gacctttttc  | ttcaaattctc | cagcttttctg | catagatcca  | tgaccatgag | 60   |
| agtctgtttc  | ttagaacgaa  | aatgaaaaaa  | atatcttcac  | attattcggg  | agtcatagcg | 120  |
| atactcggtg  | tggtgacgat  | gacctcgatg  | tgtcaagctg  | tgggtagcaa  | tgtgtaccct | 180  |
| ttgattctgg  | ttccaggaaa  | cggaggtaac  | cagctagagg  | tacggctgga  | cagagaatac | 240  |
| aagccaagta  | gtgtctgggtg | tagcagctgg  | ttatatccga  | ttcataagaa  | gagtggtgga | 300  |
| tggttttaggc | tatgggttoga | tgcagcagtg  | ttattgtctc  | ccttcaccag  | gtgcttcagc | 360  |
| gatcgaatga  | tgttgacta   | tgacctgat   | ttggatgatt  | acaaaaatgc  | tcctgggtgc | 420  |
| caaaccggg   | ttcctcattt  | cggttcgacc  | aatcacttc   | tatacctcga  | ccctcgtctc | 480  |
| cgagatgcca  | catcttacat  | ggaacatttg  | gtgaaagctc  | tagagaaaaa  | atgcgggtat | 540  |
| gttaacgacc  | aaaccatcct  | aggagctcca  | tatgatttca  | ggtacggcct  | ggctgcttcg | 600  |
| ggccaaccgt  | cccgtgtagc  | ctcacagttc  | ctacaagacc  | tcaaacaatt  | ggtggaaaaa | 660  |
| actagcagcg  | agaacgaagg  | aaagccagtg  | atactcctct  | cccatagcct  | aggaggactt | 720  |
| ttcgtcctcc  | atttcctcaa  | ccgtaccacc  | ccttcattgg  | gccgcaagta  | catcaaacac | 780  |
| tttgttgac   | tcgctgcgcc  | atgggggtgg  | acgatctctc  | agatgaagac  | atttgcttct | 840  |
| ggcaacacac  | tcggtgtccc  | tttagttaac  | cctttgctgg  | tcagacggca  | tcagaggacc | 900  |
| tccgagagta  | accaatggct  | acttccatct  | accaaagtgt  | ttcacgacag  | aactaaaccg | 960  |
| cttgtcgtaa  | ctccccaggt  | taactacaca  | gcttacgaga  | tggtatcggtt | ttttgcagac | 1020 |
| attggattct  | cacaaggagt  | tgtgccttac  | aagacaagag  | tggtgccttt  | aacagaggag | 1080 |
| ctgatgactc  | cgggagtggc  | agtcacttgc  | atatatggga  | gaggagttaga | tacaccggag | 1140 |
| gttttgatgt  | atggaaaagg  | aggattcgat  | aagcaaccag  | agattaagta  | tggagatgga | 1200 |
| gatgggacgg  | ttaatttggc  | gagcttagca  | gctttgaaag  | tcgatagctt  | gaacaccgta | 1260 |
| gagattgatg  | gagtttcgca  | tacatctata  | cttaaagacg  | agatcgact   | taaagagatt | 1320 |
| atgaagcaga  | tttcaattat  | taattatgaa  | ttagccaatg  | ttaatgccgt  | caatgaatga | 1380 |
| gagcagtcac  | ctatttcacc  | atttttagtt  | gtacatttta  | agataaagag  | ataatttaca | 1440 |
| tatatttcac  | ggtttgtttt  | aggcactcct  | tatagaagaa  | aaaaagaatt  | aaaaaccg   |      |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..432

(D) OTHER INFORMATION: / Ceres Seq. ID 1565724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ile | Ser | Ser | His | Tyr | Ser | Val | Val | Ile | Ala | Ile | Leu | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Thr | Met | Thr | Ser | Met | Cys | Gln | Ala | Val | Gly | Ser | Asn | Val | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Leu | Ile | Leu | Val | Pro | Gly | Asn | Gly | Gly | Asn | Gln | Leu | Glu | Val | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Arg | Glu | Tyr | Lys | Pro | Ser | Ser | Val | Trp | Cys | Ser | Ser | Trp | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Pro | Ile | His | Lys | Lys | Ser | Gly | Gly | Trp | Phe | Arg | Leu | Trp | Phe | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ala | Val | Leu | Leu | Ser | Pro | Phe | Thr | Arg | Cys | Phe | Ser | Asp | Arg | Met |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Met | Leu | Tyr | Tyr | Asp | Pro | Asp | Leu | Asp | Asp | Tyr | Gln | Asn | Ala | Pro | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Gln | Thr | Arg | Val | Pro | His | Phe | Gly | Ser | Thr | Lys | Ser | Leu | Leu | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asp | Pro | Arg | Leu | Arg | Asp | Ala | Thr | Ser | Tyr | Met | Glu | His | Leu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ala | Leu | Glu | Lys | Lys | Cys | Gly | Tyr | Val | Asn | Asp | Gln | Thr | Ile | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ala | Pro | Tyr | Asp | Phe | Arg | Tyr | Gly | Leu | Ala | Ala | Ser | Gly | His | Pro |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1565725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Met | Cys | Gln | Ala | Val | Gly | Ser | Asn | Val | Tyr | Pro | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Pro | Gly | Asn | Gly | Gly | Asn | Gln | Leu | Glu | Val | Arg | Leu | Asp | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Tyr | Lys | Pro | Ser | Ser | Val | Trp | Cys | Ser | Ser | Trp | Leu | Tyr | Pro | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Lys | Lys | Ser | Gly | Gly | Trp | Phe | Arg | Leu | Trp | Phe | Asp | Ala | Ala | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Ser | Pro | Phe | Thr | Arg | Cys | Phe | Ser | Asp | Arg | Met | Met | Leu | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Asp | Pro | Asp | Leu | Asp | Asp | Tyr | Gln | Asn | Ala | Pro | Gly | Val | Gln | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Val | Pro | His | Phe | Gly | Ser | Thr | Lys | Ser | Leu | Leu | Tyr | Leu | Asp | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val Lys Ala Leu  
115 120 125  
Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu Gly Ala Pro  
130 135 140  
Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro Ser Arg Val  
145 150 155 160  
Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu Lys Thr Ser  
165 170 175  
Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His Ser Leu Gly  
180 185 190  
Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro Ser Trp Arg  
195 200 205  
Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro Trp Gly Gly  
210 215 220  
Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr Leu Gly Val  
225 230 235 240  
Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg Thr Ser Glu  
245 250 255  
Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His Asp Arg Thr  
260 265 270  
Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala Tyr Glu Met  
275 280 285  
Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val Val Pro Tyr  
290 295 300  
Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr Pro Gly Val  
305 310 315 320  
Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro Glu Val Leu  
325 330 335  
Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile Lys Tyr Gly  
340 345 350  
Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala Leu Lys Val  
355 360 365  
Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His Thr Ser Ile  
370 375 380  
Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln Ile Ser Ile  
385 390 395 400  
Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu  
405 410

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1565726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Cys Gln Ala Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro  
1 5 10 15  
Gly Asn Gly Gly Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys  
20 25 30  
Pro Ser Ser Val Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys  
35 40 45  
Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser  
50 55 60  
Pro Phe Thr Arg Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro  
65 70 75 80  
Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 85  |  | 90  |  | 95  |
| His Phe Gly Ser Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg |     |  |     |  |     |
|                                                                 | 100 |  | 105 |  | 110 |
| Asp Ala Thr Ser Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys |     |  |     |  |     |
|                                                                 | 115 |  | 120 |  | 125 |
| Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe |     |  |     |  |     |
|                                                                 | 130 |  | 135 |  | 140 |
| Arg Tyr Gly Leu Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln |     |  |     |  |     |
|                                                                 | 145 |  | 150 |  | 155 |
| Phe Leu Gln Asp Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn |     |  |     |  |     |
|                                                                 | 165 |  | 170 |  | 175 |
| Glu Gly Lys Pro Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe |     |  |     |  |     |
|                                                                 | 180 |  | 185 |  | 190 |
| Val Leu His Phe Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr |     |  |     |  |     |
|                                                                 | 195 |  | 200 |  | 205 |
| Ile Lys His Phe Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser |     |  |     |  |     |
|                                                                 | 210 |  | 215 |  | 220 |
| Gln Met Lys Thr Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val |     |  |     |  |     |
|                                                                 | 225 |  | 230 |  | 235 |
| Asn Pro Leu Leu Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln |     |  |     |  |     |
|                                                                 | 245 |  | 250 |  | 255 |
| Trp Leu Leu Pro Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu |     |  |     |  |     |
|                                                                 | 260 |  | 265 |  | 270 |
| Val Val Thr Pro Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe |     |  |     |  |     |
|                                                                 | 275 |  | 280 |  | 285 |
| Phe Ala Asp Ile Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg |     |  |     |  |     |
|                                                                 | 290 |  | 295 |  | 300 |
| Val Leu Pro Leu Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr |     |  |     |  |     |
|                                                                 | 305 |  | 310 |  | 315 |
| Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly |     |  |     |  |     |
|                                                                 | 325 |  | 330 |  | 335 |
| Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp |     |  |     |  |     |
|                                                                 | 340 |  | 345 |  | 350 |
| Gly Thr Val Asn Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu |     |  |     |  |     |
|                                                                 | 355 |  | 360 |  | 365 |
| Asn Thr Val Glu Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp |     |  |     |  |     |
|                                                                 | 370 |  | 375 |  | 380 |
| Glu Ile Ala Leu Lys Glu Ile Met Lys Gln Ile Ser Ile Ile Asn Tyr |     |  |     |  |     |
|                                                                 | 385 |  | 390 |  | 395 |
| Glu Leu Ala Asn Val Asn Ala Val Asn Glu                         |     |  |     |  |     |
|                                                                 | 405 |  | 410 |  |     |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| acaattcagg gaaaatcttc aaagtgtttg cagagaaatc taaattcatc aacagttttt   | 60  |
| tacaaaagaa atggaaaacg gagaagcaaa acagagtgtc cctcttctca ctccctataa   | 120 |
| gatgggaaga ttcaatcttt cccatagggg tgttctagca ccattgacga gacagagatc   | 180 |
| gtacggaaac gttcctcagc ctacgcgtgc catatattac tctcagagaa cgactccagg   | 240 |
| aggtttttctc atcactgaag ccaactggagt ttcagatata gctcaaggat atcaagatac | 300 |
| tcctgggata tggactaaag agcatgtgga ggcattgga ccaatcggtg atgctgtaca    | 360 |
| tgccaaaggt ggtatcttct tctgtcagat ctggcatgtt ggccgcgttt ctaatagcgg   | 420 |
| gttttcagcca aatggaaaag ctccatcttc ttgttcggat aagccattga tgcctcaaat  | 480 |



```

tcgctctaataatccccggcattgtcaatgatttttaggcttgctgcaagaatgctatggaagctggttt
tgatggagttgagattcatagagctaattggctatctgattgaccagttcagaaggatac
ggatgaatgatagaactgatgaactcggtggtatcattgcaaaccggttgcaaatctcctct
agaaatagtcgatgcagttgctaaggagatcgaccagacggtgttggaatcaggctctc
tccatttgctgactacatggaatctggagacactaatccaggagcattagggttttatat
ggcgggaatctttgaacaaatcggaatcctctactgtcatgtgattgaagcgagaatgaa
aacaatgggaagaatcatgctgtgctcaacactaatgacgatgaggaagcgttttaa
ggggacttttatctccgagagggtttcacagggaagatgggaatgaggctgtgtcaaaa
gggaagaactgatttgggtgcttatgggtcgatgggttttataccaacccggacctgcaaaa
gaggttccaaatgtgatgcacgctgaataaatacgaatgacacacgttttacttctga
tccagtcgtcggttacaccgattaccctttcctgaatcaacagcttaaaattgttatca
ataatgtaatgtagtgtgtttcccttatataagatgtaataagtttctggtctttcattt
atactttttaagttaagcc

```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1565747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Glu Asn Gly Glu Ala Lys Gln Ser Val Pro Leu Leu Thr Pro Tyr
1 5 10 15
Lys Met Gly Arg Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu
20 25 30
Thr Arg Gln Arg Ser Tyr Gly Asn Val Pro Gln Pro His Ala Ala Ile
35 40 45
Tyr Tyr Ser Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Thr Glu Ala
50 55 60
Thr Gly Val Ser Asp Thr Ala Gln Gly Tyr Gln Asp Thr Pro Gly Ile
65 70 75 80
Trp Thr Lys Glu His Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val
85 90 95
His Ala Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His Val Gly Arg
100 105 110
Val Ser Asn Ser Gly Phe Gln Pro Asn Gly Lys Ala Pro Ile Ser Cys
115 120 125
Ser Asp Lys Pro Leu Met Pro Gln Ile Arg Ser Asn Gly Ile Asp Glu
130 135 140
Ala Leu Phe Thr Pro Pro Arg Arg Leu Gly Ile Glu Glu Ile Pro Gly
145 150 155 160
Ile Val Asn Asp Phe Arg Leu Ala Ala Arg Asn Ala Met Glu Ala Gly
165 170 175
Phe Asp Gly Val Glu Ile His Arg Ala Asn Gly Tyr Leu Ile Asp Gln
180 185 190
Phe Met Lys Asp Thr Val Asn Asp Arg Thr Asp Glu Tyr Gly Gly Ser
195 200 205
Leu Gln Asn Arg Cys Lys Phe Pro Leu Glu Ile Val Asp Ala Val Ala
210 215 220
Lys Glu Ile Gly Pro Asp Arg Val Gly Ile Arg Leu Ser Pro Phe Ala
225 230 235 240
Asp Tyr Met Glu Ser Gly Asp Thr Asn Pro Gly Ala Leu Gly Leu Tyr
245 250 255
Met Ala Glu Ser Leu Asn Lys Tyr Gly Ile Leu Tyr Cys His Val Ile
260 265 270
Glu Ala Arg Met Lys Thr Met Gly Glu Val His Ala Cys Pro His Thr

```

SEQUENCE - 1565747

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 275                                                             | 280 | 285 |
| Leu Met Pro Met Arg Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly |     |     |
| 290                                                             | 295 | 300 |
| Gly Phe Thr Arg Glu Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr |     |     |
| 305                                                             | 310 | 315 |
| Asp Leu Val Ala Tyr Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro |     |     |
|                                                                 | 325 | 330 |
| Lys Arg Phe Gln Val Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr |     |     |
|                                                                 | 340 | 345 |
| Phe Tyr Thr Ser Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu |     |     |
|                                                                 | 355 | 360 |
| Glu Ser Thr Ala                                                 |     | 365 |
| 370                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1565748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gly Arg Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu Thr |     |     |
| 1                                                               | 5   | 10  |
| Arg Gln Arg Ser Tyr Gly Asn Val Pro Gln Pro His Ala Ala Ile Tyr |     |     |
|                                                                 | 20  | 25  |
| Tyr Ser Gln Arg Thr Thr Pro Gly Phe Leu Ile Thr Glu Ala Thr     |     |     |
|                                                                 | 35  | 40  |
| Gly Val Ser Asp Thr Ala Gln Gly Tyr Gln Asp Thr Pro Gly Ile Trp |     |     |
|                                                                 | 50  | 55  |
| Thr Lys Glu His Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val His |     |     |
|                                                                 | 65  | 70  |
| Ala Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His Val Gly Arg Val |     |     |
|                                                                 | 85  | 90  |
| Ser Asn Ser Gly Phe Gln Pro Asn Gly Lys Ala Pro Ile Ser Cys Ser |     |     |
|                                                                 | 100 | 105 |
| Asp Lys Pro Leu Met Pro Gln Ile Arg Ser Asn Gly Ile Asp Glu Ala |     |     |
|                                                                 | 115 | 120 |
| Leu Phe Thr Pro Pro Arg Arg Leu Gly Ile Glu Glu Ile Pro Gly Ile |     |     |
|                                                                 | 130 | 135 |
| Val Asn Asp Phe Arg Leu Ala Ala Arg Asn Ala Met Glu Ala Gly Phe |     |     |
|                                                                 | 145 | 150 |
| Asp Gly Val Glu Ile His Arg Ala Asn Gly Tyr Leu Ile Asp Gln Phe |     |     |
|                                                                 | 165 | 170 |
| Met Lys Asp Thr Val Asn Asp Arg Thr Asp Glu Tyr Gly Gly Ser Leu |     |     |
|                                                                 | 180 | 185 |
| Gln Asn Arg Cys Lys Phe Pro Leu Glu Ile Val Asp Ala Val Ala Lys |     |     |
|                                                                 | 195 | 200 |
| Glu Ile Gly Pro Asp Arg Val Gly Ile Arg Leu Ser Pro Phe Ala Asp |     |     |
|                                                                 | 210 | 215 |
| Tyr Met Glu Ser Gly Asp Thr Asn Pro Gly Ala Leu Gly Leu Tyr Met |     |     |
|                                                                 | 225 | 230 |
| Ala Glu Ser Leu Asn Lys Tyr Gly Ile Leu Tyr Cys His Val Ile Glu |     |     |
|                                                                 | 245 | 250 |
| Ala Arg Met Lys Thr Met Gly Glu Val His Ala Cys Pro His Thr Leu |     |     |
|                                                                 | 260 | 265 |
| Met Pro Met Arg Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly Gly |     |     |
|                                                                 | 275 | 280 |
|                                                                 |     | 285 |

(2) INFORMATION FOR SEQ ID NO:72:

(A) LENGTH: 239 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1565749

|            |            |            |            |            |           |            |            |            |            |           |            |            |            |           |            |
|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|-----------|------------|
| Met<br>1   | Pro        | Gln        | Ile        | Arg<br>5   | Ser       | Asn        | Gly        | Ile        | Asp<br>10  | Glu       | Ala        | Leu        | Phe        | Thr<br>15 | Pro        |
| Pro        | Arg        | Arg        | Leu<br>20  | Gly        | Ile       | Glu        | Glu        | Ile<br>25  | Pro        | Gly       | Ile        | Val        | Asn<br>30  | Asp       | Phe        |
| Arg        | Leu        | Ala<br>35  | Ala        | Arg        | Asn       | Ala        | Met<br>40  | Glu        | Ala        | Gly       | Phe        | Asp<br>45  | Gly        | Val       | Glu        |
| Ile<br>50  | His        | Arg        | Ala        | Asn        | Gly       | Tyr<br>55  | Leu        | Ile        | Asp        | Gln       | Phe<br>60  | Met        | Lys        | Asp       | Thr        |
| Val<br>65  | Asn        | Asp        | Arg        | Thr        | Asp<br>70 | Glu        | Tyr        | Gly        | Gly        | Ser<br>75 | Leu        | Gln        | Asn        | Arg       | Cys<br>80  |
| Lys        | Phe        | Pro        | Leu<br>85  | Glu        | Ile       | Val        | Asp        | Ala        | Val<br>90  | Ala       | Lys        | Glu        | Ile        | Gly<br>95 | Pro        |
| Asp        | Arg        | Val        | Gly<br>100 | Ile        | Arg       | Leu        | Ser        | Pro<br>105 | Phe        | Ala       | Asp        | Tyr        | Met<br>110 | Glu       | Ser        |
| Gly        | Asp        | Thr<br>115 | Asn        | Pro        | Gly       | Ala        | Leu<br>120 | Gly        | Leu        | Tyr       | Met        | Ala<br>125 | Glu        | Ser       | Leu        |
| Asn        | Lys<br>130 | Tyr        | Gly        | Ile        | Leu       | Tyr<br>135 | Cys        | His        | Val        | Ile       | Glu<br>140 | Ala        | Arg        | Met       | Lys        |
| Thr<br>145 | Met        | Gly        | Glu        | Val<br>150 | His       | Ala        | Cys        | Pro        | His<br>155 | Thr       | Leu        | Met        | Pro        | Met       | Arg<br>160 |
| Lys        | Ala        | Phe        | Lys<br>165 | Gly        | Thr       | Phe        | Ile        | Ser        | Ala<br>170 | Gly       | Gly        | Phe        | Thr        | Arg       | Glu        |
| Asp        | Gly        | Asn<br>180 | Glu        | Ala        | Val       | Ser        | Lys<br>185 | Gly        | Arg        | Thr       | Asp        | Leu<br>190 | Val        | Ala       | Tyr        |
| Gly        | Arg<br>195 | Trp        | Phe        | Leu        | Ala       | Asn        | Pro<br>200 | Asp        | Leu        | Pro       | Lys        | Arg<br>205 | Phe        | Gln       | Val        |
| Asp        | Ala<br>210 | Pro        | Leu        | Asn        | Lys       | Tyr<br>215 | Asp        | Arg        | Pro        | Thr       | Phe<br>220 | Tyr        | Thr        | Ser       | Asp        |
| Pro<br>225 | Val        | Val        | Gly        | Tyr<br>230 | Thr       | Asp        | Tyr        | Pro        | Phe<br>235 | Leu       | Glu        | Ser        | Thr        | Ala       |            |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1012

(D) OTHER INFORMATION: / Ceres Seq. ID 1565769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| acttcagcaa | aaccactaca  | cctttcttat | ctctcagatt | ttctcaagaa  | gattgtgtgg  | 60  |
| aagatgatga | gacggaagat  | ttttctcttt | ggtgattcca | tcactgaaga  | atccttttagt | 120 |
| gacggtggct | gggggtgcttc | tctgcgcgat | cttctccgcc | gcaaggctga  | tatggtgcta  | 180 |
| cgaggataca | gtggatataa  | cacgaggtgg | gcactgaaag | tgggtggagag | agtttttccg  | 240 |
| gtggcagaag | aagacggcgg  | agattctccg | gcagctgtga | ctgttttctt  | tggagcgaac  | 300 |
| gacgcgtgtc | ttccggagag  | atgctcgggg | tttcagcatg | tgccacttca  | cgagtacaag  | 360 |
| cagaatcttc | gctctattgt  | ttcgtttctc | aagaatcggt | ggccacaaac  | ggccattatt  | 420 |
| cttataactc | cgcctccaat  | agacgaagag | gcccgcctca | gatatcctta  | tatcgaaaac  | 480 |
| acaacggggg | tgccggaaaag | aacgaatgaa | gtagccggac | tatacgcaaa  | agcatgtata  | 540 |
| scagtagctg | aggaatgtca  | aatttcgggc | actgatcttt | ggtccaaaat  | gcagcAaakt  | 600 |
| scaaattggs | aaacagaatg  | tctatgggac | gggttacatt | tgagtcgggt  | cggtaaacaaa | 660 |
| gtattgtttg | aagaagtagc  | aaagaagcgt | aaagaagaag | gcattggagc  | tgaggactta  | 720 |
| gctgtggatc | ttccctttat  | agaagatggt | gaccctaagg | atcctctcaa  | atcctttgat  | 780 |
| gagttttgat | gctttatatt  | actaccatgc | agtttggttc | ttctatcttt  | gAttactttct | 840 |
| taatttcgat | attaatttag  | ggaatgtgac | attattaggc | actttgtgag  | aatctttttg  | 900 |
| tgagaatctt | tttacgtttg  | aggcacttgt | gagagagagg | gcactttgcc  | atcttttttt  | 960 |
| agaggagatt | gaaccaat    | gtccctgaag | tgatgaaaac | acaataat    | tt          |     |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1565770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Ala | Lys | Pro | Leu | His | Leu | Ser | Tyr | Leu | Ser | Asp | Phe | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ile | Val | Trp | Lys | Met | Met | Arg | Arg | Lys | Ile | Phe | Leu | Phe | Gly | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Thr | Glu | Glu | Ser | Phe | Ser | Asp | Gly | Gly | Trp | Gly | Ala | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Asp | Leu | Leu | Arg | Arg | Lys | Ala | Asp | Met | Val | Leu | Arg | Gly | Tyr | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Tyr | Asn | Thr | Arg | Trp | Ala | Leu | Lys | Val | Val | Glu | Arg | Val | Phe | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Ala | Glu | Glu | Asp | Gly | Gly | Asp | Ser | Pro | Ala | Ala | Val | Thr | Val | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Ala | Asn | Asp | Ala | Cys | Leu | Pro | Glu | Arg | Cys | Ser | Gly | Phe | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Val | Pro | Leu | His | Glu | Tyr | Lys | Gln | Asn | Leu | Arg | Ser | Ile | Val | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Leu | Lys | Asn | Arg | Trp | Pro | Gln | Thr | Ala | Ile | Ile | Leu | Ile | Thr | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Pro | Pro | Ile | Asp | Glu | Glu | Ala | Arg | Leu | Arg | Tyr | Pro | Tyr | Ile | Glu | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Thr | Gly | Leu | Pro | Glu | Arg | Thr | Asn | Glu | Val | Ala | Gly | Leu | Tyr | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Ala | Cys | Ile | Ala | Val | Ala | Glu | Glu | Cys | Gln | Ile | Ser | Val | Thr | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Trp | Ser | Lys | Met | Gln | Gln | Xaa | Xaa | Asn | Trp | Xaa | Thr | Glu | Cys | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Asp | Gly | Leu | His | Leu | Ser | Arg | Val | Gly | Asn | Lys | Val | Leu | Phe | Glu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Val | Ala | Lys | Lys | Leu | Lys | Glu | Glu | Gly | Ile | Gly | Ala | Glu | Asp | Leu |

(2) INFORMATION FOR SEQ ID NO:75:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAM

(A) NAME/REF: peptide  
(B) LOCATION: 1 241

(D) OTHER INFORMATION

(D) OTHER INFORMATION: 7 Ceres Seq. ID 1565771  
SEQUENCE DESCRIPTION: SEQ ID NO:75.

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:75:  
Met Arg Arg Lys Ile Phe Leu Phe Gly Asp

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1565772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Arg Arg Lys Ile Phe Leu Phe Gly Asp Ser Ile Thr Glu Glu Ser  
1 5 10 15  
Phe Ser Asp Gly Trp Gly Ala Ser Leu Ala Asp Leu Leu Arg Arg  
20 25 30  
Lys Ala Asp Met Val Leu Arg Gly Tyr Ser Gly Tyr Asn Thr Arg Trp  
35 40 45  
Ala Leu Lys Val Val Glu Arg Val Phe Pro Val Ala Glu Glu Asp Gly  
50 55 60  
Gly Asp Ser Pro Ala Ala Val Thr Val Phe Phe Gly Ala Asn Asp Ala  
65 70 75 80  
Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln His Val Pro Leu His Glu  
85 90 95  
Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser Phe Leu Lys Asn Arg Trp  
100 105 110  
Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro Pro Pro Ile Asp Glu Glu  
115 120 125  
Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn Thr Thr Gly Leu Pro Glu  
130 135 140  
Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala Lys Ala Cys Ile Ala Val  
145 150 155 160  
Ala Glu Glu Cys Gln Ile Ser Val Thr Asp Leu Trp Ser Lys Met Gln  
165 170 175  
Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu Trp Asp Gly Leu His Leu  
180 185 190  
Ser Arg Val Gly Asn Lys Val Leu Phe Glu Glu Val Ala Lys Lys Leu  
195 200 205  
Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu Ala Val Asp Leu Pro Leu  
210 215 220  
Ile Glu Asp Val Asp Pro Lys Asp Pro Leu Lys Ser Phe Asp Glu Phe  
225 230 235 240

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaactttc tgttatcccc tctttctctt attctctctc tctcgctatc tctccctctt  | 60  |
| aaAgtttttt tttaaaacag actctccctc taagttattc ggtcgcaatt aaaaaagaaa  | 120 |
| acaaaatctt tataaatttt gattttctct ttttcaccgc attattttga tttgactgtt  | 180 |
| ttacgacagt caatatttca attttattat tgggtgctga cgtggcatgc atccaataga  | 240 |
| gtatcaccat gaacacccaa acgatgcgtc ttccccacgc tcgcgttcta acggcggata  | 300 |
| agcgcaaaga acgagacgcc ttcatctcct ccgtcaccga taatccgcgc gaaatcgcca  | 360 |
| agtttccctc tccgccgcct aaacttggtc ctccgcgcgt taatcccatt tccaagaaat  | 420 |
| cttcaaccgc agcagccgag ccgatcggct cgaaccaact gatgttagcc ggttatctga  | 480 |
| gccacgagta cctcacccaa ggcacactct tcggagagca atggaaccag gctcgagccc  | 540 |
| aagccgagtc cagtaagata aagccgagcc atactgttga gccggctgag gaatgtgagc  | 600 |
| cgaacggaa gaggtatagg gaggttgcta atcttctcgc gtcagatggg gcccaactgc   | 660 |
| ccggcatcgt caatcctgcc cagcttgccc gatttctcaa actgtgatcg gcgtaatccg  | 720 |
| gtgtccacgt ggagacagat cattgggtctg tcgtccggca agcgagacag ccttaaaacc | 780 |
| gaaaccttct tctctctctt tttttttcaa atgtttttt agaatcctct ctgtaaagct   | 840 |
| gactcgctcg ctctctcttc tcatcatcgt ctctctcgga aatcgactga gaaaatttag  | 900 |
| ggtttgttgt tgaggtagat gtcctctttt tgtacatcag aaatatcaat tagccaatgg  | 960 |
| attatgtttt cagatc                                                  |     |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Asn Thr Lys Thr Met Arg Leu Pro Pro Arg Arg Val Leu Thr Ala  
1 5 10 15  
Asp Lys Arg Lys Glu Arg Asp Ala Phe Ile Ser Ser Val Thr Asp Asn  
20 25 30  
Pro Pro Glu Ile Ala Lys Phe Pro Ser Pro Pro Pro Lys Leu Val Pro  
35 40 45  
Pro Pro Val Asn Pro Ile Ser Lys Lys Ser Ser Thr Ala Ala Ala Glu  
50 55 60  
Pro Ile Gly Ser Asn Gln Leu Met Leu Ala Gly Tyr Leu Ser His Glu  
65 70 75 80  
Tyr Leu Thr Gln Gly Thr Leu Phe Gly Glu Gln Trp Asn Gln Ala Arg  
85 90 95  
Ala Gln Ala Glu Ser Ser Lys Ile Lys Pro Ser His Thr Val Glu Pro  
100 105 110  
Ala Glu Glu Cys Glu Pro Lys Arg Lys Arg Tyr Arg Glu Val Ala Asn  
115 120 125  
Leu Leu Arg Ser Asp Gly Ala Gln Leu Pro Gly Ile Val Asn Pro Ala  
130 135 140  
Gln Leu Ala Arg Phe Leu Lys Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Arg Leu Pro Pro Arg Arg Val Leu Thr Ala Asp Lys Arg Lys Glu  
1 5 10 15  
Arg Asp Ala Phe Ile Ser Ser Val Thr Asp Asn Pro Pro Glu Ile Ala  
20 25 30  
Lys Phe Pro Ser Pro Pro Pro Lys Leu Val Pro Pro Pro Val Asn Pro  
35 40 45  
Ile Ser Lys Lys Ser Ser Thr Ala Ala Ala Glu Pro Ile Gly Ser Asn  
50 55 60  
Gln Leu Met Leu Ala Gly Tyr Leu Ser His Glu Tyr Leu Thr Gln Gly  
65 70 75 80  
Thr Leu Phe Gly Glu Gln Trp Asn Gln Ala Arg Ala Gln Ala Glu Ser  
85 90 95  
Ser Lys Ile Lys Pro Ser His Thr Val Glu Pro Ala Glu Glu Cys Glu  
100 105 110  
Pro Lys Arg Lys Arg Tyr Arg Glu Val Ala Asn Leu Leu Arg Ser Asp  
115 120 125  
Gly Ala Gln Leu Pro Gly Ile Val Asn Pro Ala Gln Leu Ala Arg Phe

130 135 140  
Leu Lys Leu  
145

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Leu Ala Gly Tyr Leu Ser His Glu Tyr Leu Thr Gln Gly Thr Leu  
1 5 10 15  
Phe Gly Glu Gln Trp Asn Gln Ala Arg Ala Gln Ala Glu Ser Ser Lys  
20 25 30  
Ile Lys Pro Ser His Thr Val Glu Pro Ala Glu Glu Cys Glu Pro Lys  
35 40 45  
Arg Lys Arg Tyr Arg Glu Val Ala Asn Leu Leu Arg Ser Asp Gly Ala  
50 55 60  
Gln Leu Pro Gly Ile Val Asn Pro Ala Gln Leu Ala Arg Phe Leu Lys  
65 70 75 80  
Leu

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

agccgatttc tagattctcc tccaccacca ttttaccctt cttttaaatt ccttccttca 60  
atcaaaatta gaattatttc tcaaacctct tctttatata ctaaaacgtc tcacatgaac 120  
aagaagaata aatagaaaca aagaagatga acaagaacaa gattgatgtt aagatcgaga 180  
cgaagaaagg atcgatggat gagtggcstg agccaatcgt ccgagtcag tccttagccg 240  
agagcaacct ctctctctcc cccgaccgtt acatcaaacc agcgtctcta cgccccacca 300  
cgaccgaaga cgctcctacc gcgaccaaca tcccaatcat agaccttgaa ggactctctc 360  
ggaagaaggg ttgtctgatg acgtcatcat ggctcggata tcggaggctt gccgtgggtg 420  
gggttcttc caggtgggtg accacggggg caaacgggag ctgatggacg cggctaggga 480  
saattggaga gagtttttcc atatgccggt taatgccaaa gagacttact caaactcacc 540  
aagaacctac gaaggctatg gaagtagact aggtggtgag aaaagcaagt cttgattgga 600  
gtgattatta ctttctccat cttcttctcc atcatttgaa agacttcaac aagtggcctt 660  
cttttctcc caccataaga gaagtgatcg atgaatacgg cgaagagcta gtgaagctaa 720  
gtgggagaat tatgagggtg ttatcgacaa acttgggact aaaagaggat aagtttcaag 780  
aagcatttgg aggtgaaaac attggggcgt gtttgagggt taattattac ccaaaatgcc 840  
ctcgaccggt gctggctctt ggtctctctc cacactccga tcctggcggg atgaccattc 900  
tcttaccgga cgatcaagtc ttcggtctcc aggttcgtaa agatgacacg tggatcaccg 960  
tcaagcctca tcccctgct ttcctcgta atattggtga tcaaatacag atactaagca 1020  
actcaacata caagagtgtg gagcatagag tgatagtga ctcggacaag gagagagttt 1080  
cacttgctt cttctacaat cctaaaagcg atattTccga tccaaccatt acaagaactt 1140  
gtatcaactc ataactctcc tttataacct cccatgacct ttgatcagta tagactcttt 1200  
atcagaactc aaggtccaca aggcaaatac catgttgaat ctcatatttc tcctcgttga 1260  
ttgtttttct tttatttctt cccttaaaga aaaattaatg ttttg



(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1565788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Lys Asn Lys Ile Asp Val Lys Ile Glu Thr Lys Lys Gly Ser  
1 5 10 15  
Met Asp Glu Trp Xaa Glu Pro Ile Val Arg Val Gln Ser Leu Ala Glu  
20 25 30  
Ser Asn Leu Ser Ser Leu Pro Asp Arg Tyr Ile Lys Pro Ala Ser Leu  
35 40 45  
Arg Pro Thr Thr Thr Glu Asp Ala Pro Thr Ala Thr Asn Ile Pro Ile  
50 55 60  
Ile Asp Leu Glu Gly Leu Ser Arg Lys Lys Gly Cys Leu Met Thr Ser  
65 70 75 80  
Ser Trp Leu Gly Tyr Arg Arg Leu Ala Val Gly Gly Gly Ser Ser Arg  
85 90 95  
Trp

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1565789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met Arg Val Leu Ser Thr Asn Leu Gly Leu Lys Glu Asp Lys Phe Gln  
1 5 10 15  
Glu Ala Phe Gly Gly Glu Asn Ile Gly Ala Cys Leu Arg Val Asn Tyr  
20 25 30  
Tyr Pro Lys Cys Pro Arg Pro Val Leu Ala Leu Gly Leu Ser Pro His  
35 40 45  
Ser Asp Pro Gly Gly Met Thr Ile Leu Leu Pro Asp Asp Gln Val Phe  
50 55 60  
Gly Leu Gln Val Arg Lys Asp Asp Thr Trp Ile Thr Val Lys Pro His  
65 70 75 80  
Pro His Ala Phe Ile Val Asn Ile Gly Asp Gln Ile Gln Ile Leu Ser  
85 90 95  
Asn Ser Thr Tyr Lys Ser Val Glu His Arg Val Ile Val Asn Ser Asp  
100 105 110  
Lys Glu Arg Val Ser Leu Ala Phe Phe Tyr Asn Pro Lys Ser Asp Ile  
115 120 125  
Ser Asp Pro Thr Ile Thr Arg Thr Cys Ile Asn Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
Met Thr Ile Leu Leu Pro Asp Asp Gln Val Phe Gly Leu Gln Val Arg
1 5 10 15
Lys Asp Asp Thr Trp Ile Thr Val Lys Pro His Pro His Ala Phe Ile
 20 25 30
Val Asn Ile Gly Asp Gln Ile Gln Ile Leu Ser Asn Ser Thr Tyr Lys
 35 40 45
Ser Val Glu His Arg Val Ile Val Asn Ser Asp Lys Glu Arg Val Ser
 50 55 60
Leu Ala Phe Phe Tyr Asn Pro Lys Ser Asp Ile Ser Asp Pro Thr Ile
65 70 75 80
Thr Arg Thr Cys Ile Asn Ser
 85
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1648 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1648  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
acatgtttctc tccgcctga atcatgtcaa tctcccacaa aagatctttg ataaaaagaa 60
ttgagcccta attccttgat gtttggtgaa tgcacagca gataaaaaaa aatggtggtg 120
gcggagctcg gcggccggat aaccgcgcc atacagcaga tgaacaatgt gacaataatc 180
gatgaaaagg ttttgaatga tttcttaaac gagattactc gcgctttgct ccagtccgat 240
gtttcttttg gccttggtga aaagatgcag accaatatta agaagatcgt taacctcgac 300
gatctagcag ctggccacaa caaacgcctg atcatcgagc aggcctatct caaggaactc 360
tgtaggatgc tggatccagg aaagcctgcc tttgccccca aaaaggccaa acctagtgtg 420
gtgatgttcg tcggtttaca aggtgctgga aaaaccacaa catgtaccaa gtatgcttac 480
tatcatcaga agaaagggtg caaagcagct ctagtgtgtg cggatacttt cagggccggg 540
gcttttgatc agctgaaaca gaatgccacc aaggctaaga tcccctttta tggaagctac 600
acagaatccg atcctgtgaa aattgctggt gagggagtgt ataggttcaa gaaagaaaag 660
tgtgatctta ttattgttga caccagtggc cgccataaac aagcagcttc tctctttgaa 720
gaaatgcgtc aagttgctga agcaacggaa ccagatcttg ttatatttgt tatggatagc 780
agtattggtc aagctgcatt tgaacaagct gaagctttta aggaaactgt atctgttgga 840
gctgtaatta ttactaagat ggacggccat gccaaggagag gtggtgctct tagcgctggt 900
gcagctacaa aaagtccgtg gatattcatt ggaacaggag agcatatgga tgagtttgaa 960
gtgtttgacg ttaaaccatt tgtcagcgt ctcttaggaa agggtgattg gtcctggactc 1020
gtggataaac tacaagaggt ggtacctaaa gatctacaga atgaacttgt agaaaatctc 1080
tctcagggtg actttacgtt gagaagtatg tacgaccagt tccagtgtct tctgcggatt 1140
ccacttaatc agcttttctc gatgctgcct ggaattagtg ctgaaatgat gccgaaagga 1200
catggtgaag aaagccgagt gaagatgaag cgatacatga caatgatgga ttctatgaca 1260
aataaagaac ttgacagccc aaacccaaag atttttaacg agtcaaggat aatgaggata 1320
gcgagagggg cagggagggt agtaagagaa gtgatggaga tgttggaaga gtacaagagg 1380
atagcaaaga caatgaaagg gatcaagatc ccaaagaacg gagacatgag caaggtcata 1440
ccgcctcaga tctaataaca gatgggcggc atgagcggtc tgcagagtct catgaagcag 1500
atgggttcgg ctaaggacat gatgggaatg tttggtggcg gaggcaagta gtttctatct 1560
ttcttgCaca cagtgcacgg agggcagtggt taaaactttt gttacatact gtattagtac 1620
cttataattt taacacatcc taacgacc
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..479  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565800  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Ala | Glu | Leu | Gly | Gly | Arg | Ile | Thr | Arg | Ala | Ile | Gln | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Asn | Asn | Val | Thr | Ile | Ile | Asp | Glu | Lys | Val | Leu | Asn | Asp | Phe | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Glu | Ile | Thr | Arg | Ala | Leu | Leu | Gln | Ser | Asp | Val | Ser | Phe | Gly | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Glu | Lys | Met | Gln | Thr | Asn | Ile | Lys | Lys | Ile | Val | Asn | Leu | Asp | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Ala | Gly | His | Asn | Lys | Arg | Leu | Ile | Ile | Glu | Gln | Ala | Ile | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Glu | Leu | Cys | Arg | Met | Leu | Asp | Pro | Gly | Lys | Pro | Ala | Phe | Ala | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Lys | Lys | Ala | Lys | Pro | Ser | Val | Val | Met | Phe | Val | Gly | Leu | Gln | Gly | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gly | Lys | Thr | Thr | Thr | Cys | Thr | Lys | Tyr | Ala | Tyr | Tyr | His | Gln | Lys | Lys |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Tyr | Lys | Ala | Ala | Leu | Val | Cys | Ala | Asp | Thr | Phe | Arg | Ala | Gly | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Asp | Gln | Leu | Lys | Gln | Asn | Ala | Thr | Lys | Ala | Lys | Ile | Pro | Phe | Tyr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Gly | Ser | Tyr | Thr | Glu | Ser | Asp | Pro | Val | Lys | Ile | Ala | Val | Glu | Gly | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Asp | Arg | Phe | Lys | Lys | Glu | Lys | Cys | Asp | Leu | Ile | Ile | Val | Asp | Thr | Ser |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Gly | Arg | His | Lys | Gln | Ala | Ala | Ser | Leu | Phe | Glu | Glu | Met | Arg | Gln | Val |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Glu | Ala | Thr | Glu | Pro | Asp | Leu | Val | Ile | Phe | Val | Met | Asp | Ser | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Gly | Gln | Ala | Ala | Phe | Glu | Gln | Ala | Glu | Ala | Phe | Lys | Glu | Thr | Val |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Ser | Val | Gly | Ala | Val | Ile | Ile | Thr | Lys | Met | Asp | Gly | His | Ala | Lys | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Gly | Gly | Ala | Leu | Ser | Ala | Val | Ala | Ala | Thr | Lys | Ser | Pro | Val | Ile | Phe |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Ile | Gly | Thr | Gly | Glu | His | Met | Asp | Glu | Phe | Glu | Val | Phe | Asp | Val | Lys |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Pro | Phe | Val | Ser | Arg | Leu | Leu | Gly | Lys | Gly | Asp | Trp | Ser | Gly | Leu | Val |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Asp | Lys | Leu | Gln | Glu | Val | Val | Pro | Lys | Asp | Leu | Gln | Asn | Glu | Leu | Val |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Glu | Asn | Leu | Ser | Gln | Gly | Asn | Phe | Thr | Leu | Arg | Ser | Met | Tyr | Asp | Gln |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Phe | Gln | Cys | Ser | Leu | Arg | Ile | Pro | Leu | Asn | Gln | Leu | Phe | Ser | Met | Leu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Pro | Gly | Ile | Ser | Ala | Glu | Met | Met | Pro | Lys | Gly | His | Gly | Glu | Glu | Ser |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Arg | Val | Lys | Met | Lys | Arg | Tyr | Met | Thr | Met | Met | Asp | Ser | Met | Thr | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Glu | Leu | Asp | Ser | Pro | Asn | Pro | Lys | Ile | Phe | Asn | Glu | Ser | Arg | Ile |
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |     | 400 |
| Met | Arg | Ile | Ala | Arg | Gly | Ser | Gly | Arg | Leu | Val | Arg | Glu | Val | Met | Glu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 405 |     | 410 |     | 415 |     |     |     |     |     |     |     |     |     |     |
| Met | Leu | Glu | Glu | Tyr | Lys | Arg | Ile | Ala | Lys | Thr | Met | Lys | Gly | Ile | Lys |
|     | 420 |     |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ile | Pro | Lys | Asn | Gly | Asp | Met | Ser | Lys | Val | Ile | Pro | Pro | Gln | Met | Leu |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Lys | Gln | Met | Gly | Gly | Met | Ser | Gly | Leu | Gln | Ser | Leu | Met | Lys | Gln | Met |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Ser | Ala | Lys | Asp | Met | Met | Gly | Met | Phe | Gly | Gly | Gly | Gly | Lys |     |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1565801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Asn | Val | Ile | Ile | Asp | Glu | Lys | Val | Leu | Asn | Asp | Phe | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Glu | Ile | Thr | Arg | Ala | Leu | Leu | Gln | Ser | Asp | Val | Ser | Phe | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Val | Glu | Lys | Met | Gln | Thr | Asn | Ile | Lys | Lys | Ile | Val | Asn | Leu | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Leu | Ala | Ala | Gly | His | Asn | Lys | Arg | Leu | Ile | Ile | Glu | Gln | Ala | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Lys | Glu | Leu | Cys | Arg | Met | Leu | Asp | Pro | Gly | Lys | Pro | Ala | Phe | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Lys | Ala | Lys | Pro | Ser | Val | Val | Met | Phe | Val | Gly | Leu | Gln | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |
| Gly | Lys | Thr | Thr | Thr | Cys | Thr | Lys | Tyr | Ala | Tyr | Tyr | His | Gln | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Gly | Tyr | Lys | Ala | Ala | Leu | Val | Cys | Ala | Asp | Thr | Phe | Arg | Ala | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Phe | Asp | Gln | Leu | Lys | Gln | Asn | Ala | Thr | Lys | Ala | Lys | Ile | Pro | Phe |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Gly | Ser | Tyr | Thr | Glu | Ser | Asp | Pro | Val | Lys | Ile | Ala | Val | Glu | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Asp | Arg | Phe | Lys | Lys | Glu | Lys | Cys | Asp | Leu | Ile | Ile | Val | Asp | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Arg | His | Lys | Gln | Ala | Ala | Ser | Leu | Phe | Glu | Glu | Met | Arg | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Ala | Glu | Ala | Thr | Glu | Pro | Asp | Leu | Val | Ile | Phe | Val | Met | Asp | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Ile | Gly | Gln | Ala | Ala | Phe | Glu | Gln | Ala | Glu | Ala | Phe | Lys | Glu | Thr |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Ser | Val | Gly | Ala | Val | Ile | Ile | Thr | Lys | Met | Asp | Gly | His | Ala | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Gly | Gly | Ala | Leu | Ser | Ala | Val | Ala | Ala | Thr | Lys | Ser | Pro | Val | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |
| Ile | Gly | Thr | Gly | Glu | His | Met | Asp | Glu | Phe | Glu | Val | Phe | Asp | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Pro | Phe | Val | Ser | Arg | Leu | Leu | Gly | Lys | Gly | Asp | Trp | Ser | Gly | Leu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Asp | Lys | Leu | Gln | Glu | Val | Val | Pro | Lys | Asp | Leu | Gln | Asn | Glu | Leu |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |
| Glu | Asn | Leu | Ser | Gln | Gly | Asn | Phe | Thr | Leu | Arg | Ser | Met | Tyr | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |

Phe Gln Cys Ser Leu Arg Ile Pro Leu Asn Gln Leu Phe Ser Met Leu  
325 330 335  
Pro Gly Ile Ser Ala Glu Met Met Pro Lys Gly His Gly Glu Glu Ser  
340 345 350  
Arg Val Lys Met Lys Arg Tyr Met Thr Met Met Asp Ser Met Thr Asn  
355 360 365  
Lys Glu Leu Asp Ser Pro Asn Pro Lys Ile Phe Asn Glu Ser Arg Ile  
370 375 380  
Met Arg Ile Ala Arg Gly Ser Gly Arg Leu Val Arg Glu Val Met Glu  
385 390 395 400  
Met Leu Glu Glu Tyr Lys Arg Ile Ala Lys Thr Met Lys Gly Ile Lys  
405 410 415  
Ile Pro Lys Asn Gly Asp Met Ser Lys Val Ile Pro Pro Gln Met Leu  
420 425 430  
Lys Gln Met Gly Gly Met Ser Gly Leu Gln Ser Leu Met Lys Gln Met  
435 440 445  
Gly Ser Ala Lys Asp Met Met Gly Met Phe Gly Gly Gly Lys  
450 455 460

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1565802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Gln Thr Asn Ile Lys Lys Ile Val Asn Leu Asp Asp Leu Ala Ala  
1 5 10 15  
Gly His Asn Lys Arg Leu Ile Ile Glu Gln Ala Ile Phe Lys Glu Leu  
20 25 30  
Cys Arg Met Leu Asp Pro Gly Lys Pro Ala Phe Ala Pro Lys Lys Ala  
35 40 45  
Lys Pro Ser Val Val Met Phe Val Gly Leu Gln Gly Ala Gly Lys Thr  
50 55 60  
Thr Thr Cys Thr Lys Tyr Ala Tyr Tyr His Gln Lys Lys Gly Tyr Lys  
65 70 75 80  
Ala Ala Leu Val Cys Ala Asp Thr Phe Arg Ala Gly Ala Phe Asp Gln  
85 90 95  
Leu Lys Gln Asn Ala Thr Lys Ala Lys Ile Pro Phe Tyr Gly Ser Tyr  
100 105 110  
Thr Glu Ser Asp Pro Val Lys Ile Ala Val Glu Gly Val Asp Arg Phe  
115 120 125  
Lys Lys Glu Lys Cys Asp Leu Ile Ile Val Asp Thr Ser Gly Arg His  
130 135 140  
Lys Gln Ala Ala Ser Leu Phe Glu Glu Met Arg Gln Val Ala Glu Ala  
145 150 155 160  
Thr Glu Pro Asp Leu Val Ile Phe Val Met Asp Ser Ser Ile Gly Gln  
165 170 175  
Ala Ala Phe Glu Gln Ala Glu Ala Phe Lys Glu Thr Val Ser Val Gly  
180 185 190  
Ala Val Ile Ile Thr Lys Met Asp Gly His Ala Lys Gly Gly Gly Ala  
195 200 205  
Leu Ser Ala Val Ala Ala Thr Lys Ser Pro Val Ile Phe Ile Gly Thr  
210 215 220  
Gly Glu His Met Asp Glu Phe Glu Val Phe Asp Val Lys Pro Phe Val  
225 230 235 240  
Ser Arg Leu Leu Gly Lys Gly Asp Trp Ser Gly Leu Val Asp Lys Leu

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(2) INFORMATION FOR SEO ID NO:89:

(A) LENGTH: 1687 base pairs

(C) STRANDEDNESS: sing

MOLECULE TYPE: DNA (α

FEATURE:

(A) NAME / KEY: -

(A) NAME/REF.

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:89:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
cagaaac caaatctcta tctctctcca ttagagcttg

|              |             |            |             |            |             |      |
|--------------|-------------|------------|-------------|------------|-------------|------|
| gggaacaaac   | caaatctctc  | tctctctcca | ttagagcttg  | aagcagccat | agcctaacaa  | 80   |
| aaccttcaac   | aatggcttca  | atggctgccg | tcttaagcaa  | aactccattc | ctctctcaac  | 120  |
| cactaaccaa   | atcatctcca  | aactccgatc | tccccctcgc  | cgcggtttcc | ttcccttcca  | 180  |
| aatccctacg   | ccgcgcgcgt  | ggatcaatcc | gagccggatt  | aatcgctccc | gacgggtggt  | 240  |
| agcttgtaga   | gctcatcgtg  | gaagagccaa | agcgacgaga  | gaagaaacac | gagggcgccg  | 300  |
| atttgccacg   | tgttgagctg  | acggcgattg | acttgcaatg  | gatgcattga | ttaagcgaag  | 360  |
| gctggacaag   | tccactcgga  | ggttttatga | gagaatccga  | gttcctccaa | actcttctatt | 420  |
| ttaaactcgt   | acgtcttgac  | gacggctccg | tcgttaacat  | gtccgtgcct | attgttctcg  | 480  |
| ctattgacga   | tgaacaaaaa  | gcagctatcg | gcgagctcac  | acgtgtcgct | cttttcaatt  | 540  |
| ccgatggtaa   | ccccgtctct  | atcctcagcg | atattgagat  | ttataagcat | ccaaaggaag  | 600  |
| aaaggatagc   | tagaacatgg  | ggtacgacgg | ctccagggtt  | gccttacgta | gacgaggcga  | 660  |
| taactaatgc   | tggaaactgg  | ctcattgggg | gtgatcttga  | ggttcttgag | ccagtgaagt  | 720  |
| acaatgatgg   | gcttgatcgt  | ttcaggcttt | cgctgctga   | gttacgtaaa | gagttggaga  | 780  |
| agcgtaatgc   | ggatgcggtg  | tttgctttcc | agctgaggaa  | tcctgttcat | aatgggtcatg | 840  |
| ctcttcttat   | gactgatact  | cgtaggagac | ttcttgagat  | gggttacaaa | aaccctattc  | 900  |
| ttttgcttca   | tccggttaggt | gggtttacaa | aggctgatga  | tgttccttta | gattggagga  | 960  |
| tgaagcaaca   | cgaaacggtt  | ctagaggatg | gtgttctcga  | tccggagact | acagtggttt  | 1020 |
| ctgactattccc | gtcacctatg  | cattacgctg | gtccaaccga  | agtgagctgg | cacgcaaagg  | 1080 |
| ctagaatcaa   | tgctggtgct  | aacttttaca | ttgtgggtcg  | tgatcctgct | gggatgggtc  | 1140 |
| atccagtaga   | gaaacgtgat  | ctttacgatg | ctgatcatgg  | aaagaaagta | ctaagcatgg  | 1200 |
| caccaggact   | cgaacgactc  | aacatccttc | Ctttcagggt  | tgctgcata  | gacaagacgc  | 1260 |
| aaggcaagat   | ggctttcttc  | gatccctcga | ggcctcaaga  | tttcttgttc | atctccggca  | 1320 |
| ctaagatgcg   | cacattggca  | aagaacaacg | aaaaccctgc  | agcaggtttt | atgtgccacg  | 1380 |
| gtggatggaa   | agttctcggt  | gattactatg | agaaccttgac | tccggcggtg | aatggttcag  | 1440 |
| taccgaagtg   | ggttccggtg  | taagacaaaa | ctgttcgttt  | caaattgtaa | cgtttggtgt  | 1500 |
| qtgaagcctt   | gtagcaacaa  | tcattgttgt | attgggagag  | aagcctatgt | ataatctggc  | 1560 |

ttgacctttt tccaaataaa atacagaaga aaaaaagact gtttttcggtt tgcaagataa 1620  
tttacgaaac ttgtaatat tgggcctcaa actttgtacc atattaatga aacgattgtg 1680  
tttacat

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1565811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Met | Ala | Ala | Val | Leu | Ser | Lys | Thr | Pro | Phe | Leu | Ser | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Thr | Lys | Ser | Ser | Pro | Asn | Ser | Asp | Leu | Pro | Phe | Ala | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Pro | Ser | Lys | Ser | Leu | Arg | Arg | Arg | Val | Gly | Ser | Ile | Arg | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Ile | Ala | Pro | Asp | Gly | Gly | Lys | Leu | Val | Glu | Leu | Ile | Val | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Pro | Lys | Arg | Arg | Glu | Lys | Lys | His | Glu | Ala | Ala | Asp | Leu | Pro | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Glu | Leu | Thr | Ala | Ile | Asp | Leu | Gln | Trp | Met | His | Val | Leu | Ser | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Trp | Thr | Ser | Pro | Leu | Gly | Gly | Phe | Met | Arg | Glu | Ser | Glu | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Thr | Leu | His | Phe | Asn | Ser | Leu | Arg | Leu | Asp | Asp | Gly | Ser | Val | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Met | Ser | Val | Pro | Ile | Val | Leu | Ala | Ile | Asp | Asp | Glu | Gln | Lys | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Arg | Ile | Gly | Glu | Ser | Thr | Arg | Val | Ala | Leu | Phe | Asn | Ser | Asp | Gly | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Val | Ser | Ile | Leu | Ser | Asp | Ile | Glu | Ile | Tyr | Lys | His | Pro | Lys | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Arg | Ile | Ala | Arg | Thr | Trp | Gly | Thr | Thr | Ala | Pro | Gly | Leu | Pro | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Asp | Glu | Ala | Ile | Thr | Asn | Ala | Gly | Asn | Trp | Leu | Ile | Gly | Gly | Asp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Glu | Val | Leu | Glu | Pro | Val | Lys | Tyr | Asn | Asp | Gly | Leu | Asp | Arg | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Leu | Ser | Pro | Ala | Glu | Leu | Arg | Lys | Glu | Leu | Glu | Lys | Arg | Asn | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Ala | Val | Phe | Ala | Phe | Gln | Leu | Arg | Asn | Pro | Val | His | Asn | Gly | His |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Leu | Met | Thr | Asp | Thr | Arg | Arg | Arg | Leu | Leu | Glu | Met | Gly | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Asn | Pro | Ile | Leu | Leu | Leu | His | Pro | Leu | Gly | Gly | Phe | Thr | Lys | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Asp | Val | Pro | Leu | Asp | Trp | Arg | Met | Lys | Gln | His | Glu | Lys | Val | Leu |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Glu | Asp | Gly | Val | Leu | Asp | Pro | Glu | Thr | Thr | Val | Val | Ser | Ile | Phe | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ser | Pro | Met | His | Tyr | Ala | Gly | Pro | Thr | Glu | Val | Gln | Trp | His | Ala | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Arg | Ile | Asn | Ala | Gly | Ala | Asn | Phe | Tyr | Ile | Val | Gly | Arg | Asp | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Gly | Met | Gly | His | Pro | Val | Glu | Lys | Arg | Asp | Leu | Tyr | Asp | Ala | Asp |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |

His Gly Lys Lys Val Leu Ser Met Ala Pro Gly Leu Glu Arg Leu Asn  
370 375 380  
Ile Leu Pro Phe Arg Val Ala Ala Tyr Asp Lys Thr Gln Gly Lys Met  
385 390 395 400  
Ala Phe Phe Asp Pro Ser Arg Pro Gln Asp Phe Leu Phe Ile Ser Gly  
405 410 415  
Thr Lys Met Arg Thr Leu Ala Lys Asn Asn Glu Asn Pro Pro Asp Gly  
420 425 430  
Phe Met Cys Pro Gly Gly Trp Lys Val Leu Val Asp Tyr Tyr Glu Ser  
435 440 445  
Leu Thr Pro Ala Gly Asn Gly Arg Leu Pro Glu Val Val Pro Val  
450 455 460

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1565812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ala Val Leu Ser Lys Thr Pro Phe Leu Ser Gln Pro Leu Thr  
1 5 10 15  
Lys Ser Ser Pro Asn Ser Asp Leu Pro Phe Ala Ala Val Ser Phe Pro  
20 25 30  
Ser Lys Ser Leu Arg Arg Arg Val Gly Ser Ile Arg Ala Gly Leu Ile  
35 40 45  
Ala Pro Asp Gly Gly Lys Leu Val Glu Leu Ile Val Glu Glu Pro Lys  
50 55 60  
Arg Arg Glu Lys Lys His Glu Ala Ala Asp Leu Pro Arg Val Glu Leu  
65 70 75 80  
Thr Ala Ile Asp Leu Gln Trp Met His Val Leu Ser Glu Gly Trp Thr  
85 90 95  
Ser Pro Leu Gly Gly Phe Met Arg Glu Ser Glu Phe Leu Gln Thr Leu  
100 105 110  
His Phe Asn Ser Leu Arg Leu Asp Asp Gly Ser Val Val Asn Met Ser  
115 120 125  
Val Pro Ile Val Leu Ala Ile Asp Asp Glu Gln Lys Ala Arg Ile Gly  
130 135 140  
Glu Ser Thr Arg Val Ala Leu Phe Asn Ser Asp Gly Asn Pro Val Ser  
145 150 155 160  
Ile Leu Ser Asp Ile Glu Ile Tyr Lys His Pro Lys Glu Glu Arg Ile  
165 170 175  
Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu  
180 185 190  
Ala Ile Thr Asn Ala Gly Asn Trp Leu Ile Gly Gly Asp Leu Glu Val  
195 200 205  
Leu Glu Pro Val Lys Tyr Asn Asp Gly Leu Asp Arg Phe Arg Leu Ser  
210 215 220  
Pro Ala Glu Leu Arg Lys Glu Leu Glu Lys Arg Asn Ala Asp Ala Val  
225 230 235 240  
Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu  
245 250 255  
Met Thr Asp Thr Arg Arg Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro  
260 265 270  
Ile Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val  
275 280 285  
Pro Leu Asp Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Asp Gly



290 295 300  
Val Leu Asp Pro Glu Thr Thr Val Val Ser Ile Phe Pro Ser Pro Met  
305 310 315 320  
His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile  
325 330 335  
Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met  
340 345 350  
Gly His Pro Val Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys  
355 360 365  
Lys Val Leu Ser Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro  
370 375 380  
Phe Arg Val Ala Ala Tyr Asp Lys Thr Gln Gly Lys Met Ala Phe Phe  
385 390 395 400  
Asp Pro Ser Arg Pro Gln Asp Phe Leu Phe Ile Ser Gly Thr Lys Met  
405 410 415  
Arg Thr Leu Ala Lys Asn Asn Glu Asn Pro Pro Asp Gly Phe Met Cys  
420 425 430  
Pro Gly Gly Trp Lys Val Leu Val Asp Tyr Tyr Glu Ser Leu Thr Pro  
435 440 445  
Ala Gly Asn Gly Arg Leu Pro Glu Val Val Pro Val  
450 455 460

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..373

(D) OTHER INFORMATION: / Ceres Seq. ID 1565813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met His Val Leu Ser Glu Gly Trp Thr Ser Pro Leu Gly Gly Phe Met  
1 5 10 15  
Arg Glu Ser Glu Phe Leu Gln Thr Leu His Phe Asn Ser Leu Arg Leu  
20 25 30  
Asp Asp Gly Ser Val Val Asn Met Ser Val Pro Ile Val Leu Ala Ile  
35 40 45  
Asp Asp Glu Gln Lys Ala Arg Ile Gly Glu Ser Thr Arg Val Ala Leu  
50 55 60  
Phe Asn Ser Asp Gly Asn Pro Val Ser Ile Leu Ser Asp Ile Glu Ile  
65 70 75 80  
Tyr Lys His Pro Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr Thr  
85 90 95  
Ala Pro Gly Leu Pro Tyr Val Asp Glu Ala Ile Thr Asn Ala Gly Asn  
100 105 110  
Trp Leu Ile Gly Gly Asp Leu Glu Val Leu Glu Pro Val Lys Tyr Asn  
115 120 125  
Asp Gly Leu Asp Arg Phe Arg Leu Ser Pro Ala Glu Leu Arg Lys Glu  
130 135 140  
Leu Glu Lys Arg Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg Asn  
145 150 155 160  
Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Arg Arg  
165 170 175  
Leu Leu Glu Met Gly Tyr Lys Asn Pro Ile Leu Leu Leu His Pro Leu  
180 185 190  
Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Asp Trp Arg Met Lys  
195 200 205  
Gln His Glu Lys Val Leu Glu Asp Gly Val Leu Asp Pro Glu Thr Thr  
210 215 220

Val Val Ser Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr Glu  
225 230 235 240  
Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe Tyr  
245 250 255  
Ile Val Gly Arg Asp Pro Ala Gly Met Gly His Pro Val Glu Lys Arg  
260 265 270  
Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala Pro  
275 280 285  
Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Arg Val Ala Ala Tyr Asp  
290 295 300  
Lys Thr Gln Gly Lys Met Ala Phe Phe Asp Pro Ser Arg Pro Gln Asp  
305 310 315 320  
Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn Asn  
325 330 335  
Glu Asn Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val Leu  
340 345 350  
Val Asp Tyr Tyr Glu Ser Leu Thr Pro Ala Gly Asn Gly Arg Leu Pro  
355 360 365  
Glu Val Val Pro Val  
370

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..747
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| ctcttcatta  | tcttcaaaat | cgctcgagag | tgagaactct | actcttcttc  | ttcttcctcc | 60  |
| gccatagcta  | caatgcttag | tctctcaata | gctacgccgg | ggacggCggc  | gatttttcgt | 120 |
| agaggaactg  | cttcggcgac | ttcaacttcg | tcttcattcc | atggtgtcag  | aatccagcac | 180 |
| caggttttctg | ctcgcgtccc | cgcggcggcg | acgatatcgt | cgtcgtctcc  | taaaccgtcg | 240 |
| gtggtgatga  | tgtcgaaaag | agaggcggaa | ttgaaagaga | taagatcgaa  | gacgacggag | 300 |
| cagttacaag  | aggaggttgt | tgaccttaaa | ggtgagctct | ttatgcttcg  | tctccagaaa | 360 |
| toggcaagga  | atgagttcaa | atctagcGac | tttcgtcgtg | tgaagaaaaca | agttgctcgg | 420 |
| atgttgacgg  | ttaaaagaga | gagggagatc | aaagaaggga | taaagaaaag  | gttgtcgagg | 480 |
| aaacttgaca  | gacaatggaa | gaaaagcata | gtaccaagac | cacctccgtc  | tctgaagaaa | 540 |
| cttcaagaag  | aagaagctgc | agaagaaGca | gctgaagctg | ctaaatctgc  | ttgaaaaaac | 600 |
| ccgctattga  | tttatggtct | cttccttggt | gtttcctcga | gatgttgta   | atctctgtta | 660 |
| tttgttgctg  | aaccatcttg | tatttgtttt | tcttttggtg | taaacacttt  | ccttatcaag | 720 |
| tagtttacat  | gaatccctta | aagattg    |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Leu | Ser | Ile | Ala | Thr | Pro | Gly | Thr | Ala | Ala | Ile | Phe | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Thr | Ala | Ser | Ala | Thr | Ser | Thr | Ser | Ser | Ser | Phe | His | Gly | Val |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |

Arg Ile Gln His Gln Val Ser Ala Arg Val Pro Ala Ala Ala Thr Ile  
35 40 45  
Ser Ser Ser Ser Pro Lys Pro Ser Val Val Met Met Ser Lys Arg Glu  
50 55 60  
Ala Glu Leu Lys Glu Ile Arg Ser Lys Thr Thr Glu Gln Leu Gln Glu  
65 70 75 80  
Glu Val Val Asp Leu Lys Gly Glu Leu Phe Met Leu Arg Leu Gln Lys  
85 90 95  
Ser Ala Arg Asn Glu Phe Lys Ser Ser Asp Phe Arg Arg Met Lys Lys  
100 105 110  
Gln Val Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Lys Glu  
115 120 125  
Gly Ile Lys Lys Arg Leu Ser Arg Lys Leu Asp Arg Gln Trp Lys Lys  
130 135 140  
Ser Ile Val Pro Arg Pro Pro Pro Ser Leu Lys Lys Leu Gln Glu Glu  
145 150 155 160  
Glu Ala Ala Glu Glu Ala Ala Glu Ala Ala Lys Ser Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1565818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Met Ser Lys Arg Glu Ala Glu Leu Lys Glu Ile Arg Ser Lys Thr  
1 5 10 15  
Thr Glu Gln Leu Gln Glu Glu Val Val Asp Leu Lys Gly Glu Leu Phe  
20 25 30  
Met Leu Arg Leu Gln Lys Ser Ala Arg Asn Glu Phe Lys Ser Ser Asp  
35 40 45  
Phe Arg Arg Met Lys Lys Gln Val Ala Arg Met Leu Thr Val Lys Arg  
50 55 60  
Glu Arg Glu Ile Lys Glu Gly Ile Lys Lys Arg Leu Ser Arg Lys Leu  
65 70 75 80  
Asp Arg Gln Trp Lys Lys Ser Ile Val Pro Arg Pro Pro Pro Ser Leu  
85 90 95  
Lys Lys Leu Gln Glu Glu Glu Ala Ala Glu Glu Ala Ala Glu Ala Ala  
100 105 110  
Lys Ser Ala  
115

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1565819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Ser Lys Arg Glu Ala Glu Leu Lys Glu Ile Arg Ser Lys Thr Thr  
1 5 10 15  
Glu Gln Leu Gln Glu Glu Val Val Asp Leu Lys Gly Glu Leu Phe Met

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Leu Arg Leu Gln Lys Ser Ala Arg Asn Glu Phe Lys Ser Asp Phe     |     |     |
| 35                                                              | 40  | 45  |
| Arg Arg Met Lys Lys Gln Val Ala Arg Met Leu Thr Val Lys Arg Glu |     |     |
| 50                                                              | 55  | 60  |
| Arg Glu Ile Lys Glu Gly Ile Lys Lys Arg Leu Ser Arg Lys Leu Asp |     |     |
| 65                                                              | 70  | 75  |
| Arg Gln Trp Lys Lys Ser Ile Val Pro Arg Pro Pro Pro Ser Leu Lys |     |     |
| 85                                                              | 90  | 95  |
| Lys Leu Gln Glu Glu Glu Ala Ala Glu Glu Ala Ala Glu Ala Lys     |     |     |
| 100                                                             | 105 | 110 |
| Ser Ala                                                         |     |     |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2216

(D) OTHER INFORMATION: / Ceres Seq. ID 1565820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| ggtttttcg   | gatccatcga  | acttcttctc | tcttcttctt  | ctgactcctt  | agccgacgac | 60   |
| acagagaaga  | agaagacgaa  | gacgttggag | agtcacatca  | aagcttaa    | ctttcgtgat | 120  |
| ttattctcct  | ttttcccg    | ttcggattaa | tttttcaa    | tccgacgaaa  | ttcgctatct | 180  |
| tctggtgctt  | gagctgctta  | gctaagtga  | gcagagagag  | tacaattggt  | tatgttttgt | 240  |
| taaattaagg  | agattcttgg  | caaaattctg | aagtagcagc  | agtagctgtg  | ttttgtgttc | 300  |
| atagagaatg  | ggagcagaag  | aatttccgag | tgttccgttc  | aactcaaatg  | caatggacaa | 360  |
| cgctgaatat  | accgacacag  | atgttggtgt | tgcggttaga  | aaggcccttg  | catctgtcca | 420  |
| aaatggagat  | accgacgatt  | atagtcagct | taaaacagtg  | atgtgcctta  | cagaagacgc | 480  |
| tgattttcgat | gcagtggcac  | agcttgagac | agtcttgaaa  | agtctatcag  | tttccgttgc | 540  |
| ttggatagat  | ttagttcatc  | ataaagatct | tcttgaagct  | atttttaaga  | tgagcttgtg | 600  |
| gtatcatagt  | cacagacctt  | gtgtaatgga | tgcattgggtg | gacctaatca  | tatcactggc | 660  |
| cgctactagt  | ggaaaatatc  | tggatccttg | tttgaatatg  | ctcgtaagaa  | atttcagtca | 720  |
| acctactttt  | aagcataaag  | tttcacaaac | ccagttagtc  | aaaaagatgc  | aggaagtcca | 780  |
| tccacgggtg  | catcgacccc  | ttcacaagat | ttcttattta  | attcctcttg  | ctccctggaa | 840  |
| tttagtgtct  | atacttgcgc  | agaacatgcg | taaaattgac  | aaaaaggacc  | cttctatagt | 900  |
| gacatatgtg  | gataacctgt  | tgagggttga | gaatagctca  | atcgagagaag | ttgttggcag | 960  |
| cgtagattctt | atgatggcaa  | tggagaggat | gctagattta  | gatttggtaa  | gtggatgtga | 1020 |
| tgactcta    | ggaggcatgt  | ttgatatgga | acttgaagat  | gcagttgaaa  | gcactatgaa | 1080 |
| tgaaggagac  | gagtttccag  | tgggggctct | aaaacaaaat  | acttcagggtg | gaaatgtagt | 1140 |
| ctctgaaactg | ttggacaaa   | tgatggctct | attttttcat  | catctagaat  | cctgtcaaaa | 1200 |
| ctctgatcgt  | ttggatgaga  | tcttgaaaat | tgtggtgtga  | gatttggccag | taagctgttg | 1260 |
| gacatatatc  | tctccagcaa  | cacatgtcga | cttactagga  | tgagtgcagt  | ggcttatcta | 1320 |
| gctagctatt  | tgtctogtgg  | aaagtttttg | cctgcttctt  | ttgtggctag  | catgttgaaa | 1380 |
| agattgggtg  | acgagtgatg  | ggaatattgc | ggaacatgca  | atgatgatgt  | gaagccagaa | 1440 |
| gcacatcaag  | tgttctatct  | tggatgtcag | gcaatcttgt  | atgtgctatg  | cttccgaatg | 1500 |
| agatccatag  | tggagattcc  | tgcctttcaa | tgcagtttta  | gatcattgga  | gtcaatttta | 1560 |
| tctcacaac   | taaaccact   | actggtgtgt | cttccatctg  | tagtttccga  | gttccttaaa | 1620 |
| caagccaaag  | ctggtggtct  | gttcattgtc | tcaRgaAtcc  | ttcattttcg  | atgacctaca | 1680 |
| cgagtctgag  | ctctctcggtg | cttttgggtg | ctttgaaagg  | cttgacacat  | tcttcccggt | 1740 |
| tgaccctgtc  | ttgttgaaaa  | tgtctagcag | ctacatctcc  | ccgaacttca  | acttctggtc | 1800 |
| aatggtgaaa  | acgacttatg  | gagaagatgg | tgacgaagag  | ctttgtgatg  | aggtcatagt | 1860 |
| gaatggagat  | gcagacagtg  | cggaggaacc | tgacgatgac  | gttgaacttg  | atagtgagat | 1920 |
| gaacacgatg  | tctacaactc  | cgaacacttc | tttcatgcca  | gaaacagaga  | ggctcttgaa | 1980 |
| gatgccttca  | agaatcagac  | catccactag | tcttcttgaa  | tcttctttaa  | tctaatagtc | 2040 |
| atagagagag  | ggaatgcaat  | tttgcaatgt | aggtttctta  | ttacaatctc  | ttagctagt  | 2100 |
| cgtaaaactct | aaaaaaaaa   | agttgacatg | agttttgtgc  | gagtcctgtg  | tattatctga | 2160 |

tgcgcatgtgg tttttagtagca aaatttttgaa gaacatctat gaagtaatat ttagtc

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1565821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Gly Ala Glu Glu Phe Pro Ser Val Pro Phe Asn Ser Asn Ala Met  
1 5 10 15  
Asp Asn Ala Glu Tyr Thr Asp Thr Asp Leu Val Phe Ala Val Arg Lys  
20 25 30  
Ala Leu Ala Ser Val Gln Asn Gly Asp Thr Asp Asp Tyr Ser Gln Leu  
35 40 45  
Lys Thr Val Met Cys Leu Thr Glu Asp Ala Asp Phe Asp Ala Val Ala  
50 55 60  
Gln Leu Glu Thr Val Leu Lys Ser Leu Ser Val Ser Val Ala Trp Ile  
65 70 75 80  
Asp Leu Val His His Lys Asp Leu Leu Glu Ala Ile Phe Lys Met Ser  
85 90 95  
Leu Trp Tyr His Ser His Arg Pro Ser Val Met Asp Ala Leu Val Asp  
100 105 110  
Leu Ile Ile Ser Leu Ala Ala Thr Ser Gly Lys Tyr Leu Asp Pro Cys  
115 120 125  
Leu Asn Met Leu Val Arg Asn Phe Ser Gln Pro Thr Phe Lys His Lys  
130 135 140  
Val Ser Gln Thr Gln Leu Val Lys Lys Met Gln Glu Val His Pro Arg  
145 150 155 160  
Val His Ala Ala Leu His Lys Ile Ser Tyr Leu Ile Pro Leu Ala Pro  
165 170 175  
Trp Asn Leu Val Ser Ile Leu Ala Gln Asn Met Arg Lys Ile Asp Lys  
180 185 190  
Lys Asp Pro Ser Ile Val Thr Tyr Val Asp Asn Leu Leu Arg Leu Glu  
195 200 205  
Asn Ser Ser Ile Gly Glu Val Val Gly Ser Val Ile Leu Met Met Ala  
210 215 220  
Met Glu Arg Met Leu Asp Leu Asp Leu Val Ser Gly Cys Asp Asp Ser  
225 230 235 240  
Asn Gly Gly Met Phe Asp Met Glu Leu Glu Asp Ala Val Glu Ser Thr  
245 250 255  
Met Asn Glu Gly Asp Glu Phe Pro Val Gly Ala Leu Lys Gln Asn Thr  
260 265 270  
Ser Gly Gly Asn Val Val Ser Glu Leu Leu Asp Lys Leu Met Val Leu  
275 280 285  
Phe Phe His His Leu Glu Ser Cys Gln Asn Ser Asp Arg Leu Asp Glu  
290 295 300  
Ile Leu Lys Ile Val Val  
305 310

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..295  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asn | Ala | Glu | Tyr | Thr | Asp | Thr | Asp | Leu | Val | Phe | Ala | Val | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Leu | Ala | Ser | Val | Gln | Asn | Gly | Asp | Thr | Asp | Asp | Tyr | Ser | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Thr | Val | Met | Cys | Leu | Thr | Glu | Asp | Ala | Asp | Phe | Asp | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gln | Leu | Glu | Thr | Val | Leu | Lys | Ser | Leu | Ser | Val | Ser | Val | Ala | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asp | Leu | Val | His | His | Lys | Asp | Leu | Leu | Glu | Ala | Ile | Phe | Lys | Met |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Leu | Trp | Tyr | His | Ser | His | Arg | Pro | Ser | Val | Met | Asp | Ala | Leu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Leu | Ile | Ile | Ser | Leu | Ala | Ala | Thr | Ser | Gly | Lys | Tyr | Leu | Asp | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Leu | Asn | Met | Leu | Val | Arg | Asn | Phe | Ser | Gln | Pro | Thr | Phe | Lys | His |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Val | Ser | Gln | Thr | Gln | Leu | Val | Lys | Lys | Met | Gln | Glu | Val | His | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Val | His | Ala | Ala | Leu | His | Lys | Ile | Ser | Tyr | Leu | Ile | Pro | Leu | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Trp | Asn | Leu | Val | Ser | Ile | Leu | Ala | Gln | Asn | Met | Arg | Lys | Ile | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Lys | Asp | Pro | Ser | Ile | Val | Thr | Tyr | Val | Asp | Asn | Leu | Leu | Arg | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Asn | Ser | Ser | Ile | Gly | Glu | Val | Gly | Ser | Val | Ile | Leu | Met | Met |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ala | Met | Glu | Arg | Met | Leu | Asp | Leu | Asp | Leu | Val | Ser | Gly | Cys | Asp | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Asn | Gly | Gly | Met | Phe | Asp | Met | Glu | Leu | Glu | Asp | Ala | Val | Glu | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Met | Asn | Glu | Gly | Asp | Glu | Phe | Pro | Val | Gly | Ala | Leu | Lys | Gln | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ser | Gly | Gly | Asn | Val | Val | Ser | Glu | Leu | Leu | Asp | Lys | Leu | Met | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Phe | Phe | His | His | Leu | Glu | Ser | Cys | Gln | Asn | Ser | Asp | Arg | Leu | Asp |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Glu | Ile | Leu | Lys | Ile | Val | Val |     |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 259 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..259  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Leu | Thr | Glu | Asp | Ala | Asp | Phe | Asp | Ala | Val | Ala | Gln | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Leu | Lys | Ser | Leu | Ser | Val | Ser | Val | Ala | Trp | Ile | Asp | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | His | Lys | Asp | Leu | Leu | Glu | Ala | Ile | Phe | Lys | Met | Ser | Leu | Trp | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| His | Ser | His | Arg | Pro | Ser | Val | Met | Asp | Ala | Leu | Val | Asp | Leu | Ile | Ile |

|                                                                 |                                             |                     |
|-----------------------------------------------------------------|---------------------------------------------|---------------------|
| 50                                                              | 55                                          | 60                  |
| Ser Leu Ala Ala Thr                                             | Ser Gly Lys Tyr Leu Asp                     | Pro Cys Leu Asn Met |
| 65                                                              | 70                                          | 75                  |
| Leu Val Arg Asn Phe                                             | Ser Gln Pro Thr Phe Lys His Lys Val Ser Gln | 80                  |
| 85                                                              | 90                                          | 95                  |
| Thr Gln Leu Val Lys Lys Met Gln Glu Val His Pro Arg Val His Ala | 100                                         | 110                 |
| Ala Leu His Lys Ile Ser Tyr Leu Ile Pro Leu Ala Pro Trp Asn Leu | 115                                         | 125                 |
| Val Ser Ile Leu Ala Gln Asn Met Arg Lys Ile Asp Lys Lys Asp Pro | 130                                         | 140                 |
| Ser Ile Val Thr Tyr Val Asp Asn Leu Leu Arg Leu Glu Asn Ser Ser | 145                                         | 155                 |
| Ile Gly Glu Val Val Gly Ser Val Ile Leu Met Met Ala Met Glu Arg | 165                                         | 175                 |
| Met Leu Asp Leu Asp Leu Val Ser Gly Cys Asp Asp Ser Asn Gly Gly | 180                                         | 190                 |
| Met Phe Asp Met Glu Leu Glu Asp Ala Val Glu Ser Thr Met Asn Glu | 195                                         | 205                 |
| Gly Asp Glu Phe Pro Val Gly Ala Leu Lys Gln Asn Thr Ser Gly Gly | 210                                         | 220                 |
| Asn Val Val Ser Glu Leu Asp Lys Leu Met Val Leu Phe Phe His     | 225                                         | 235                 |
| His Leu Glu Ser Cys Gln Asn Ser Asp Arg Leu Asp Glu Ile Leu Lys | 245                                         | 255                 |
| Ile Val Val                                                     |                                             |                     |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1717
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| ataaataaaaa | ccactctcgt | tgctgattcc  | atttatcggt  | cttattgacc  | ctagccgcta | 60   |
| cacacttttc  | tgcgatatct | ctgagatttg  | ttgacagtct  | ctaaccatgg  | gtaaaaagaa | 120  |
| gtttcacatc  | aacattgtgg | tcattggcca  | cgctcgattct | ggaaagtcga  | ccaccactgg | 180  |
| acacttgatc  | tacaagttgg | gtggtattga  | caagcgtgtc  | attgagaggt  | tcgagaagga | 240  |
| ggctgctgag  | atgaacaaga | ggctccttcaa | gtaogcatgg  | gttttgagca  | aacttaaggc | 300  |
| tgagcgtgag  | cgtggtatca | ccattgacat  | tgctctctgg  | aagttcgaga  | ccaccaagta | 360  |
| ctactgcact  | gtcattgatg | ctcctgggtca | tcgtgatttc  | atcaagaaca  | tgatcactgg | 420  |
| tacctcccag  | gctgattgtg | ctgtccttat  | cattgactcc  | accactgggtg | Gttttgaggc | 480  |
| tggtatctcc  | aaggatggtc | agaccocgtga | gcacgctcta  | cttgctttca  | cccttggtgt | 540  |
| caagcagatg  | atctgctgtt | gtaacaagat  | ggatgccact  | acccccaagt  | actccaaggc | 600  |
| caggtacgat  | gaaatcatca | aggaggtgtc  | ttcctacttg  | aagaagggtg  | gttacaaccc | 660  |
| cgacaaaatc  | ccatttgtgc | ccatctctgg  | atttgagggt  | gacaacatga  | ttgagaggtc | 720  |
| caccaacctt  | gactggtaca | agggaccaac  | tctccttgag  | gctcttgacc  | agatcaacga | 780  |
| gcccaagagg  | ccgtcagaca | agcccccttcg | tctcccactt  | caggatgtct  | acaagattgg | 840  |
| tggtattgga  | acggtgccag | tgggacgtgt  | tgagactggg  | atgatcaagc  | ctggtatggg | 900  |
| tgtgaccttt  | gctcccacag | gattgaccac  | tgaggccaag  | tctgttgaga  | tgcaccacga | 960  |
| gtctcttctt  | gaggcacttc | caggtgacaa  | cggtgggttc  | aatgttaaga  | atgttgctgt | 1020 |
| caaggatctt  | aagagagggt | acgtgcgcac  | caactccaag  | gatgaccctg  | ccaagggtgc | 1080 |
| tgctaacttc  | acctcccagg | tcatcatcat  | gaaccaccct  | ggtcagattg  | gtaacgggta | 1140 |
| cgccccagtc  | ctggattgcc | acacctctca  | cattgcagtc  | aagttctctg  | agatcttgac | 1200 |
| caagattgac  | aggcgttctg | gtaaggagat  | tgagaaggag  | cctaaattct  | tgaagaatgg | 1260 |
| tgatgctggg  | atggtgaaga | tgactccaac  | caagcccatg  | gttgtggaga  | ccttctctga | 1320 |

(2) INFORMATION FOR SEO ID NO:102:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1565829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|            |            |            |            |          |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Gly        | Lys        | Lys        | Lys<br>5 | Phe        | His        | Ile        | Asn        | Ile<br>10  | Val        | Val        | Ile        | Gly        | His<br>15  | Val        |
| Asp        | Ser        | Gly        | Lys<br>20  | Ser      | Thr        | Thr        | Thr        | Gly<br>25  | His        | Leu        | Ile        | Tyr        | Lys<br>30  | Leu        | Gly        |
| Gly        | Ile        | Asp<br>35  | Lys        | Arg      | Val        | Ile        | Glu<br>40  | Arg        | Phe        | Glu        | Lys        | Glu<br>45  | Ala        | Ala        | Glu        |
| Met        | Asn<br>50  | Lys        | Arg        | Ser      | Phe        | Lys<br>55  | Tyr        | Ala        | Trp        | Val        | Leu<br>60  | Asp        | Lys        | Leu        | Lys        |
| Ala<br>65  | Glu        | Arg        | Glu        | Arg      | Gly<br>70  | Ile        | Thr        | Ile        | Asp        | Ile<br>75  | Ala        | Leu        | Trp        | Lys        | Phe<br>80  |
| Glu        | Thr        | Thr        | Lys<br>85  | Tyr      | Tyr        | Cys        | Thr        | Val        | Ile<br>90  | Asp        | Ala        | Pro        | Gly<br>95  | His        | Arg        |
| Asp        | Phe        | Ile        | Lys<br>100 | Asn      | Met        | Ile        | Thr        | Gly<br>105 | Thr        | Ser        | Gln        | Ala        | Asp<br>110 | Cys        | Ala        |
| Val        | Leu        | Ile<br>115 | Ile        | Asp      | Ser        | Thr        | Thr<br>120 | Gly        | Gly        | Phe        | Glu        | Ala<br>125 | Gly        | Ile        | Ser        |
| Lys        | Asp<br>130 | Gly        | Gln        | Thr      | Arg        | Glu<br>135 | His        | Ala        | Leu        | Leu        | Ala<br>140 | Phe        | Thr        | Leu        | Gly        |
| Val<br>145 | Lys        | Gln        | Met        | Ile      | Cys<br>150 | Cys        | Cys        | Asn        | Lys        | Met<br>155 | Asp        | Ala        | Thr        | Thr        | Pro<br>160 |
| Lys        | Tyr        | Ser        | Lys<br>165 | Ala      | Arg        | Tyr        | Asp        | Glu<br>170 | Ile        | Ile        | Lys        | Glu        | Val<br>175 | Ser        | Ser        |
| Tyr        | Leu        | Lys        | Lys<br>180 | Val      | Gly        | Tyr        | Asn<br>185 | Pro        | Asp        | Lys        | Ile        | Pro<br>190 | Phe        | Val        | Pro        |
| Ile        | Ser        | Gly<br>195 | Phe        | Glu      | Gly        | Asp<br>200 | Asn        | Met        | Ile        | Glu        | Arg<br>205 | Ser        | Thr        | Asn        | Leu        |
| Asp        | Trp<br>210 | Tyr        | Lys        | Gly      | Pro        | Thr<br>215 | Leu        | Leu        | Glu        | Ala<br>220 | Leu        | Asp        | Gln        | Ile        | Asn        |
| Glu<br>225 | Pro        | Lys        | Arg        | Pro      | Ser<br>230 | Asp        | Lys        | Pro        | Leu        | Arg<br>235 | Leu        | Pro        | Leu        | Gln        | Asp<br>240 |
| Val        | Tyr        | Lys        | Ile<br>245 | Gly      | Gly        | Ile        | Gly        | Thr        | Val<br>250 | Pro        | Val        | Gly        | Arg<br>255 | Val        | Glu        |
| Thr        | Gly        | Met        | Ile<br>260 | Lys      | Pro        | Gly        | Met<br>265 | Val        | Val        | Thr        | Phe        | Ala<br>270 | Pro        | Thr        | Gly        |
| Leu        | Thr<br>275 | Thr        | Glu        | Val      | Lys        | Ser        | Val<br>280 | Glu        | Met        | His        | His<br>285 | Glu        | Ser        | Leu        | Leu        |
| Glu        | Ala<br>290 | Leu        | Pro        | Gly      | Asp        | Asn<br>295 | Val        | Gly        | Phe        | Asn<br>300 | Val        | Lys        | Asn        | Val        | Ala        |
| Val<br>305 | Lys        | Asp        | Leu        | Lys      | Arg<br>310 | Gly        | Tyr        | Val        | Ala        | Ser<br>315 | Asn        | Ser        | Lys        | Asp        | Asp<br>320 |
| Pro        | Ala        | Lys        | Gly<br>325 | Ala      | Ala        | Asn        | Phe        | Thr        | Ser<br>330 | Gln        | Val        | Ile        | Ile        | Met<br>335 | Asn        |



His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His  
340 345 350  
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp  
355 360 365  
Arg Arg Ser Gly Lys Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn  
370 375 380  
Gly Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val  
385 390 395 400  
Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp  
405 410 415  
Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys  
420 425 430  
Asp Pro Thr Gly Ala Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala  
435 440 445  
Lys

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1565830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys  
1 5 10 15  
Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe  
20 25 30  
Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg  
35 40 45  
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala  
50 55 60  
Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser  
65 70 75 80  
Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly  
85 90 95  
Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro  
100 105 110  
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser  
115 120 125  
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro  
130 135 140  
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu  
145 150 155 160  
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn  
165 170 175  
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp  
180 185 190  
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu  
195 200 205  
Thr Gly Met Ile Lys Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly  
210 215 220  
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ser Leu Leu  
225 230 235 240  
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala  
245 250 255  
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp

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(2) INFORMATION FOR SEO ID NO:104:

(A) LENGTH: 348 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1565831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|            |            |            |            |            |     |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Ile        | Thr        | Gly        | Thr<br>5   | Ser | Gln        | Ala        | Asp        | Cys<br>10  | Ala        | Val        | Leu        | Ile        | Ile<br>15 | Asp        |
| Ser        | Thr        | Thr        | Gly<br>20  | Gly        | Phe | Glu        | Ala        | Gly<br>25  | Ile        | Ser        | Lys        | Asp        | Gly<br>30  | Gln       | Thr        |
| Arg        | Glu        | His<br>35  | Ala        | Leu        | Leu | Ala        | Phe<br>40  | Thr        | Leu        | Gly        | Val        | Lys<br>45  | Gln        | Met       | Ile        |
| Cys        | Cys<br>50  | Cys        | Asn        | Lys        | Met | Asp<br>55  | Ala        | Thr        | Thr        | Pro        | Lys<br>60  | Tyr        | Ser        | Lys       | Ala        |
| Arg<br>65  | Tyr        | Asp        | Glu        | Ile<br>70  | Ile | Lys        | Glu        | Val        | Ser        | Ser<br>75  | Tyr        | Leu        | Lys        | Lys       | Val<br>80  |
| Gly        | Tyr        | Asn        | Pro        | Asp<br>85  | Lys | Ile        | Pro        | Phe        | Val<br>90  | Pro        | Ile        | Ser        | Gly<br>95  | Phe       | Glu        |
| Gly        | Asp        | Asn        | Met<br>100 | Ile        | Glu | Arg        | Ser        | Thr<br>105 | Asn        | Leu        | Asp        | Trp        | Tyr<br>110 | Lys       | Gly        |
| Pro        | Thr        | Leu<br>115 | Leu        | Glu        | Ala | Leu        | Asp<br>120 | Gln        | Ile        | Asn        | Glu        | Pro<br>125 | Lys        | Arg       | Pro        |
| Ser        | Asp<br>130 | Lys        | Pro        | Leu        | Arg | Leu<br>135 | Pro        | Leu        | Gln        | Asp        | Val<br>140 | Tyr        | Lys        | Ile       | Gly        |
| Gly<br>145 | Ile        | Gly        | Thr        | Val<br>150 | Pro | Val        | Gly        | Arg        | Val<br>155 | Glu        | Thr        | Gly        | Met        | Ile       | Lys<br>160 |
| Pro        | Gly        | Met        | Val<br>165 | Val        | Thr | Phe        | Ala        | Pro        | Thr<br>170 | Gly        | Leu        | Thr        | Thr        | Glu       | Val<br>175 |
| Lys        | Ser        | Val        | Glu<br>180 | Met        | His | His        | Glu        | Ser<br>185 | Leu        | Leu        | Glu        | Ala        | Leu<br>190 | Pro       | Gly        |
| Asp        | Asn<br>195 | Val        | Gly        | Phe        | Asn | Val        | Lys<br>200 | Asn        | Val        | Ala        | Val        | Lys<br>205 | Asp        | Leu       | Lys        |
| Arg        | Gly<br>210 | Tyr        | Val        | Ala        | Ser | Asn<br>215 | Ser        | Lys        | Asp        | Asp        | Pro<br>220 | Ala        | Lys        | Gly       | Ala        |
| Ala<br>225 | Asn        | Phe        | Thr        | Ser<br>230 | Gln | Val        | Ile        | Ile        | Met        | Asn<br>235 | His        | Pro        | Gly        | Gln       | Ile<br>240 |

Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala  
245 250 255  
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys  
260 265 270  
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met  
275 280 285  
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu  
290 295 300  
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val  
305 310 315 320  
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala  
325 330 335  
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys  
340 345

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..635
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| tctctctaca | acaaaatcag  | cgacaGctca | aacgtcgata | tttttctccg | gcttttctag | 60  |
| ggttttaatt | ttctttccga  | tcagagatta | atggcgactc | tagactccga | cgttaccatg | 120 |
| attcctgcog | gagaagcctc  | cagcagcgta | gccgcgtcgt | cttccaacaa | gaaagctaag | 180 |
| cgattcgaaa | ttaagaagtg  | gagcgccggt | gctctctggg | cttgggatat | cgttgttgac | 240 |
| aactgtgcga | tctgcagaaa  | ccacatcatg | gatctttgta | tcgagtgtca | ggctaatacg | 300 |
| gccagtgcca | caagtgaaga  | gtgcactgta | gcttgggggg | tttgcaatca | cgccttccac | 360 |
| tttactgca  | tcagcagatg  | gctaaagact | cgtcaagttt | gtccattgga | taacagtga  | 420 |
| tgggagtttc | agaaatatgg  | toactaaatc | aacaaatggg | tccagcaagc | atgtgtctaa | 480 |
| tcgtgaagac | atcagggttca | tttggttacc | accgcatatg | ataactaaag | attgttcaag | 540 |
| tttttgccct | ttttttggta  | ctgtatttta | caatttgtgg | aaacagagat | ttactgttca | 600 |
| gtgttcacta | aacctattat  | ggttgtgctt | tggtg      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Thr Leu Asp Ser Asp Val Thr Met Ile Pro Ala Gly Glu Ala |  |
| 1 5 10 15                                                       |  |
| Ser Ser Ser Val Ala Ala Ser Ser Ser Asn Lys Lys Ala Lys Arg Phe |  |
| 20 25 30                                                        |  |
| Glu Ile Lys Lys Trp Ser Ala Val Ala Leu Trp Ala Trp Asp Ile Val |  |
| 35 40 45                                                        |  |
| Val Asp Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile |  |
| 50 55 60                                                        |  |
| Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val |  |
| 65 70 75 80                                                     |  |
| Ala Trp Gly Val Cys Asn His Ala Phe His Phe His Cys Ile Ser Arg |  |
| 85 90 95                                                        |  |

Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Ser Glu Trp Glu  
100 105 110  
Phe Gln Lys Tyr Gly His  
115

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Ile Pro Ala Gly Glu Ala Ser Ser Ser Val Ala Ala Ser Ser Ser  
1 5 10 15  
Asn Lys Lys Ala Lys Arg Phe Glu Ile Lys Lys Trp Ser Ala Val Ala  
20 25 30  
Leu Trp Ala Trp Asp Ile Val Val Asp Asn Cys Ala Ile Cys Arg Asn  
35 40 45  
His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala  
50 55 60  
Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe  
65 70 75 80  
His Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro  
85 90 95  
Leu Asp Asn Ser Glu Trp Glu Phe Gln Lys Tyr Gly His  
100 105

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Val Thr Lys Ser Thr Asn Gly Ser Ser Lys His Val Ser Asn Arg  
1 5 10 15  
Glu Asp Ile Arg Phe Ile Trp Leu Pro Pro His Met Ile Thr Lys Asp  
20 25 30  
Cys Ser Ser Phe Cys Pro Phe Phe Gly Thr Val Phe Tyr Asn Leu Trp  
35 40 45  
Lys Gln Arg Phe Thr Val Gln Cys Ser Leu Asn Leu Leu Trp Leu Cys  
50 55 60  
Phe Gly  
65

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1618

(D) OTHER INFORMATION: / Ceres Seq. ID 1565840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| aatagattag  | ttttgtactt  | ctgttacgtg  | gtgattatta | aaacttgtaa | taacagtata | 60   |
| atctggtttt  | gttgggtgtag | attgatgatt  | tcaacattgc | aaagaaggaa | gaggacattg | 120  |
| ggttctacgc  | tggatttggt  | ggttgctctt  | tcatgctcgg | acgagctttt | acatctgtgg | 180  |
| catggggact  | tgttgctgat  | cgttatggta  | gaaaacctgt | aatcctcata | ggaaccgctt | 240  |
| cagtggtcgt  | ttttaatact  | ctgtttggcc  | taagtttaaa | tttctggatg | gctattatca | 300  |
| caagattttg  | cctcggtagt  | ttcaacgggt  | tacttgggtc | tatcaaggct | tacgcaatgg | 360  |
| aaatattccg  | tgatgagtat  | caagggttag  | cactctcagc | agttagtaca | gcttggggaa | 420  |
| ttggactcat  | catttggcct  | gctataggag  | gttttcttgc | tcagcctgca | aagcaatatc | 480  |
| caagttttatt | cttcacaggac | tccattttttg | gcaaatttcc | cttctttttg | ccatgcttag | 540  |
| caatatccgt  | ttttgcattc  | ttggtgacca  | tagtttcatc | aaggattccg | gaaacattgc | 600  |
| acaatcacaa  | gtttaatgat  | gatgagtctt  | atgatgctct | caaagatttg | tctgatgacc | 660  |
| ctgaatctaa  | taaagtggca  | gagagaaatg  | gaaaaagttc | tctcttgaac | aactggccat | 720  |
| taatttcatc  | tatcatcgta  | tactgcgtct  | tttactaca  | tgatatggct | tacacagaga | 780  |
| tcttttcatt  | gtgggcaaac  | agtcogagga  | aatatggagg | tttgggatac | tccactgcag | 840  |
| atgttgggtc  | tgttcttggc  | ttttcaggct  | ttggtctcct | tatctttcag | ctttcgctct | 900  |
| actcttacgc  | agagaggctt  | ttaggaccta  | tcatagttac | acgtatatct | gggagcctag | 960  |
| caatggtcgt  | ctttatcatgt | taccactaa   | tagcaaagtt | atctggttta | gtccttaccg | 1020 |
| tgactgtaac  | ttctgcattc  | gtagcaaaga  | gtgttttagg | tacttctgct | ataactggat | 1080 |
| tattcatcct  | tcaaaacaag  | gctgtgagac  | aagaccaWag | aggagcagct | aatggaattg | 1140 |
| ccatgacagc  | gatgtctctt  | ttcaaagcca  | taggtccagc | agcagcagga | atcatttttt | 1200 |
| cgtggagcga  | gaaacgtcag  | ggtgctgctt  | ttctccctgg | cacccaaatg | gtattcttta | 1260 |
| tactgaatgt  | ggttttggca  | cttggagttg  | tattgacatt | caaaccattt | ctagctgaaa | 1320 |
| cacaacagta  | gaaaatgatg  | aagattttga  | tggtattcaa | attacataat | cagaatgtat | 1380 |
| tgtataatat  | atagatYtgt  | atgtctgata  | caaagttaga | ttagaaaaat | ggcaagagaa | 1440 |
| aaagaaaaaa  | aacttgtag   | aattgttgtc  | atcatccttt | gtatgttata | ggacaagttg | 1500 |
| ttcacaaaaa  | tttgtcta    | gtgtcagaac  | cattgtaaga | aggattcaat | aatgtttttt | 1560 |
| gtacatgatg  | tttcgcgaat  | aatattgaca  | agtcgtcaaa | tcctatcctg | agattccc   |      |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1565841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Arg | Ala | Phe | Thr | Ser | Val | Ala | Trp | Gly | Leu | Val | Ala | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Tyr | Gly | Arg | Lys | Pro | Val | Ile | Leu | Ile | Gly | Thr | Ala | Ser | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Phe | Asn | Thr | Leu | Phe | Gly | Leu | Ser | Leu | Asn | Phe | Trp | Met | Ala | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Thr | Arg | Phe | Cys | Leu | Gly | Ser | Phe | Asn | Gly | Leu | Leu | Gly | Pro | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Ala | Tyr | Ala | Met | Glu | Ile | Phe | Arg | Asp | Glu | Tyr | Gln | Gly | Leu | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Ala | Val | Ser | Thr | Ala | Trp | Gly | Ile | Gly | Leu | Ile | Ile | Gly | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ile | Gly | Gly | Phe | Leu | Ala | Gln | Pro | Ala | Lys | Gln | Tyr | Pro | Ser | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Gln | Asp | Ser | Ile | Phe | Gly | Lys | Phe | Pro | Phe | Phe | Leu | Pro | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ala | Ile | Ser | Val | Phe | Ala | Phe | Leu | Val | Thr | Ile | Val | Ser | Ser | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Pro | Glu | Thr | Leu | His | Asn | His | Lys | Phe | Asn | Asp | Asp | Glu | Ser | Tyr |

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145 150 155 160
Asp Ala Leu Lys Asp Leu Ser Asp Asp Pro Glu Ser Asn Lys Val Ala
 165 170 175
Glu Arg Asn Gly Lys Ser Ser Leu Leu Asn Asn Trp Pro Leu Ile Ser
 180 185 190
Ser Ile Ile Val Tyr Cys Val Phe Ser Leu His Asp Met Ala Tyr Thr
 195 200 205
Glu Ile Phe Ser Leu Trp Ala Asn Ser Pro Arg Lys Tyr Gly Gly Leu
 210 215 220
Gly Tyr Ser Thr Ala Asp Val Gly Ser Val Leu Ala Phe Ser Gly Phe
225 230 235 240
Gly Leu Leu Ile Phe Gln Leu Ser Leu Tyr Ser Tyr Ala Glu Arg Leu
 245 250 255
Leu Gly Pro Ile Ile Val Thr Arg Ile Ser Gly Ser Leu Ala Met Val
 260 265 270
Val Leu Ser Cys Tyr Pro Leu Ile Ala Lys Leu Ser Gly Leu Val Leu
 275 280 285
Thr Val Thr Val Thr Ser Ala Ser Val Ala Lys Ser Val Leu Gly Thr
 290 295 300
Ser Ala Ile Thr Gly Leu Phe Ile Leu Gln Asn Lys Ala Val Arg Gln
305 310 315 320
Asp Xaa Arg Gly Ala Ala Asn Gly Ile Ala Met Thr Ala Met Ser Leu
 325 330 335
Phe Lys Ala Ile Gly Pro Ala Ala Ala Gly Ile Ile Phe Ser Trp Ser
 340 345 350
Glu Lys Arg Gln Gly Ala Ala Phe Leu Pro Gly Thr Gln Met Val Phe
 355 360 365
Phe Ile Leu Asn Val Val Leu Ala Leu Gly Val Val Leu Thr Phe Lys
 370 375 380
Pro Phe Leu Ala Glu Thr Gln Gln
385 390

```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```

Met Ala Ile Ile Thr Arg Phe Cys Leu Gly Ser Phe Asn Gly Leu Leu
1 5 10 15
Gly Pro Ile Lys Ala Tyr Ala Met Glu Ile Phe Arg Asp Glu Tyr Gln
 20 25 30
Gly Leu Ala Leu Ser Ala Val Ser Thr Ala Trp Gly Ile Gly Leu Ile
 35 40 45
Ile Gly Pro Ala Ile Gly Gly Phe Leu Ala Gln Pro Ala Lys Gln Tyr
 50 55 60
Pro Ser Leu Phe Ser Gln Asp Ser Ile Phe Gly Lys Phe Pro Phe Phe
65 70 75 80
Leu Pro Cys Leu Ala Ile Ser Val Phe Ala Phe Leu Val Thr Ile Val
 85 90 95
Ser Ser Arg Ile Pro Glu Thr Leu His Asn His Lys Phe Asn Asp Asp
 100 105 110
Glu Ser Tyr Asp Ala Leu Lys Asp Leu Ser Asp Asp Pro Glu Ser Asn
 115 120 125
Lys Val Ala Glu Arg Asn Gly Lys Ser Ser Leu Leu Asn Asn Trp Pro
 130 135 140

```

Leu Ile Ser Ser Ile Ile Val Tyr Cys Val Phe Ser Leu His Asp Met  
145 150 155 160  
Ala Tyr Thr Glu Ile Phe Ser Leu Trp Ala Asn Ser Pro Arg Lys Tyr  
165 170 175  
Gly Gly Leu Gly Tyr Ser Thr Ala Asp Val Gly Ser Val Leu Ala Phe  
180 185 190  
Ser Gly Phe Gly Leu Leu Ile Phe Gln Leu Ser Leu Tyr Ser Tyr Ala  
195 200 205  
Glu Arg Leu Leu Gly Pro Ile Ile Val Thr Arg Ile Ser Gly Ser Leu  
210 215 220  
Ala Met Val Val Leu Ser Cys Tyr Pro Leu Ile Ala Lys Leu Ser Gly  
225 230 235 240  
Leu Val Leu Thr Val Thr Val Thr Ser Ala Ser Val Ala Lys Ser Val  
245 250 255  
Leu Gly Thr Ser Ala Ile Thr Gly Leu Phe Ile Leu Gln Asn Lys Ala  
260 265 270  
Val Arg Gln Asp Xaa Arg Gly Ala Ala Asn Gly Ile Ala Met Thr Ala  
275 280 285  
Met Ser Leu Phe Lys Ala Ile Gly Pro Ala Ala Ala Gly Ile Ile Phe  
290 295 300  
Ser Trp Ser Glu Lys Arg Gln Gly Ala Ala Phe Leu Pro Gly Thr Gln  
305 310 315 320  
Met Val Phe Phe Ile Leu Asn Val Val Leu Ala Leu Gly Val Val Leu  
325 330 335  
Thr Phe Lys Pro Phe Leu Ala Glu Thr Gln Gln  
340 345

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1565843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Glu Ile Phe Arg Asp Glu Tyr Gln Gly Leu Ala Leu Ser Ala Val  
1 5 10 15  
Ser Thr Ala Trp Gly Ile Gly Leu Ile Ile Gly Pro Ala Ile Gly Gly  
20 25 30  
Phe Leu Ala Gln Pro Ala Lys Gln Tyr Pro Ser Leu Phe Ser Gln Asp  
35 40 45  
Ser Ile Phe Gly Lys Phe Pro Phe Phe Leu Pro Cys Leu Ala Ile Ser  
50 55 60  
Val Phe Ala Phe Leu Val Thr Ile Val Ser Ser Arg Ile Pro Glu Thr  
65 70 75 80  
Leu His Asn His Lys Phe Asn Asp Asp Glu Ser Tyr Asp Ala Leu Lys  
85 90 95  
Asp Leu Ser Asp Asp Pro Glu Ser Asn Lys Val Ala Glu Arg Asn Gly  
100 105 110  
Lys Ser Ser Leu Leu Asn Asn Trp Pro Leu Ile Ser Ser Ile Ile Val  
115 120 125  
Tyr Cys Val Phe Ser Leu His Asp Met Ala Tyr Thr Glu Ile Phe Ser  
130 135 140  
Leu Trp Ala Asn Ser Pro Arg Lys Tyr Gly Gly Leu Gly Tyr Ser Thr  
145 150 155 160  
Ala Asp Val Gly Ser Val Leu Ala Phe Ser Gly Phe Gly Leu Leu Ile  
165 170 175  
Phe Gln Leu Ser Leu Tyr Ser Tyr Ala Glu Arg Leu Leu Gly Pro Ile

|                                                                 |                                 |  |     |  |     |
|-----------------------------------------------------------------|---------------------------------|--|-----|--|-----|
|                                                                 | 180                             |  | 185 |  | 190 |
| Ile Val Thr Arg Ile Ser Gly Ser                                 | Leu Ala Met Val Val Leu Ser Cys |  |     |  |     |
| 195                                                             | 200                             |  | 205 |  |     |
| Tyr Pro Leu Ile Ala Lys Leu Ser Gly Leu Val                     | Leu Thr Val Thr Val             |  |     |  |     |
| 210                                                             | 215                             |  | 220 |  |     |
| Thr Ser Ala Ser Val Ala Lys Ser Val Leu Gly Thr Ser Ala Ile Thr |                                 |  |     |  |     |
| 225                                                             | 230                             |  | 235 |  | 240 |
| Gly Leu Phe Ile Leu Gln Asn Lys Ala Val Arg Gln Asp Xaa Arg Gly |                                 |  |     |  |     |
| 245                                                             | 250                             |  | 255 |  |     |
| Ala Ala Asn Gly Ile Ala Met Thr Ala Met Ser Leu Phe Lys Ala Ile |                                 |  |     |  |     |
| 260                                                             | 265                             |  | 270 |  |     |
| Gly Pro Ala Ala Ala Gly Ile Ile Phe Ser Trp Ser Glu Lys Arg Gln |                                 |  |     |  |     |
| 275                                                             | 280                             |  | 285 |  |     |
| Gly Ala Ala Phe Leu Pro Gly Thr Gln Met Val Phe Phe Ile Leu Asn |                                 |  |     |  |     |
| 290                                                             | 295                             |  | 300 |  |     |
| Val Val Leu Ala Leu Gly Val Val Leu Thr Phe Lys Pro Phe Leu Ala |                                 |  |     |  |     |
| 305                                                             | 310                             |  | 315 |  | 320 |
| Glu Thr Gln Gln                                                 |                                 |  |     |  |     |

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| agattcacgc atcacacaat cgagtttttta gggtttttagc ggttgctctc tcggaagcca | 60   |
| gagagaagag ggaagaggaa gtctaattcc tctgcgtttt ttgcaattag ggtttttctca  | 120  |
| attggaatcg aaaatggtga cagacaagag caagaaggcg aaaaccgaag aagaaaacgt   | 180  |
| cgagcaaatc gatgcagagc ttgtcctctc aatcgaaaag cttcaagaga tccaagacga   | 240  |
| cctcgagaag ataaatgaaa aggctagtga tgaagtgttg gaagtggagc agaaatataa   | 300  |
| tgtgataagg aaacctgttt atgacaagcg taacgagatc atcaaaacca tccctgattt   | 360  |
| ctggttaact gctttcttga gtcacctgc tttagggtgaa cttttgactg aagaagacca   | 420  |
| aaagattttc aaatatctta gctctcttga tgttgaggat gccaaagatg tgaaatctgg   | 480  |
| atactctatc actttttcct tcaatcccaa tccatttttt gaagatggaa aactgacaaa   | 540  |
| gacttttacc tttctcgaag aaggggacaac caaaatcaca gccacgccta tcaaattggaa | 600  |
| agagggcaaa ggctgtgcga atggagtga tcatgagaag aatggaaaca aacgtgcact    | 660  |
| acctgaagag agcttcttta cctggtttag tgatgctcaa cacaaggagg atgttgagga   | 720  |
| tgagatgcaa gacgagcagg ttgcagatat catcaaggaa gatttgtggc ccaaccctct   | 780  |
| cacctacttc aacaatgacg ctgatgaaga ggactttgat ggagacgatg atggagatga   | 840  |
| agaggagaaa gaaggtgact ctgatgaaga tgatgacgaa gaagacgaag ttggtgagga   | 900  |
| atgatggcag ggatacccag aaaccacaty tgcttacatg tcttctctat aacagagtgt   | 960  |
| gtaaagtttt gtgtgttgaa aggtKtttta attYttaagc aaaagtggat tatgacNgac   | 1020 |
| aacagacaag cttttaattt tatttttaCcc gtaatatgta tatcttggtg taagaaacca  | 1080 |
| ttttcagcct tttgttgga aatcctgc                                       |      |

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565864

1108-1065863



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Val Thr Asp Lys Ser Lys Lys Ala Lys Thr Glu Glu Glu Asn Val  
1 5 10 15  
Glu Gln Ile Asp Ala Glu Leu Val Leu Ser Ile Glu Lys Leu Gln Glu  
20 25 30  
Ile Gln Asp Asp Leu Glu Lys Ile Asn Glu Lys Ala Ser Asp Glu Val  
35 40 45  
Leu Glu Val Glu Gln Lys Tyr Asn Val Ile Arg Lys Pro Val Tyr Asp  
50 55 60  
Lys Arg Asn Glu Ile Ile Lys Thr Ile Pro Asp Phe Trp Leu Thr Ala  
65 70 75 80  
Phe Leu Ser His Pro Ala Leu Gly Glu Leu Thr Glu Glu Asp Gln  
85 90 95  
Lys Ile Phe Lys Tyr Leu Ser Ser Leu Asp Val Glu Asp Ala Lys Asp  
100 105 110  
Val Lys Ser Gly Tyr Ser Ile Thr Phe Ser Phe Asn Pro Asn Pro Phe  
115 120 125  
Phe Glu Asp Gly Lys Leu Thr Lys Thr Phe Thr Phe Leu Glu Glu Gly  
130 135 140  
Thr Thr Lys Ile Thr Ala Thr Pro Ile Lys Trp Lys Glu Gly Lys Gly  
145 150 155 160  
Leu Ala Asn Gly Val Asn His Glu Lys Asn Gly Asn Lys Arg Ala Leu  
165 170 175  
Pro Glu Glu Ser Phe Phe Thr Trp Phe Ser Asp Ala Gln His Lys Glu  
180 185 190  
Asp Val Glu Asp Glu Met Gln Asp Glu Gln Val Ala Asp Ile Ile Lys  
195 200 205  
Glu Asp Leu Trp Pro Asn Pro Leu Thr Tyr Phe Asn Asn Asp Ala Asp  
210 215 220  
Glu Glu Asp Phe Asp Gly Asp Asp Asp Gly Asp Glu Glu Glu Lys Glu  
225 230 235 240  
Gly Asp Ser Asp Glu Asp Asp Asp Glu Glu Asp Glu Val Gly Glu Glu  
245 250 255

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1710
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

atgcaacatt ataaaatatac Ttattttcat aaccaaCccc gatatggctg ctccacaaaa 60  
gaaaccaggc ctacgtaacg tggagctact ttgtaattat aaagatttat tgtttcccat 120  
aaactggtta aatgatttta gaaactaaag taaaatgagc ttgacactag agtttctgct 180  
tcttctgatt gtacttatct tgagtcacca tgctcattct ggctctattg tcaaattcct 240  
tcttggtttt gaaggccccc ttccttttga actcgaaacc gggtagattg gtattggtga 300  
ggaagaggaa gtgcaattat totactatct catcaaactc gagaagaatc cagaagaaga 360  
ccctcttctt ctatgggttaa gtggaggacc tggatgttcc tctcttactg gccttctttt 420  
tgagaatgga cgggtggctt tgaagttcga ggtttacaat ggaagtgttc catctttggt 480  
ctctactaca tattcatgga caaagatggc gaacataata ttcttgatc agccagttgg 540  
atctggcttc tctatttcaa gaactccact tggttgataaa attagtgaac ctggtgaagt 600  
taagaggatt tatgagtttc ttcaaaagtg gtttaagcaaa catcaacaat ttttttccaa 660  
cccttttttac gttggtggag attcttattc aggtatgatt gttccacccc tagttcaaga 720  
aatcgaaaaa ggtatgttcg ttaattcata tcaatcaatc cccatacact tttcttgga 780  
tattgttttaa ttgtctgtct ctcaataatt aacaatatat acaatgatgc aggaaattat 840

caaataaatc tacaggttgt agatatattat ttgtttctta tattttgtta tttaaaaaaa 900  
tattgaagat taatagtaat atgttcttac gaaaataggg ttatatcctc ggaaacccga 960  
taacagatac tgaatctgaa caaaactatc agattccata tgctcatgga atggcattaa 1020  
tctctgatga actatacaag tcaatggaga gaatctgcaa aggaaattat gtgaaagtgg 1080  
attcacttaa cacaaaatgc tataaactaa tcaaagatta tcaaaagtgt attcataaac 1140  
tgaataagta tcatatatta ttacctgact gcgatataac atctcctgat tgctttgtaa 1200  
ttatataggt atactctcat aaccttttgg gccacaaca agagcgttcg cgaagctctg 1260  
caagtcaata agtggtgacc atgatatgat ggtgcctttc cttgcaactc aagcctggat 1320  
aagatctctc aattattcca tcaactgatga ttggaagcct tggatgataa acgatcaaat 1380  
tgctggatac acgagaagtt attccaataa gatgacattt gctactatca aagcaagtct 1440  
tcttgtgtca acttaaatatt tgtattgtcc ttagactgca ataaaaaaga ctttgtttta 1500  
attgttttga gtttgtttta tttatttttt tgttaaaggg aagtggacac acagcagagt 1560  
ataaaccaaa agagacctct atcatgttca aaagatggat cagtgccag cctttgtaaa 1620  
agaggatgat ggtcttttgcg tatgtagaat aaaactatgt aacataaaaa atgtttgtat 1680  
acaatataat catctacttg gtaattaagt

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ser Leu Thr Leu Glu Phe Leu Leu Leu Leu Ile Val Leu Ile Leu  
1 5 10 15  
Ser His His Ala His Ser Gly Ser Ile Val Lys Phe Leu Pro Gly Phe  
20 25 30  
Glu Gly Pro Leu Pro Phe Glu Leu Glu Thr Gly Tyr Ile Gly Ile Gly  
35 40 45  
Glu Glu Glu Glu Val Gln Leu Phe Tyr Tyr Phe Ile Lys Ser Glu Lys  
50 55 60  
Asn Pro Glu Glu Asp Pro Leu Leu Leu Trp Leu Ser Gly Gly Pro Gly  
65 70 75 80  
Cys Ser Ser Leu Thr Gly Leu Leu Phe Glu Asn Gly Pro Val Ala Leu  
85 90 95  
Lys Phe Glu Val Tyr Asn Gly Ser Val Pro Ser Leu Val Ser Thr Thr  
100 105 110  
Tyr Ser Trp Thr Lys Met Ala Asn Ile Ile Phe Leu Asp Gln Pro Val  
115 120 125  
Gly Ser Gly Phe Ser Tyr Ser Arg Thr Pro Leu Val Asp Lys Ile Ser  
130 135 140  
Asp Thr Gly Glu Val Lys Arg Ile Tyr Glu Phe Leu Gln Lys Trp Leu  
145 150 155 160  
Ser Lys His Gln Gln Phe Phe Ser Asn Pro Phe Tyr Val Gly Gly Asp  
165 170 175  
Ser Tyr Ser Gly Met Ile Val Pro Pro Leu Val Gln Glu Ile Gly Lys  
180 185 190  
Gly Met Phe Val Asn Ser Tyr Gln Ser Ile Pro Ile His Phe Ser Trp  
195 200 205  
Asn Ile Val  
210

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1673

(D) OTHER INFORMATION: / Ceres Seq. ID 1565880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| aatattaatt | tcttcaatta  | accttgataa  | gagttaaaaa | agtaaaaaaac | ctcgagaaga  | 60   |
| gttgtagctg | tgggtcaacac | ttgagaggca  | gcacgatgag | ctccatatgg  | gacgttgcaa  | 120  |
| tgttgatggt | agctttggtg  | gttggtgagga | tcagccactg | gctttaccga  | tgggtcaaacc | 180  |
| ctaagtcccc | tggcaagtta  | ccacctggat  | cgatgggttt | tccaatcatt  | ggagagactc  | 240  |
| tcgatttctt | taagccttgt  | ggagtcgaag  | gtatcccaac | ctttgtcaag  | aagaggatga  | 300  |
| taaggatagg | gccgttgttt  | cgaacaaaaca | tttttggttc | caaaaccgtg  | gtttcgacag  | 360  |
| atccggatgt | gatccaccag  | attttccggc  | aagagaacac | gtcttttgag  | ctaggctatc  | 420  |
| cagacatatt | tgtgaaagta  | tttggaagaa  | ataatttggt | cttgaaggaa  | gtgttcatcc  | 480  |
| acaagtacct | ccaaaaaatc  | actatgcaaa  | ttcttggttc | cgaggggttg  | aagcaaacia  | 540  |
| tgtaggaaa  | catggacaaa  | gcaacccgcg  | accatattag | gtccattgct  | agccagggga  | 600  |
| gcttcaatgt | tcgtaaagaa  | gttgaaaact  | tggtagtagc | gtacatgaca  | ccaaagctga  | 660  |
| taagtaacct | taaaccagag  | acgcaatcaa  | agcttataga | taatctcaac  | gccttcaatc  | 720  |
| ttgattggtt | taagtccttc  | ttaagactct  | ctacttgga  | agctgtcacc  | aaagccctca  | 780  |
| agtcacgtga | agaagctatc  | caggtgatga  | aagacgttct | catgatgaga  | aaagagacgc  | 840  |
| gagagaagca | agaagacttc  | cttaaacacgc | ttctagaaga | actggagaaa  | gacggtagct  | 900  |
| ttttcgacca | aggatcggct  | ataaatctca  | tcttctctct | ggcggttgcc  | ttgagagaag  | 960  |
| gtacctctag | ttgtactgct  | ttggccgtga  | agttcatatc | caaagaccgc  | aaagtgcctg  | 1020 |
| cagagctcaa | gcgtgagcat  | aaggcaattg  | tagacaacag | aaaagataag  | gaagctggag  | 1080 |
| ttagctggga | agaatataga  | cacaacatga  | ctttcaccaa | catggttagc  | aatgaggtGc  | 1140 |
| ttcgcctagc | aaacacgacc  | cctttgttgt  | ttcgaaaggc | ggtgcaagat  | gttgagatca  | 1200 |
| aaggatatac | aattccggct  | ggttggaattg | tggcGgttg  | accttcagcg  | gttcattttg  | 1260 |
| atcctgcaat | ctatgagaac  | ccatttgagt  | ttaatccatg | gagatgggag  | gggaaagaaa  | 1320 |
| tgatttgggg | atctaaaacg  | ttcatggcgt  | ttggatatgg | agttagactt  | tgtgtaggtg  | 1380 |
| cagagttttc | gcggcttcaa  | atggcaatct  | tcctccatga | tcttgtggca  | tattacgatt  | 1440 |
| tctcaatggt | ccaagactcc  | gagatcattc  | gttcaccatt | ccatcaatac  | accaaggatc  | 1500 |
| tgcttataaa | catctctcag  | tctcttacca  | agtgaacat  | gcattgcagtt | tccaaatctt  | 1560 |
| aataatcaga | tcattatatg  | caataatctc  | atttctGct  | tcgcgaaaat  | ctctggagtc  | 1620 |
| tttttatatg | taatatgcga  | tctctataat  | ttttaaaaag | tatctatctt  | gcc         |      |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1565881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ile | Trp | Asp | Val | Ala | Met | Leu | Met | Val | Ala | Leu | Val | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Arg | Ile | Ser | His | Trp | Leu | Tyr | Arg | Trp | Ser | Asn | Pro | Lys | Cys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Lys | Leu | Pro | Pro | Gly | Ser | Met | Gly | Phe | Pro | Ile | Ile | Gly | Glu | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Asp | Phe | Phe | Lys | Pro | Cys | Gly | Val | Glu | Gly | Ile | Pro | Thr | Phe | Val |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Lys | Lys | Arg | Met | Ile | Arg | Tyr | Gly | Pro | Leu | Phe | Arg | Thr | Asn | Ile | Phe |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Gly | Ser | Lys | Thr | Val | Val | Ser | Thr | Asp | Pro | Asp | Val | Ile | His | Gln | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Arg | Gln | Glu | Asn | Thr | Ser | Phe | Glu | Leu | Gly | Tyr | Pro | Asp | Ile | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Lys | Val | Phe | Gly | Lys | Asp | Asn | Leu | Phe | Leu | Lys | Glu | Val | Phe | Ile |

Met Leu Met Val Ala Leu Val Val Val Arg Ile Ser His Trp Leu Tyr  
1 5 10 15  
Arg Trp Ser Asn Pro Lys Cys Pro Gly Lys Leu Pro Pro Gly Ser Met  
20 25 30

Gly Phe Pro Ile Ile Gly Glu Thr Leu Asp Phe Phe Lys Pro Cys Gly  
35 40 45  
Val Glu Gly Ile Pro Thr Phe Val Lys Lys Arg Met Ile Arg Tyr Gly  
50 55 60  
Pro Leu Phe Arg Thr Asn Ile Phe Gly Ser Lys Thr Val Val Ser Thr  
65 70 75 80  
Asp Pro Asp Val Ile His Gln Ile Phe Arg Gln Glu Asn Thr Ser Phe  
85 90 95  
Glu Leu Gly Tyr Pro Asp Ile Phe Val Lys Val Phe Gly Lys Asp Asn  
100 105 110  
Leu Phe Leu Lys Glu Val Phe Ile His Lys Tyr Leu Gln Lys Ile Thr  
115 120 125  
Met Gln Ile Leu Gly Ser Glu Gly Leu Lys Gln Thr Met Leu Gly Asn  
130 135 140  
Met Asp Lys Ala Thr Arg Asp His Ile Arg Ser Ile Ala Ser Gln Gly  
145 150 155 160  
Ser Phe Asn Val Arg Lys Glu Val Glu Asn Leu Val Val Ala Tyr Met  
165 170 175  
Thr Pro Lys Leu Ile Ser Asn Leu Lys Pro Glu Thr Gln Ser Lys Leu  
180 185 190  
Ile Asp Asn Leu Asn Ala Phe Asn Leu Asp Trp Phe Lys Ser Phe Leu  
195 200 205  
Arg Leu Ser Thr Trp Lys Ala Val Thr Lys Ala Leu Lys Ser Arg Glu  
210 215 220  
Glu Ala Ile Gln Val Met Lys Asp Val Leu Met Met Arg Lys Glu Thr  
225 230 235 240  
Arg Glu Lys Gln Glu Asp Phe Leu Asn Thr Leu Leu Glu Glu Leu Glu  
245 250 255  
Lys Asp Gly Ser Phe Phe Asp Gln Gly Ser Ala Ile Asn Leu Ile Phe  
260 265 270  
Leu Leu Ala Phe Ala Leu Arg Glu Gly Thr Ser Ser Cys Thr Ala Leu  
275 280 285  
Ala Val Lys Phe Ile Ser Lys Asp Pro Lys Val Leu Ala Glu Leu Lys  
290 295 300  
Arg Glu His Lys Ala Ile Val Asp Asn Arg Lys Asp Lys Glu Ala Gly  
305 310 315 320  
Val Ser Trp Glu Glu Tyr Arg His Asn Met Thr Phe Thr Asn Met Val  
325 330 335  
Ser Asn Glu Val Leu Arg Leu Ala Asn Thr Thr Pro Leu Leu Phe Arg  
340 345 350  
Lys Ala Val Gln Asp Val Glu Ile Lys Gly Tyr Thr Ile Pro Ala Gly  
355 360 365  
Trp Ile Val Ala Val Ala Pro Ser Ala Val His Phe Asp Pro Ala Ile  
370 375 380  
Tyr Glu Asn Pro Phe Glu Phe Asn Pro Trp Arg Trp Glu Gly Lys Glu  
385 390 395 400  
Met Ile Trp Gly Ser Lys Thr Phe Met Ala Phe Gly Tyr Gly Val Arg  
405 410 415  
Leu Cys Val Gly Ala Glu Phe Ser Arg Leu Gln Met Ala Ile Phe Leu  
420 425 430  
His His Leu Val Ala Tyr Tyr Asp Phe Ser Met Val Gln Asp Ser Glu  
435 440 445  
Ile Ile Arg Ser Pro Phe His Gln Tyr Thr Lys Asp Leu Leu Ile Asn  
450 455 460  
Ile Ser Gln Ser Pro Thr Lys  
465 470

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..469  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565883  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Leu | Val | Val | Val | Arg | Ile | Ser | His | Trp | Leu | Tyr | Arg | Trp | 1   | 5   | 10  | 15  |
| Ser | Asn | Pro | Lys | Cys | Pro | Gly | Lys | Leu | Pro | Pro | Gly | Ser | Met | Gly | Phe | 20  | 25  | 30  |     |
| Pro | Ile | Ile | Gly | Glu | Thr | Leu | Asp | Phe | Phe | Lys | Pro | Cys | Gly | Val | Glu | 35  | 40  | 45  |     |
| Gly | Ile | Pro | Thr | Phe | Val | Lys | Lys | Arg | Met | Ile | Arg | Tyr | Gly | Pro | Leu | 50  | 55  | 60  |     |
| Phe | Arg | Thr | Asn | Ile | Phe | Gly | Ser | Lys | Thr | Val | Val | Ser | Thr | Asp | Pro | 65  | 70  | 75  | 80  |
| Asp | Val | Ile | His | Gln | Ile | Phe | Arg | Gln | Glu | Asn | Thr | Ser | Phe | Glu | Leu | 85  | 90  | 95  |     |
| Gly | Tyr | Pro | Asp | Ile | Phe | Val | Lys | Val | Phe | Gly | Lys | Asp | Asn | Leu | Phe | 100 | 105 | 110 |     |
| Leu | Lys | Glu | Val | Phe | Ile | His | Lys | Tyr | Leu | Gln | Lys | Ile | Thr | Met | Gln | 115 | 120 | 125 |     |
| Ile | Leu | Gly | Ser | Glu | Gly | Leu | Lys | Gln | Thr | Met | Leu | Gly | Asn | Met | Asp | 130 | 135 | 140 |     |
| Lys | Ala | Thr | Arg | Asp | His | Ile | Arg | Ser | Ile | Ala | Ser | Gln | Gly | Ser | Phe | 145 | 150 | 155 | 160 |
| Asn | Val | Arg | Lys | Glu | Val | Glu | Asn | Leu | Val | Val | Ala | Tyr | Met | Thr | Pro | 165 | 170 | 175 |     |
| Lys | Leu | Ile | Ser | Asn | Leu | Lys | Pro | Glu | Thr | Gln | Ser | Lys | Leu | Ile | Asp | 180 | 185 | 190 |     |
| Asn | Leu | Asn | Ala | Phe | Asn | Leu | Asp | Trp | Phe | Lys | Ser | Phe | Leu | Arg | Leu | 195 | 200 | 205 |     |
| Ser | Thr | Trp | Lys | Ala | Val | Thr | Lys | Ala | Leu | Lys | Ser | Arg | Glu | Glu | Ala | 210 | 215 | 220 |     |
| Ile | Gln | Val | Met | Lys | Asp | Val | Leu | Met | Met | Arg | Lys | Glu | Thr | Arg | Glu | 225 | 230 | 235 | 240 |
| Lys | Gln | Glu | Asp | Phe | Leu | Asn | Thr | Leu | Leu | Glu | Glu | Leu | Glu | Lys | Asp | 245 | 250 | 255 |     |
| Gly | Ser | Phe | Phe | Asp | Gln | Gly | Ser | Ala | Ile | Asn | Leu | Ile | Phe | Leu | Leu | 260 | 265 | 270 |     |
| Ala | Phe | Ala | Leu | Arg | Glu | Gly | Thr | Ser | Ser | Cys | Thr | Ala | Leu | Ala | Val | 275 | 280 | 285 |     |
| Lys | Phe | Ile | Ser | Lys | Asp | Pro | Lys | Val | Leu | Ala | Glu | Leu | Lys | Arg | Glu | 290 | 295 | 300 |     |
| His | Lys | Ala | Ile | Val | Asp | Asn | Arg | Lys | Asp | Lys | Glu | Ala | Gly | Val | Ser | 305 | 310 | 315 | 320 |
| Trp | Glu | Glu | Tyr | Arg | His | Asn | Met | Thr | Phe | Thr | Asn | Met | Val | Ser | Asn | 325 | 330 | 335 |     |
| Glu | Val | Leu | Arg | Leu | Ala | Asn | Thr | Thr | Pro | Leu | Leu | Phe | Arg | Lys | Ala | 340 | 345 | 350 |     |
| Val | Gln | Asp | Val | Glu | Ile | Lys | Gly | Tyr | Thr | Ile | Pro | Ala | Gly | Trp | Ile | 355 | 360 | 365 |     |
| Val | Ala | Val | Ala | Pro | Ser | Ala | Val | His | Phe | Asp | Pro | Ala | Ile | Tyr | Glu | 370 | 375 | 380 |     |
| Asn | Pro | Phe | Glu | Phe | Asn | Pro | Trp | Arg | Trp | Glu | Gly | Lys | Glu | Met | Ile | 385 | 390 | 395 | 400 |
| Trp | Gly | Ser | Lys | Thr | Phe | Met | Ala | Phe | Gly | Tyr | Gly | Val | Arg | Leu | Cys | 405 | 410 | 415 |     |
| Val | Gly | Ala | Glu | Phe | Ser | Arg | Leu | Gln | Met | Ala | Ile | Phe | Leu | His | His | 420 | 425 | 430 |     |

Leu Val Ala Tyr Tyr Asp Phe Ser Met Val Gln Asp Ser Glu Ile Ile  
435 440 445  
Arg Ser Pro Phe His Gln Tyr Thr Lys Asp Leu Leu Ile Asn Ile Ser  
450 455 460  
Gln Ser Pro Thr Lys  
465

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| attgggttct  | ttcctctttt  | ctcccagatt | catcaatccc  | tcctgctacc  | gcgagagagt  | 60   |
| aacaactcac  | cggacgtttc  | aaatccatcc | tccgataact  | atattcgttt  | cgttagatct  | 120  |
| agatctgagc  | gtcgggtgaga | gattttctgg | atctgtgata  | cgttccagga  | aacatggcga  | 180  |
| cgatgaaaag  | tttgataggt  | ctgataaaca | aaatccagag  | ggcgtgtact  | gtcctcggag  | 240  |
| atcatggcgg  | tgaagggaatg | tcgctttggg | aagctctccc  | aaccgtcgct  | gtcgttggtg  | 300  |
| gccagagttc  | cggaaaatct  | tcagttctag | aaagtgttgt  | gggaagagat  | tttctgcctc  | 360  |
| gtggatctgg  | tatcggttaca | aggaggccat | tgggtgttgc  | acttcataag  | actgaagacg  | 420  |
| ggacaactga  | gtacgctgag  | tttcttcatg | ctcctaagaa  | gagatttgct  | gattttgctg  | 480  |
| ctgtgcggaa  | agaaattgag  | gatgaaactg | atcgtattac  | tgggaagtca  | aaacaaatct  | 540  |
| caaacattcc  | aattcagctg  | agcatatatt | ctcctaattg  | tgtaaatctg  | acgctcatag  | 600  |
| atcttccggg  | tttgaccaag  | gtcgtctgag | atggacaacc  | ggaaagtatt  | gtccaagaca  | 660  |
| ttgaaaatat  | ggtccggtct  | tatggttgaa | agccaaattg  | catcatattg  | gctatttctc  | 720  |
| cagcaaatca  | agatatgtct  | acctcagatg | ctataaaact  | tgctagagaa  | gttgatccta  | 780  |
| caggcgaag   | gacttttggt  | gttgcaacca | agcttgatat  | catggataaa  | ggaacagatt  | 840  |
| gtctagatgt  | tcttgaggga  | aggtcatacc | gtttgcaaca  | tccttgggtt  | ggaattgtga  | 900  |
| atcggtcaca  | agctgatatt  | aataagagag | tcgatatgat  | tgctgcacgt  | agaaaagagc  | 960  |
| aagaatattt  | tgaacaagc   | cctgaatacg | ggcacttagc  | cagtagaatg  | ggatcagaat  | 1020 |
| atctagcaaa  | actcttgtct  | cagcacttag | agactgttat  | caggcagaaa  | atccccagta  | 1080 |
| ttgttgcttt  | gatcaacaaa  | agcatcgatg | agataaatgc  | agaacttgat  | aggattggga  | 1140 |
| gacccattgc  | agtagattca  | ggagcccaac | tttacacaa   | tttggaactc  | tgccgggcat  | 1200 |
| ttgatcgtgt  | ctttaaggag  | cacttggatg | gaggacgacc  | tgggtggagac | cgaatttatg  | 1260 |
| gagttttcga  | ccatcaatta  | ccagcagcct | taaagaaact  | tccttttgat  | cgacatctgt  | 1320 |
| ctaccaaaaa  | tgttcagaag  | gttgtttcag | aagcagatgg  | ttatcagccg  | catcttattg  | 1380 |
| ctcctgaaca  | aggatacaga  | aggctcattg | atggatccat  | aagctatttc  | aaaggaccag  | 1440 |
| ctgaagccac  | tgctgatgca  | gtgcatttgc | tattgaagga  | gctggtcaga  | aagtcaattt  | 1500 |
| cagaaacaga  | ggaactgaag  | cgtttccoga | ctctagcaag  | cgatatagca  | gctgctgcaa  | 1560 |
| atgaagctct  | tgaagatttc  | agagacgaaa | gcaggaaaac  | ggttttgcgt  | ctggtggata  | 1620 |
| tggaatctag  | ctacctcacg  | gttgagttct | tcaggaaaact | ccatcttgaa  | cccagagaaag | 1680 |
| agaaacaaaa  | cccaaggaat  | gccccagcac | caaacgcaga  | cccctactcc  | gataatcact  | 1740 |
| tcagaaagat  | cggatccaac  | gBgagtgc   | acataaacat  | ggtctgcgac  | acattgagaa  | 1800 |
| actctcttcc  | caaagctgtc  | gtttactgcc | aagttagaga  | agctaagaga  | tcgcttctca  | 1860 |
| acttcttcta  | cgctcaagtt  | ggcaggaaag | agaaggagaa  | gctgggtgct  | atgttggacg  | 1920 |
| aagaccacaca | gctgatggaa  | cgaagaggaa | ccttagctaa  | acggctagag  | ctttacaaac  | 1980 |
| aagctagaga  | cgacatcgat  | gcagtggctt | ggaagtaagg  | gggtttgcta  | agacatattc  | 2040 |
| tttatattgt  | taatttcttt  | gttcgtgtgg | gcacactgca  | ttataataga  | tatgtttgga  | 2100 |
| gttctaactt  | ccagtctaca  | caaacataca | cgcgactact  | catgttttct  | tgggtcgcta  | 2160 |
| atttctatca  | caactttccc  | actttttttt | ggtgtgtatc  | ttcgattctt  | gaatactggt  | 2220 |
| ttttaagaaca | gttaagacat  | attttgaagt | cgc         |             |             |      |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..614  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1565899  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Met | Lys | Ser | Leu | Ile | Gly | Leu | Ile | Asn | Lys | Ile | Gln | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Cys | Thr | Val | Leu | Gly | Asp | His | Gly | Gly | Glu | Gly | Met | Ser | Leu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Leu | Pro | Thr | Val | Ala | Val | Val | Gly | Gly | Gln | Ser | Ser | Gly | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Val | Leu | Glu | Ser | Val | Val | Gly | Arg | Asp | Phe | Leu | Pro | Arg | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ile | Val | Thr | Arg | Arg | Pro | Leu | Val | Leu | Gln | Leu | His | Lys | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Asp | Gly | Thr | Thr | Glu | Tyr | Ala | Glu | Phe | Leu | His | Ala | Pro | Lys | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Phe | Ala | Asp | Phe | Ala | Ala | Val | Arg | Lys | Glu | Ile | Glu | Asp | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Arg | Ile | Thr | Gly | Lys | Ser | Lys | Gln | Ile | Ser | Asn | Ile | Pro | Ile | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Ile | Tyr | Ser | Pro | Asn | Val | Val | Asn | Leu | Thr | Leu | Ile | Asp | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gly | Leu | Thr | Lys | Val | Ala | Val | Asp | Gly | Gln | Pro | Glu | Ser | Ile | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Asp | Ile | Glu | Asn | Met | Val | Arg | Ser | Tyr | Val | Glu | Lys | Pro | Asn | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ile | Leu | Ala | Ile | Ser | Pro | Ala | Asn | Gln | Asp | Ile | Ala | Thr | Ser | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Lys | Leu | Ala | Arg | Glu | Val | Asp | Pro | Thr | Gly | Glu | Arg | Thr | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Val | Ala | Thr | Lys | Leu | Asp | Ile | Met | Asp | Lys | Gly | Thr | Asp | Cys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Val | Leu | Glu | Gly | Arg | Ser | Tyr | Arg | Leu | Gln | His | Pro | Trp | Val | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Val | Asn | Arg | Ser | Gln | Ala | Asp | Ile | Asn | Lys | Arg | Val | Asp | Met | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala | Arg | Arg | Lys | Glu | Gln | Glu | Tyr | Phe | Glu | Thr | Ser | Pro | Glu | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | His | Leu | Ala | Ser | Arg | Met | Gly | Ser | Glu | Tyr | Leu | Ala | Lys | Leu | Leu |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Gln | His | Leu | Glu | Thr | Val | Ile | Arg | Gln | Lys | Ile | Pro | Ser | Ile | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Leu | Ile | Asn | Lys | Ser | Ile | Asp | Glu | Ile | Asn | Ala | Glu | Leu | Asp | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ile | Gly | Arg | Pro | Ile | Ala | Val | Asp | Ser | Gly | Ala | Gln | Leu | Tyr | Thr | Ile |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Glu | Leu | Cys | Arg | Ala | Phe | Asp | Arg | Val | Phe | Lys | Glu | His | Leu | Asp |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Gly | Arg | Pro | Gly | Gly | Asp | Arg | Ile | Tyr | Gly | Val | Phe | Asp | His | Gln |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Leu | Pro | Ala | Ala | Leu | Lys | Lys | Leu | Pro | Phe | Asp | Arg | His | Leu | Ser | Thr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Asn | Val | Gln | Lys | Val | Ser | Glu | Ala | Asp | Gly | Tyr | Gln | Pro | His |     |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     | 400 |     |
| Leu | Ile | Ala | Pro | Glu | Gln | Gly | Tyr | Arg | Arg | Leu | Ile | Asp | Gly | Ser | Ile |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Ser | Tyr | Phe | Lys | Gly | Pro | Ala | Glu | Ala | Thr | Val | Asp | Ala | Val | His | Phe |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |



|            |            |            |            |          |            |            |            |            |           |            |            |            |            |            |     |
|------------|------------|------------|------------|----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Lys        | Ser        | Leu        | Ile<br>5 | Gly        | Leu        | Ile        | Asn        | Lys<br>10 | Ile        | Gln        | Arg        | Ala        | Cys<br>15  | Thr |
| Val        | Leu        | Gly        | Asp<br>20  | His      | Gly        | Gly        | Glu        | Gly<br>25  | Met       | Ser        | Leu        | Trp        | Glu<br>30  | Ala        | Leu |
| Pro        | Thr        | Val        | Ala<br>35  | Val      | Val        | Gly        | Gly<br>40  | Gln        | Ser       | Ser        | Gly        | Lys<br>45  | Ser        | Ser        | Val |
| Leu        | Glu<br>50  | Ser        | Val        | Val      | Gly        | Arg<br>55  | Asp        | Phe        | Leu       | Pro        | Arg<br>60  | Gly        | Ser        | Gly        | Ile |
| Val<br>65  | Thr        | Arg        | Arg        | Pro      | Leu<br>70  | Val        | Leu        | Gln        | Leu       | His<br>75  | Lys        | Thr        | Glu        | Asp<br>80  | Gly |
| Thr        | Thr        | Glu        | Tyr<br>85  | Ala      | Glu        | Phe        | Leu        | His<br>90  | Ala       | Pro        | Lys        | Lys        | Arg        | Phe<br>95  | Ala |
| Asp        | Phe        | Ala        | Ala<br>100 | Val      | Arg        | Lys        | Glu        | Ile<br>105 | Glu       | Asp        | Glu        | Thr        | Asp<br>110 | Arg        | Ile |
| Thr        | Gly        | Lys<br>115 | Ser        | Lys      | Gln        | Ile        | Ser<br>120 | Asn        | Ile       | Pro        | Ile        | Gln<br>125 | Leu        | Ser        | Ile |
| Tyr        | Ser<br>130 | Pro        | Asn        | Val      | Val        | Asn<br>135 | Leu        | Thr        | Leu       | Ile        | Asp<br>140 | Leu        | Pro        | Gly        | Leu |
| Thr<br>145 | Lys        | Val        | Ala        | Val      | Asp<br>150 | Gly        | Gln        | Pro        | Glu       | Ser<br>155 | Ile        | Val        | Gln        | Asp<br>160 | Ile |
| Glu        | Asn        | Met        | Val<br>165 | Arg      | Ser        | Tyr        | Val        | Glu<br>170 | Lys       | Pro        | Asn        | Cys        | Ile        | Ile<br>175 | Leu |
| Ala        | Ile        | Ser        | Pro<br>180 | Ala      | Asn        | Gln        | Asp        | Ile<br>185 | Ala       | Thr        | Ser        | Asp        | Ala<br>190 | Ile        | Lys |
| Leu        | Ala        | Arg        | Glu        | Val      | Asp        | Pro        | Thr        | Gly        | Glu       | Arg        | Thr        | Phe        | Gly        | Val        | Ala |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Thr Lys Leu Asp Ile Met Asp Lys Gly Thr Asp Cys Leu Asp Val Leu |     |     |
| 210                                                             | 215 | 220 |
| Glu Gly Arg Ser Tyr Arg Leu Gln His Pro Trp Val Gly Ile Val Asn |     |     |
| 225                                                             | 230 | 235 |
| Arg Ser Gln Ala Asp Ile Asn Lys Arg Val Asp Met Ile Ala Ala Arg |     |     |
| 245                                                             | 250 | 255 |
| Arg Lys Glu Gln Glu Tyr Phe Glu Thr Ser Pro Glu Tyr Gly His Leu |     |     |
| 260                                                             | 265 | 270 |
| Ala Ser Arg Met Gly Ser Glu Tyr Leu Ala Lys Leu Leu Ser Gln His |     |     |
| 275                                                             | 280 | 285 |
| Leu Glu Thr Val Ile Arg Gln Lys Ile Pro Ser Ile Val Ala Leu Ile |     |     |
| 290                                                             | 295 | 300 |
| Asn Lys Ser Ile Asp Glu Ile Asn Ala Glu Leu Asp Arg Ile Gly Arg |     |     |
| 305                                                             | 310 | 315 |
| Pro Ile Ala Val Asp Ser Gly Ala Gln Leu Tyr Thr Ile Leu Glu Leu |     |     |
| 325                                                             | 330 | 335 |
| Cys Arg Ala Phe Asp Arg Val Phe Lys Glu His Leu Asp Gly Gly Arg |     |     |
| 340                                                             | 345 | 350 |
| Pro Gly Gly Asp Arg Ile Tyr Gly Val Phe Asp His Gln Leu Pro Ala |     |     |
| 355                                                             | 360 | 365 |
| Ala Leu Lys Lys Leu Pro Phe Asp Arg His Leu Ser Thr Lys Asn Val |     |     |
| 370                                                             | 375 | 380 |
| Gln Lys Val Val Ser Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala |     |     |
| 385                                                             | 390 | 395 |
| Pro Glu Gln Gly Tyr Arg Arg Leu Ile Asp Gly Ser Ile Ser Tyr Phe |     |     |
| 405                                                             | 410 | 415 |
| Lys Gly Pro Ala Glu Ala Thr Val Asp Ala Val His Phe Val Leu Lys |     |     |
| 420                                                             | 425 | 430 |
| Glu Leu Val Arg Lys Ser Ile Ser Glu Thr Glu Glu Leu Lys Arg Phe |     |     |
| 435                                                             | 440 | 445 |
| Pro Thr Leu Ala Ser Asp Ile Ala Ala Ala Ala Asn Glu Ala Leu Glu |     |     |
| 450                                                             | 455 | 460 |
| Arg Phe Arg Asp Glu Ser Arg Lys Thr Val Leu Arg Leu Val Asp Met |     |     |
| 465                                                             | 470 | 475 |
| Glu Ser Ser Tyr Leu Thr Val Glu Phe Phe Arg Lys Leu His Leu Glu |     |     |
| 485                                                             | 490 | 495 |
| Pro Glu Lys Glu Lys Pro Asn Pro Arg Asn Ala Pro Ala Pro Asn Ala |     |     |
| 500                                                             | 505 | 510 |
| Asp Pro Tyr Ser Asp Asn His Phe Arg Lys Ile Gly Ser Asn Xaa Ser |     |     |
| 515                                                             | 520 | 525 |
| Ala Tyr Ile Asn Met Val Cys Asp Thr Leu Arg Asn Ser Leu Pro Lys |     |     |
| 530                                                             | 535 | 540 |
| Ala Val Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Ser Leu Leu Asn |     |     |
| 545                                                             | 550 | 555 |
| Phe Phe Tyr Ala Gln Val Gly Arg Lys Glu Lys Glu Lys Leu Gly Ala |     |     |
| 565                                                             | 570 | 575 |
| Met Leu Asp Glu Asp Pro Gln Leu Met Glu Arg Arg Gly Thr Leu Ala |     |     |
| 580                                                             | 585 | 590 |
| Lys Arg Leu Glu Leu Tyr Lys Gln Ala Arg Asp Asp Ile Asp Ala Val |     |     |
| 595                                                             | 600 | 605 |
| Ala Trp Lys                                                     |     |     |
| 610                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

U.S. Pat. No. 4,444,444

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Ser        | Leu        | Trp        | Glu<br>5   | Ala        | Leu        | Pro        | Thr        | Val<br>10  | Ala        | Val        | Val        | Gly        | Gly<br>15  | Gln        |
| Ser        | Ser        | Gly        | Lys<br>20  | Ser        | Ser        | Val        | Leu        | Glu<br>25  | Ser        | Val        | Val        | Gly        | Arg<br>30  | Asp        | Phe        |
| Leu        | Pro        | Arg<br>35  | Gly        | Ser        | Gly        | Ile        | Val<br>40  | Thr        | Arg        | Arg        | Pro        | Leu<br>45  | Val        | Leu        | Gln        |
| Leu        | His<br>50  | Lys        | Thr        | Glu        | Asp<br>55  | Gly        | Thr        | Thr        | Glu        | Tyr        | Ala<br>60  | Glu        | Phe        | Leu        | His        |
| Ala<br>65  | Pro        | Lys        | Lys        | Arg        | Phe<br>70  | Ala        | Asp        | Phe        | Ala        | Ala<br>75  | Val        | Arg        | Lys        | Glu        | Ile<br>80  |
| Glu        | Asp        | Glu        | Thr        | Asp<br>85  | Arg        | Ile        | Thr        | Gly        | Lys<br>90  | Ser        | Lys        | Gln        | Ile<br>95  | Ser        | Asn        |
| Ile        | Pro        | Ile        | Gln<br>100 | Leu        | Ser        | Ile        | Tyr        | Ser<br>105 | Pro        | Asn        | Val        | Val        | Asn<br>110 | Leu        | Thr        |
| Leu        | Ile        | Asp<br>115 | Leu        | Pro        | Gly        | Leu        | Thr<br>120 | Lys        | Val        | Ala        | Val        | Asp<br>125 | Gly        | Gln        | Pro        |
| Glu        | Ser<br>130 | Ile        | Val        | Gln        | Asp<br>135 | Ile        | Glu        | Asn        | Met        | Val        | Arg<br>140 | Ser        | Tyr        | Val        | Glu        |
| Lys<br>145 | Pro        | Asn        | Cys        | Ile<br>150 | Ile        | Leu        | Ala        | Ile        | Ser        | Pro        | Ala<br>155 | Asn        | Gln        | Asp<br>160 | Ile        |
| Ala        | Thr        | Ser        | Asp<br>165 | Ala        | Ile        | Lys        | Leu        | Ala        | Arg<br>170 | Glu        | Val        | Asp        | Pro<br>175 | Thr        | Gly        |
| Glu        | Arg        | Thr        | Phe<br>180 | Gly        | Val        | Ala        | Thr        | Lys<br>185 | Leu        | Asp        | Ile        | Met<br>190 | Asp        | Lys        | Gly        |
| Thr        | Asp<br>195 | Cys        | Leu        | Asp        | Val        | Leu        | Glu<br>200 | Gly        | Arg        | Ser        | Tyr<br>205 | Arg        | Leu        | Gln        | His        |
| Pro        | Trp<br>210 | Val        | Gly        | Ile        | Val        | Asn<br>215 | Arg        | Ser        | Gln        | Ala        | Asp<br>220 | Ile        | Asn        | Lys        | Arg        |
| Val<br>225 | Asp        | Met        | Ile        | Ala<br>230 | Ala        | Arg        | Arg        | Lys        | Glu        | Gln<br>235 | Glu        | Tyr        | Phe        | Glu<br>240 | Thr        |
| Ser        | Pro        | Glu        | Tyr<br>245 | Gly        | His        | Leu        | Ala        | Ser        | Arg<br>250 | Met        | Gly        | Ser        | Glu<br>255 | Tyr        | Leu        |
| Ala        | Lys        | Leu<br>260 | Leu        | Ser        | Gln        | His        | Leu        | Glu<br>265 | Thr        | Val        | Ile        | Arg<br>270 | Gln        | Lys        | Ile        |
| Pro        | Ser<br>275 | Ile        | Val        | Ala        | Leu        | Ile        | Asn<br>280 | Lys        | Ser        | Ile        | Asp<br>285 | Glu        | Ile        | Asn        | Ala        |
| Glu<br>290 | Leu        | Asp        | Arg        | Ile        | Gly<br>295 | Arg        | Pro        | Ile        | Ala        | Val        | Asp<br>300 | Ser        | Gly        | Ala        | Gln        |
| Leu<br>305 | Tyr        | Thr        | Ile        | Leu<br>310 | Glu        | Leu        | Cys        | Arg        | Ala        | Phe<br>315 | Asp        | Arg        | Val        | Phe        | Lys<br>320 |
| Glu        | His        | Leu        | Asp<br>325 | Gly        | Gly        | Arg        | Pro        | Gly        | Gly<br>330 | Asp        | Arg        | Ile        | Tyr<br>335 | Gly        | Val        |
| Phe        | Asp        | His<br>340 | Gln        | Leu        | Pro        | Ala        | Ala<br>345 | Leu        | Lys        | Lys        | Leu        | Pro<br>350 | Phe        | Asp        | Arg        |
| His        | Leu<br>355 | Ser        | Thr        | Lys        | Asn        | Val        | Gln<br>360 | Lys        | Val        | Val        | Ser<br>365 | Glu        | Ala        | Asp        | Gly        |
| Tyr        | Gln<br>370 | Pro        | His        | Leu        | Ile<br>375 | Ala        | Pro        | Glu        | Gln        | Gly<br>380 | Tyr        | Arg        | Arg        | Leu        | Ile        |
| Asp<br>385 | Gly        | Ser        | Ile        | Ser<br>390 | Tyr        | Phe        | Lys        | Gly        | Pro        | Ala<br>395 | Glu        | Ala        | Thr        | Val        | Asp<br>400 |
| Ala        | Val        | His<br>405 | Phe        | Val        | Leu        | Lys        | Glu        | Leu<br>410 | Val        | Arg        | Lys        | Ser        | Ile<br>415 | Ser        | Glu        |
| Thr        | Glu        | Glu<br>420 | Leu        | Lys        | Arg        | Phe        | Pro<br>425 | Thr        | Leu        | Ala        | Ser        | Asp<br>430 | Ile        | Ala        | Ala        |
| Ala        | Ala<br>435 | Asn        | Glu        | Ala        | Leu        | Glu        | Arg<br>440 | Phe        | Arg        | Asp        | Glu<br>445 | Ser        | Arg        | Lys        | Thr        |
| Val        | Leu        | Arg        | Leu        | Val        | Asp        | Met        | Glu        | Ser        | Ser        | Tyr        | Leu        | Thr        | Val        | Glu        | Phe        |

450 455 460  
Phe Arg Lys Leu His Leu Glu Pro Glu Lys Glu Lys Pro Asn Pro Arg  
465 470 475 480  
Asn Ala Pro Ala Pro Asn Ala Asp Pro Tyr Ser Asp Asn His Phe Arg  
485 490 495  
Lys Ile Gly Ser Asn Xaa Ser Ala Tyr Ile Asn Met Val Cys Asp Thr  
500 505 510  
Leu Arg Asn Ser Leu Pro Lys Ala Val Val Tyr Cys Gln Val Arg Glu  
515 520 525  
Ala Lys Arg Ser Leu Leu Asn Phe Phe Tyr Ala Gln Val Gly Arg Lys  
530 535 540  
Glu Lys Glu Lys Leu Gly Ala Met Leu Asp Glu Asp Pro Gln Leu Met  
545 550 555 560  
Glu Arg Arg Gly Thr Leu Ala Lys Arg Leu Glu Leu Tyr Lys Gln Ala  
565 570 575  
Arg Asp Asp Ile Asp Ala Val Ala Trp Lys  
580 585

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
catctcttct tgaagctgct ttcttctctca aattcttttt ttttcagat tcttctcctt 60
tcttcttctt tcttctcttat ttcgatttgc aattttgaat tttctcaatg gctcaatcgt 120
gtcttaaaat tgttcgaatc aacaatctaa ggaacagagt gaatcgctcg attttgattc 180
tccgacgatt cacacggttg ttatggagta gaatcggtgc ttgtactcct ggcaaatctc 240
ggagatatct cttgctttct cgcgcctctc cgtctccgac tgtttctcgt ccttctcctt 300
ctccgatccc cgcgcgcgat gtcgctcgctg gtggtggtgg tgggtggtgg gagtttggtc 360
gtcgttcgtc ggttggttac gataatgata acagtcacog gagatcggat tctgatttgg 420
tttctttgaa gattagtctc ttaggagatc cagaaatcgg aaaaactagc ttcctggcga 480
aatatgttgg agaagagaaa gaagtagaaa tgagagaatt ggagaaagg ataaattgta 540
cggacaagac gttatacatg ggaggtgctc gcatttcata tagtatctgg gaattagaag 600
ctgagagatc acgagatcaa atccctgtgg cttgcaagga ctctgttgcc attctcttta 660
tgtttgattt aaccagtcgt tgcacgctta atagtgtcat tagctggtat caacaagcta 720
ggaagtcaaa tcagacggcg ataccagtta tggtaggaac caagtttgat gagtttattc 780
agcttcctat tgatctgcaa tggacaattg ctagccaggc gagaacatat gcgaaggcct 840
taaacgcgac gctcttcttc tcgagtgtct catacaacat aaacgtgaat aagatcttta 900
agTtttgtga cggcgaagct cttcgactta ccatggacgg tggaaacgca tctcacaatc 960
ggagaaccaa tcatcgactt ctagaatatg tatttgata taatataaaa gaagcgaatc 1020
ctgaagaatg cgtttttttt tttttttttt ttaattcaGc cgctaaagct tgtcgcgctg 1080
ggactgatcg gactagtcgt atttaagcga aatggagaga tgaagcggcg gagatttcgc 1140
ccgctttttt cc
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

2025 RELEASE UNDER E.O. 14176

```

Met Ala Gln Ser Cys Leu Lys Ile Val Arg Ile Asn Asn Leu Arg Asn
1 5 10 15
Arg Val Asn Arg Arg Ile Leu Ile Leu Arg Arg Phe Thr Arg Leu Leu
 20 25 30
Trp Ser Arg Ile Val Ala Cys Thr Pro Gly Lys Ser Arg Arg Tyr Leu
 35 40 45
Leu Leu Ser Arg Ala Leu Pro Ser Pro Thr Val Ser Arg Pro Ser Pro
 50 55 60
Ser Pro Ile Pro Ala Val Asp Val Val Val Gly Gly Gly Gly Gly Gly
65 70 75 80
Gly Glu Phe Val Arg Arg Ser Ser Val Val Tyr Asp Asn Asp Asn Ser
 85 90 95
His Arg Arg Ser Asp Ser Asp Leu Val Ser Leu Lys Ile Ser Leu Leu
 100 105 110
Gly Asp Pro Glu Ile Gly Lys Thr Ser Phe Leu Ala Lys Tyr Val Gly
 115 120 125
Glu Glu Lys Glu Val Glu Met Arg Glu Leu Glu Lys Gly Ile Asn Cys
 130 135 140
Thr Asp Lys Thr Leu Tyr Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile
145 150 155 160
Trp Glu Leu Glu Ala Glu Arg Ser Arg Asp Gln Ile Pro Val Ala Cys
 165 170 175
Lys Asp Ser Val Ala Ile Leu Phe Met Phe Asp Leu Thr Ser Arg Cys
 180 185 190
Thr Leu Asn Ser Val Ile Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn
 195 200 205
Gln Thr Ala Ile Pro Val Met Val Gly Thr Lys Phe Asp Glu Phe Ile
 210 215 220
Gln Leu Pro Ile Asp Leu Gln Trp Thr Ile Ala Ser Gln Ala Arg Thr
225 230 235 240
Tyr Ala Lys Ala Leu Asn Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr
 245 250 255
Asn Ile Asn Val Asn Lys Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu
 260 265 270
Arg Leu Thr Met Asp Gly Gly Thr Gln Ser His Asn Arg Arg Thr Asn
 275 280 285
His Arg Leu Leu Glu Tyr Val Phe Val Tyr Asn Ile Lys Glu Ala Asn
 290 295 300
Pro Glu Glu Cys Val Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys
305 310 315 320
Ala Cys Arg Arg Gly Thr Asp Arg Thr Ser Arg Ile
 325 330

```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```

Met Arg Glu Leu Glu Lys Gly Ile Asn Cys Thr Asp Lys Thr Leu Tyr
1 5 10 15
Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile Trp Glu Leu Glu Ala Glu
 20 25 30
Arg Ser Arg Asp Gln Ile Pro Val Ala Cys Lys Asp Ser Val Ala Ile
 35 40 45
Leu Phe Met Phe Asp Leu Thr Ser Arg Cys Thr Leu Asn Ser Val Ile

```

50 55 60  
Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn Gln Thr Ala Ile Pro Val  
65 70 75 80  
Met Val Gly Thr Lys Phe Asp Glu Phe Ile Gln Leu Pro Ile Asp Leu  
85 90 95  
Gln Trp Thr Ile Ala Ser Gln Ala Arg Thr Tyr Ala Lys Ala Leu Asn  
100 105 110  
Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr Asn Ile Asn Val Asn Lys  
115 120 125  
Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu Arg Leu Thr Met Asp Gly  
130 135 140  
Gly Thr Gln Ser His Asn Arg Arg Thr Asn His Arg Leu Leu Glu Tyr  
145 150 155 160  
Val Phe Val Tyr Asn Ile Lys Glu Ala Asn Pro Glu Glu Cys Val Phe  
165 170 175  
Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys Ala Cys Arg Arg Gly Thr  
180 185 190  
Asp Arg Thr Ser Arg Ile  
195

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1565925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile Trp Glu Leu Glu Ala Glu  
1 5 10 15  
Arg Ser Arg Asp Gln Ile Pro Val Ala Cys Lys Asp Ser Val Ala Ile  
20 25 30  
Leu Phe Met Phe Asp Leu Thr Ser Arg Cys Thr Leu Asn Ser Val Ile  
35 40 45  
Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn Gln Thr Ala Ile Pro Val  
50 55 60  
Met Val Gly Thr Lys Phe Asp Glu Phe Ile Gln Leu Pro Ile Asp Leu  
65 70 75 80  
Gln Trp Thr Ile Ala Ser Gln Ala Arg Thr Tyr Ala Lys Ala Leu Asn  
85 90 95  
Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr Asn Ile Asn Val Asn Lys  
100 105 110  
Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu Arg Leu Thr Met Asp Gly  
115 120 125  
Gly Thr Gln Ser His Asn Arg Arg Thr Asn His Arg Leu Leu Glu Tyr  
130 135 140  
Val Phe Val Tyr Asn Ile Lys Glu Ala Asn Pro Glu Glu Cys Val Phe  
145 150 155 160  
Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys Ala Cys Arg Arg Gly Thr  
165 170 175  
Asp Arg Thr Ser Arg Ile  
180

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1599 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1599

(D) OTHER INFORMATION: / Ceres Seq. ID 1565926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| gaagatgatg | aaacctgagt | ttctgagaca | gaaggaagag | cttttaacat  | cccttctgtt  | 60   |
| tatggtcgga | ttccaactcc | ggacttcttg | gctttaaccc | tttacgtccg  | atcttgtcgc  | 120  |
| tgaaatcttt | ctttctcctt | ttacatgggt | ttcacgacga | caaaagtttg  | cctttttcta  | 180  |
| gttgctgcct | tgacttcaga | tagcatcaca | aggttcggct | tcagataaca  | tcacaagttg  | 240  |
| agggaaacat | gaattcgaca | tcgacacatt | ttgtgccacc | gagaagagtt  | ggtatatacg  | 300  |
| aacctgtcca | tcaattcggg | atgtgggggg | agagtttcaa | aagcaatatt  | agcaatggga  | 360  |
| ctatgaacac | accaaaccac | ataataatc  | cgaataatca | gaaactagac  | aacaacgtgt  | 420  |
| cagaggatac | ttcccatgga | acagcaggaa | ctcctcacat | gttcgatcaa  | gaagcttcaa  | 480  |
| cgtctagaca | tcccgataag | atacaaagac | ggcttgctca | aaaccgagag  | gctgctagga  | 540  |
| aaagtgcgtt | gcgcaagaag | gcttatgttc | agcaactgga | aacaagcagg  | ttgaagctaa  | 600  |
| ttcaattaga | gcaagaactc | gacgtgctga | gacaacaggg | attctatgta  | ggaaacggaa  | 660  |
| tagatactaa | ttctctcggt | ttttcggaaa | ccatgaatcc | agggattgct  | gcatttgaaa  | 720  |
| tggaatatgg | acattggggt | gaagaacaga | acagacagat | atgtgaacta  | agaacagttt  | 780  |
| tacacggaca | cattaacgat | atcgagcttc | gttcgctagt | cgaaaacgcc  | atgaaacatt  | 840  |
| actttgagct | tttcoggatg | aaatcgtctg | ctgcaaagc  | cgatgtcttc  | ttcgtcatgt  | 900  |
| cagggatgtg | gagaacttca | gcagaacgat | tcttcttatg | gattggcgga  | tttcgaccct  | 960  |
| cogatcttct | caaggttctt | ttgccacatt | ttgatgtctt | gacggatcaa  | caacttctag  | 1020 |
| atgtatgcaa | tctaaaacaa | tcgtgtcagc | aagcagaaga | cgcgttgact  | caaggtatgg  | 1080 |
| agaagctgca | acacaccctt | gcggaCtgcg | ttgcagcggg | acaactcggg  | gaaggaagtt  | 1140 |
| acattctcca | ggtgaattct | gctatggata | gattagaagc | tttggtcagt  | ttcgtaaatac | 1200 |
| aggctgatca | cttgagacat | gaaacattgc | aacaaatgta | tcggatattg  | acaacgcgac  | 1260 |
| aagcggctcg | aggattatta | gctcttggtg | agtattttca | acggcttaga  | gccttgagct  | 1320 |
| caagttgggc | aactcgacat | cgtgaaccaa | cgtaggtttg | agttattttg  | taacaaccaa  | 1380 |
| atgaagaaaa | tggaaagacc | tcaaaaaatg | aagaatgggt | gcactctgaaa | acagaggact  | 1440 |
| actctgaata | aatagagggg | ttgctgctga | tatttatttt | tactctgcgg  | cggaatagaa  | 1500 |
| aatttgaaaa | acatcatgta | ttgataagtt | gtaaatatca | gaaaaagggtg | ggggtgcaaa  | 1560 |
| aatttgact  | ttttagcttt | tgaagaggc  | aagtttttc  |             |             |      |

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1565927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ser | Thr | Ser | Thr | His | Phe | Val | Pro | Pro | Arg | Arg | Val | Gly | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Glu | Pro | Val | His | Gln | Phe | Gly | Met | Trp | Gly | Glu | Ser | Phe | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Ser | Asn | Gly | Thr | Met | Asn | Thr | Pro | Asn | His | Ile | Ile | Ile | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asn | Asn | Gln | Lys | Leu | Asp | Asn | Asn | Val | Ser | Glu | Asp | Thr | Ser | His | Gly |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Thr | Ala | Gly | Thr | Pro | His | Met | Phe | Asp | Gln | Glu | Ala | Ser | Thr | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Pro | Asp | Lys | Ile | Gln | Arg | Arg | Leu | Ala | Gln | Asn | Arg | Glu | Ala | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Lys | Ser | Arg | Leu | Arg | Lys | Lys | Ala | Tyr | Val | Gln | Gln | Leu | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Leu | Lys | Leu | Ile | Gln | Leu | Glu | Gln | Glu | Leu | Asp | Arg | Ala | Arg |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Gly | Phe | Tyr | Val | Gly | Asn | Gly | Ile | Asp | Thr | Asn | Ser | Leu | Gly |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Glu | Thr | Met | Asn | Pro | Gly | Ile | Ala | Ala | Phe | Glu | Met | Glu | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | His | Trp | Val | Glu | Glu | Gln | Asn | Arg | Gln | Ile | Cys | Glu | Leu | Arg | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Leu | His | Gly | His | Ile | Asn | Asp | Ile | Glu | Leu | Arg | Ser | Leu | Val | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Ala | Met | Lys | His | Tyr | Phe | Glu | Leu | Phe | Arg | Met | Lys | Ser | Ser | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Lys | Ala | Asp | Val | Phe | Phe | Val | Met | Ser | Gly | Met | Trp | Arg | Thr | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Glu | Arg | Phe | Phe | Leu | Trp | Ile | Gly | Gly | Phe | Arg | Pro | Ser | Asp | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Lys | Val | Leu | Leu | Pro | His | Phe | Asp | Val | Leu | Thr | Asp | Gln | Gln | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Asp | Val | Cys | Asn | Leu | Lys | Gln | Ser | Cys | Gln | Gln | Ala | Glu | Asp | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Leu | Thr | Gln | Gly | Met | Glu | Lys | Leu | Gln | His | Thr | Leu | Ala | Asp | Cys | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Ala | Ala | Gly | Gln | Leu | Gly | Glu | Gly | Ser | Tyr | Ile | Pro | Gln | Val | Asn | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Met | Asp | Arg | Leu | Glu | Ala | Leu | Val | Ser | Phe | Val | Asn | Gln | Ala | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| His | Leu | Arg | His | Glu | Thr | Leu | Gln | Gln | Met | Tyr | Arg | Ile | Leu | Thr | Thr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Gln | Ala | Ala | Arg | Gly | Leu | Leu | Ala | Leu | Gly | Glu | Tyr | Phe | Gln | Arg |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Arg | Ala | Leu | Ser | Ser | Ser | Trp | Ala | Thr | Arg | His | Arg | Glu | Pro | Thr |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Gly | Glu | Ser | Phe | Lys | Ser | Asn | Ile | Ser | Asn | Gly | Thr | Met | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Pro | Asn | His | Ile | Ile | Ile | Pro | Asn | Asn | Gln | Lys | Leu | Asp | Asn | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Glu | Asp | Thr | Ser | His | Gly | Thr | Ala | Gly | Thr | Pro | His | Met | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Glu | Ala | Ser | Thr | Ser | Arg | His | Pro | Asp | Lys | Ile | Gln | Arg | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Ala | Gln | Asn | Arg | Glu | Ala | Ala | Arg | Lys | Ser | Arg | Leu | Arg | Lys | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Tyr | Val | Gln | Gln | Leu | Glu | Thr | Ser | Arg | Leu | Lys | Leu | Ile | Gln | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Gln | Glu | Leu | Asp | Arg | Ala | Arg | Gln | Gln | Gly | Phe | Tyr | Val | Gly | Asn |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Asp | Thr | Asn | Ser | Leu | Gly | Phe | Ser | Glu | Thr | Met | Asn | Pro | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Ala | Phe | Glu | Met | Glu | Tyr | Gly | His | Trp | Val | Glu | Glu | Gln | Asn |



```
(2) INFORMATION FOR SEQ ID NO:132:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..330
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565929
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Pro | Asn | His | Ile | Ile | Ile | Pro | Asn | Asn | Gln | Lys | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asn | Val | Ser | Glu | Asp | Thr | Ser | His | Gly | Thr | Ala | Gly | Thr | Pro | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Phe | Asp | Gln | Glu | Ala | Ser | Thr | Ser | Arg | His | Pro | Asp | Lys | Ile | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Leu | Ala | Gln | Asn | Arg | Glu | Ala | Ala | Arg | Lys | Ser | Arg | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Lys | Ala | Tyr | Val | Gln | Gln | Leu | Glu | Thr | Ser | Arg | Leu | Lys | Leu | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Leu | Glu | Gln | Glu | Leu | Asp | Arg | Ala | Arg | Gln | Gln | Gly | Phe | Tyr | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Asn | Gly | Ile | Asp | Thr | Asn | Ser | Leu | Gly | Phe | Ser | Glu | Thr | Met | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Gly | Ile | Ala | Ala | Phe | Glu | Met | Glu | Tyr | Gly | His | Trp | Val | Glu | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Asn | Arg | Gln | Ile | Cys | Glu | Leu | Arg | Thr | Val | Leu | His | Gly | His | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Asp | Ile | Glu | Leu | Arg | Ser | Leu | Val | Glu | Asn | Ala | Met | Lys | His | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Glu | Leu | Phe | Arg | Met | Lys | Ser | Ser | Ala | Ala | Lys | Ala | Asp | Val | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

Phe Val Met Ser Gly Met Trp Arg Thr Ser Ala Glu Arg Phe Phe Leu  
180 185 190  
Trp Ile Gly Gly Phe Arg Pro Ser Asp Leu Leu Lys Val Leu Leu Pro  
195 200 205  
His Phe Asp Val Leu Thr Asp Gln Gln Leu Leu Asp Val Cys Asn Leu  
210 215 220  
Lys Gln Ser Cys Gln Gln Ala Glu Asp Ala Leu Thr Gln Gly Met Glu  
225 230 235 240  
Lys Leu Gln His Thr Leu Ala Asp Cys Val Ala Ala Gly Gln Leu Gly  
245 250 255  
Glu Gly Ser Tyr Ile Pro Gln Val Asn Ser Ala Met Asp Arg Leu Glu  
260 265 270  
Ala Leu Val Ser Phe Val Asn Gln Ala Asp His Leu Arg His Glu Thr  
275 280 285  
Leu Gln Gln Met Tyr Arg Ile Leu Thr Thr Arg Gln Ala Ala Arg Gly  
290 295 300  
Leu Leu Ala Leu Gly Glu Tyr Phe Gln Arg Leu Arg Ala Leu Ser Ser  
305 310 315 320  
Ser Trp Ala Thr Arg His Arg Glu Pro Thr  
325 330

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

|             |             |             |            |             |            |      |
|-------------|-------------|-------------|------------|-------------|------------|------|
| tagttttcgtc | ctccgtcaat  | ctctctcgcc  | gctttatcct | tgttacaaat  | cccatcgatc | 60   |
| ttttcggaat  | cttccctcat  | tatgctcagc  | caccattacc | agagctccat  | tgtttcagtt | 120  |
| ctccgttcaa  | cgattatcgg  | aattattcac  | aacactatta | gtatcacccg  | cgccaaccga | 180  |
| ttttgattac  | cagctttggg  | gacgacagtc  | gtgattaagg | aggttttggg  | aaattttctt | 240  |
| gttctctgtt  | gttttcaaag  | atggctgctt  | tgaaagggtt | tggttgtgt   | tctatggact | 300  |
| ctgctcttca  | attcccctgt  | cctaagctat  | tcaatggcta | taagagaagg  | agctcgaaat | 360  |
| gggtctctcc  | caaagcagct  | gttgaccaca  | atttccatct | cccaatgcgc  | agcttgagg  | 420  |
| ttaaaaacag  | gacaaacaca  | gacgacatta  | aagctctacg | tgtgatcaca  | gctatcaaaa | 480  |
| caccgtatct  | acctgatgga  | agattcgacc  | ttgaagccta | cgatgactta  | gtcaacattc | 540  |
| agatacaaaa  | cggtgctgaa  | ggtgtcattg  | ttggtggtac | aactgtgaag  | gacaactgat | 600  |
| gagctgggac  | gaacacatta  | tgcttatagg  | ccataccgtt | aactgttttg  | gcggaagcat | 660  |
| caaagtcatt  | ggaaacactg  | gaagcaattc  | gactagagaa | gcaatccacg  | cgactgaaca | 720  |
| aggattcgcg  | gttggaatgc  | atgctgctct  | tcatataaac | ccttactatg  | gcaagacttc | 780  |
| tattgaggga  | ctgattgcac  | atttccagtc  | tgttcttcat | atgggaccga  | cgattatata | 840  |
| caatgtgcct  | ggtcgaacag  | ggcaagatat  | accgcctcgt | gccatcttca  | aactttctca | 900  |
| gaatccgaat  | ttagctggtg  | tgaaggaaatg | tgttgggaac | aagcgagtcg  | aagagtacac | 960  |
| tgagaatggg  | gttggtgtgt  | ggagtgggaa  | tgatgatgag | tgatcatgatt | ccagatggga | 1020 |
| ttatggagca  | acaggagtta  | tatcagttac  | tagtaattta | gttccgggtt  | tgatgaggaa | 1080 |
| gttgatgttt  | gaaggtagga  | attcatcttt  | gaactcaaag | cttctacctt  | tgatggcttg | 1140 |
| gctgttccac  | gagccaaacc  | cgattggaat  | caacactgct | ttggctcagc  | ttggagtttc | 1200 |
| gaggccgggt  | tttaggttac  | catatgtacc  | attgccactg | tctaagaggc  | ttgagtttgt | 1260 |
| gaaactgggtg | aaggagattg  | gacgagagca  | ttttgtgggt | gagaaagatg  | ttcaggctct | 1320 |
| tgatgatgat  | gatttttatcc | ttatcggtcg  | atattagcat | actttttttt  | ttgaattttt | 1380 |
| gggtccctttt | tgtttggtgt  | taatgaagaa  | gagatggttc | tatcatttgg  | ttttatgtag | 1440 |
| ctgatgaatg  | aatgaaaact  | caaggaatga  | tttcatc    |             |            |      |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..252  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1565939  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn Cys  
1                   5                   10                   15  
Phe Gly Gly Ser Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr  
                  20                   25                   30  
Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Val Gly Met His  
                  35                   40                   45  
Ala Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu Gly  
50                   55                   60  
Leu Ile Ala His Phe Gln Ser Val Leu His Met Gly Pro Thr Ile Ile  
65                   70                   75                   80  
Tyr Asn Val Pro Gly Arg Thr Gly Gln Asp Ile Pro Pro Arg Ala Ile  
                  85                   90                   95  
Phe Lys Leu Ser Gln Asn Pro Asn Leu Ala Gly Val Lys Glu Cys Val  
                  100                   105                   110  
Gly Asn Lys Arg Val Glu Glu Tyr Thr Glu Asn Gly Val Val Val Trp  
                  115                   120                   125  
Ser Gly Asn Asp Asp Glu Cys His Asp Ser Arg Trp Asp Tyr Gly Ala  
130                   135                   140  
Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met Arg  
145                   150                   155                   160  
Lys Leu Met Phe Glu Gly Arg Asn Ser Ser Leu Asn Ser Lys Leu Leu  
                  165                   170                   175  
Pro Leu Met Ala Trp Leu Phe His Glu Pro Asn Pro Ile Gly Ile Asn  
                  180                   185                   190  
Thr Ala Leu Ala Gln Leu Gly Val Ser Arg Pro Val Phe Arg Leu Pro  
                  195                   200                   205  
Tyr Val Pro Leu Pro Leu Ser Lys Arg Leu Glu Phe Val Lys Leu Val  
210                   215                   220  
Lys Glu Ile Gly Arg Glu His Phe Val Gly Glu Lys Asp Val Gln Ala  
225                   230                   235                   240  
Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr  
                  245                   250

- (2) INFORMATION FOR SEQ ID NO:135:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 245 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..245  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1565940  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Leu Ile Gly His Thr Val Asn Cys Phe Gly Gly Ser Ile Lys Val  
1                   5                   10                   15  
Ile Gly Asn Thr Gly Ser Asn Ser Thr Arg Glu Ala Ile His Ala Thr  
                  20                   25                   30  
Glu Gln Gly Phe Ala Val Gly Met His Ala Ala Leu His Ile Asn Pro  
35                   40                   45  
Tyr Tyr Gly Lys Thr Ser Ile Glu Gly Leu Ile Ala His Phe Gln Ser  
50                   55                   60  
Val Leu His Met Gly Pro Thr Ile Ile Tyr Asn Val Pro Gly Arg Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Gly | Gln | Asp | Ile | Pro | Pro | Arg | Ala | Ile | Phe | Lys | Leu | Ser | Gln | Asn | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Leu | Ala | Gly | Val | Lys | Glu | Cys | Val | Gly | Asn | Lys | Arg | Val | Glu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Thr | Glu | Asn | Gly | Val | Val | Val | Trp | Ser | Gly | Asn | Asp | Asp | Glu | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Asp | Ser | Arg | Trp | Asp | Tyr | Gly | Ala | Thr | Gly | Val | Ile | Ser | Val | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Asn | Leu | Val | Pro | Gly | Leu | Met | Arg | Lys | Leu | Met | Phe | Glu | Gly | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Ser | Ser | Leu | Asn | Ser | Lys | Leu | Leu | Pro | Leu | Met | Ala | Trp | Leu | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Glu | Pro | Asn | Pro | Ile | Gly | Ile | Asn | Thr | Ala | Leu | Ala | Gln | Leu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ser | Arg | Pro | Val | Phe | Arg | Leu | Pro | Tyr | Val | Pro | Leu | Pro | Leu | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Arg | Leu | Glu | Phe | Val | Lys | Leu | Val | Lys | Glu | Ile | Gly | Arg | Glu | His |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Val | Gly | Glu | Lys | Asp | Val | Gln | Ala | Leu | Asp | Asp | Asp | Asp | Phe | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Ile | Gly | Arg | Tyr |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ala | Ala | Leu | His | Ile | Asn | Pro | Tyr | Tyr | Gly | Lys | Thr | Ser | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gly | Leu | Ile | Ala | His | Phe | Gln | Ser | Val | Leu | His | Met | Gly | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Tyr | Asn | Val | Pro | Gly | Arg | Thr | Gly | Gln | Asp | Ile | Pro | Pro | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ile | Phe | Lys | Leu | Ser | Gln | Asn | Pro | Asn | Leu | Ala | Gly | Val | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Cys | Val | Gly | Asn | Lys | Arg | Val | Glu | Glu | Tyr | Thr | Glu | Asn | Gly | Val | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Trp | Ser | Gly | Asn | Asp | Asp | Glu | Cys | His | Asp | Ser | Arg | Trp | Asp | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ala | Thr | Gly | Val | Ile | Ser | Val | Thr | Ser | Asn | Leu | Val | Pro | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Arg | Lys | Leu | Met | Phe | Glu | Gly | Arg | Asn | Ser | Ser | Leu | Asn | Ser | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Leu | Pro | Leu | Met | Ala | Trp | Leu | Phe | His | Glu | Pro | Asn | Pro | Ile | Gly |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ile | Asn | Thr | Ala | Leu | Ala | Gln | Leu | Gly | Val | Ser | Arg | Pro | Val | Phe | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Pro | Tyr | Val | Pro | Leu | Pro | Leu | Ser | Lys | Arg | Leu | Glu | Phe | Val | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Val | Lys | Glu | Ile | Gly | Arg | Glu | His | Phe | Val | Gly | Glu | Lys | Asp | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Ala | Leu | Asp | Asp | Asp | Asp | Phe | Ile | Leu | Ile | Gly | Arg | Tyr |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..858
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| attgaatacc | atatatatat | agatacacag | acataataaac | acacaaatat | tcgtgttttt  | 60  |
| ttcaaactgt | gagagaaaaa | gaaagagaga | aagagatggg  | agagattggg | tttacagaga  | 120 |
| agcaagaagc | tttggtgaag | gaatcgtggg | agatactgaa  | acaagacatc | cccaaataca  | 180 |
| gccttcaact | cttctcacag | atactggaga | tagcaccagc  | agcaaaaggc | ttgttctctt  | 240 |
| tcctaagaga | ctcagatgaa | gtccctcaca | acaatcctaa  | actcaaagct | catgctgtta  | 300 |
| aagtcttcaa | gatgacatgt | gaaacagcta | tacagctgag  | ggaggaagga | aagggtggtag | 360 |
| tggctgacac | aaccctccaa | tatttaggct | caattcatct  | caaaagcggc | gttattgacc  | 420 |
| ctcacttcga | ggtggtgaaa | gaagctttgc | taaggacatt  | gaaagagggg | ttgggggaga  | 480 |
| aatacaatga | agaagtggaa | ggtgcttggt | ctcaagctta  | tgatcacttg | gctttagCca  | 540 |
| tcaagaccga | gatgaacaaa | gaagatgcat | aaaaccctat  | tgatcatttg | ggtatcgcat  | 600 |
| acatgaatct | attccacata | catgatacac | atatacgtgt  | ttctgtgtgt | gtactatggt  | 660 |
| gctctctaac | tttctacagt | tcactatttt | aattataaag  | aaggatcttg | tgctatcatt  | 720 |
| agggagatag | gtgatactgt | agttcttctt | gaaattgtta  | ttcgtgagaa | atatcatggt  | 780 |
| ttgaagtatt | tattttcaca | agatggatgt | taacgtgggg  | atcattttac | aatcattcta  | 840 |
| caaataattt | tactttctc  |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Glu | Ile | Gly | Phe | Thr | Glu | Lys | Gln | Glu | Ala | Leu | Val | Lys | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Trp | Glu | Ile | Leu | Lys | Gln | Asp | Ile | Pro | Lys | Tyr | Ser | Leu | His | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Gln | Ile | Leu | Glu | Ile | Ala | Pro | Ala | Ala | Lys | Gly | Leu | Phe | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Phe | Leu | Arg | Asp | Ser | Asp | Glu | Val | Pro | His | Asn | Asn | Pro | Lys | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | His | Ala | Val | Lys | Val | Phe | Lys | Met | Thr | Cys | Glu | Thr | Ala | Ile | Gln |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Arg | Glu | Glu | Gly | Lys | Val | Val | Val | Ala | Asp | Thr | Thr | Leu | Gln | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Gly | Ser | Ile | His | Leu | Lys | Ser | Gly | Val | Ile | Asp | Pro | His | Phe | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Val | Lys | Glu | Ala | Leu | Leu | Arg | Thr | Leu | Lys | Glu | Gly | Leu | Gly | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Tyr | Asn | Glu | Glu | Val | Glu | Gly | Ala | Trp | Ser | Gln | Ala | Tyr | Asp | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ala | Leu | Ala | Ile | Lys | Thr | Glu | Met | Lys | Gln | Glu | Glu | Ser |     |     |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..86  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565948  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:  
Met Thr Cys Glu Thr Ala Ile Gln Leu Arg Glu Glu Gly Lys Val Val  
1 5 10 15  
Val Ala Asp Thr Leu Gln Tyr Leu Gly Ser Ile His Leu Lys Ser  
20 25 30  
Gly Val Ile Asp Pro His Phe Glu Val Val Lys Glu Ala Leu Leu Arg  
35 40 45  
Thr Leu Lys Glu Gly Leu Gly Glu Lys Tyr Asn Glu Glu Val Glu Gly  
50 55 60  
Ala Trp Ser Gln Ala Tyr Asp His Leu Ala Leu Ala Ile Lys Thr Glu  
65 70 75 80  
Met Lys Gln Glu Glu Ser  
85

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1262  
(D) OTHER INFORMATION: / Ceres Seq. ID 1565957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

aaagcaacaa aaacttaacc catttcttct tctttttttg tttctctctc acaaacacaa 60  
caaatatgga atacagctgt gtagacgaca gtagtactac gtcagaatct ctctccatct 120  
ctactactcc aaagccgaca acgacaacgg agaagaaact ctcttctcca ccggcgactt 180  
cgatgcgtct ctacagaatg ggaagcggcg gaagcagcgt tgttttggat tcagagaacg 240  
cgtctgagac cgagtcacga aagcttccgt cgtcgaaata caaaggcgtt gtgcctcagc 300  
ctaacggaag atggggagct cagattttacg agaagcatca gcgagtttg ctcggtactt 360  
tcaacgagga agaagaagct gcgtcttctt acgacatcgc cgtgaggagg ttccgaggcc 420  
gcgacgccgt cactaaactt aaatctcaag ttgatggaaa cgacgccgaa tcggcttttc 480  
ttgacgtctc ttctaaagct gagatcgttg atatgttgag gaaacacact tacgccgatg 540  
agtttgagca gagtagacgg aagtttgtaa acggcgacgg aaaacgctct gggttggaga 600  
cggcgacgta cggaaacgac gctgttttga gagcgcgatg ggttttggtc gagaagactg 660  
ttacgccgag cgacgtcggg aagctgaacc gtttagtgat accgaaacaa cagcgggaga 720  
agcattttcc gttatcggcg atgacgacgg cgatggggat gaatccGtct ccgacgaaag 780  
gcgttttgat taacttggaa gatagaacag ggaaagtgtg gcggttccgt tacagttact 840  
ggaacagcag tcaaagttag gtgttgacca agggctggag ccggttcgtt aaagagaaga 900  
atcttcgagc cggatgatgt gtttgtttcg agagatcaac cggaccagac cggcaattgt 960  
atatccactg gaaagtccgg tctagtccgg ttcagactgt ggtaggcta ttcggagtca 1020  
acattttcaa tgtgagtaac gagaaaccaa acgacgtcgc agtagagtgt gttggcaaga 1080  
agagatctcg ggaagatgat ttgttttcgt taggggtgtt caagaagcag gcgattatca 1140  
acatcttgtg acaaattctt ttttttttgt tttttttctt caatttgttt ctcttttttc 1200  
aatattttgt attgaaatga caagttgtaa attaggacaa tacaagaaaa aatgacaact 1260  
ag

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..382  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1565958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Lys | Asn | Leu | Thr | His | Phe | Phe | Phe | Phe | Phe | Cys | Phe | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asn | Thr | Thr | Asn | Met | Glu | Tyr | Ser | Cys | Val | Asp | Asp | Ser | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Glu | Ser | Leu | Ser | Ile | Ser | Thr | Thr | Pro | Lys | Pro | Thr | Thr | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Glu | Lys | Lys | Leu | Ser | Ser | Pro | Pro | Ala | Thr | Ser | Met | Arg | Leu | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Met | Gly | Ser | Gly | Gly | Ser | Ser | Val | Val | Leu | Asp | Ser | Glu | Asn | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Glu | Thr | Glu | Ser | Arg | Lys | Leu | Pro | Ser | Ser | Lys | Tyr | Lys | Gly | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Pro | Gln | Pro | Asn | Gly | Arg | Trp | Gly | Ala | Gln | Ile | Tyr | Glu | Lys | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Arg | Val | Trp | Leu | Gly | Thr | Phe | Asn | Glu | Glu | Glu | Glu | Ala | Ala | Ser |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Tyr | Asp | Ile | Ala | Val | Arg | Arg | Phe | Arg | Gly | Arg | Asp | Ala | Val | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Phe | Lys | Ser | Gln | Val | Asp | Gly | Asn | Asp | Ala | Glu | Ser | Ala | Phe | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Ala | His | Ser | Lys | Ala | Glu | Ile | Val | Asp | Met | Leu | Arg | Lys | His | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Ala | Asp | Glu | Phe | Glu | Gln | Ser | Arg | Arg | Lys | Phe | Val | Asn | Gly | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Lys | Arg | Ser | Gly | Leu | Glu | Thr | Ala | Thr | Tyr | Gly | Asn | Asp | Ala | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Arg | Ala | Arg | Glu | Val | Leu | Phe | Glu | Lys | Thr | Val | Thr | Pro | Ser | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Gly | Lys | Leu | Asn | Arg | Leu | Val | Ile | Pro | Lys | Gln | His | Ala | Glu | Lys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Phe | Pro | Leu | Ser | Ala | Met | Thr | Thr | Ala | Met | Gly | Met | Asn | Pro | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Thr | Lys | Gly | Val | Leu | Ile | Asn | Leu | Glu | Asp | Arg | Thr | Gly | Lys | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Arg | Phe | Arg | Tyr | Ser | Tyr | Trp | Asn | Ser | Ser | Gln | Ser | Tyr | Val | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Lys | Gly | Trp | Ser | Arg | Phe | Val | Lys | Glu | Lys | Asn | Leu | Arg | Ala | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Val | Val | Cys | Phe | Glu | Arg | Ser | Thr | Gly | Pro | Asp | Arg | Gln | Leu | Tyr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | His | Trp | Lys | Val | Arg | Ser | Ser | Pro | Val | Gln | Thr | Val | Val | Arg | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Gly | Val | Asn | Ile | Phe | Asn | Val | Ser | Asn | Glu | Lys | Pro | Asn | Asp | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Val | Glu | Cys | Val | Gly | Lys | Lys | Arg | Ser | Arg | Glu | Asp | Asp | Leu | Phe |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Ser | Leu | Gly | Cys | Ser | Lys | Lys | Gln | Ala | Ile | Ile | Asn | Ile | Leu |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 361 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:143:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 322 amino acids  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS:  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
     (A) NAME/KEY: peptide



(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1565960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Arg Leu Tyr Arg Met Gly Ser Gly Ser Ser Val Val Leu Asp  
1 5 10 15  
Ser Glu Asn Gly Val Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys  
20 25 30  
Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile  
35 40 45  
Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Glu  
50 55 60  
Glu Ala Ala Ser Ser Tyr Asp Ile Ala Val Arg Arg Phe Arg Gly Arg  
65 70 75 80  
Asp Ala Val Thr Asn Phe Lys Ser Gln Val Asp Gly Asn Asp Ala Glu  
85 90 95  
Ser Ala Phe Leu Asp Ala His Ser Lys Ala Glu Ile Val Asp Met Leu  
100 105 110  
Arg Lys His Thr Tyr Ala Asp Glu Phe Glu Gln Ser Arg Arg Lys Phe  
115 120 125  
Val Asn Gly Asp Gly Lys Arg Ser Gly Leu Glu Thr Ala Thr Tyr Gly  
130 135 140  
Asn Asp Ala Val Leu Arg Ala Arg Glu Val Leu Phe Glu Lys Thr Val  
145 150 155 160  
Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln  
165 170 175  
His Ala Glu Lys His Phe Pro Leu Ser Ala Met Thr Thr Ala Met Gly  
180 185 190  
Met Asn Pro Ser Pro Thr Lys Gly Val Leu Ile Asn Leu Glu Asp Arg  
195 200 205  
Thr Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln  
210 215 220  
Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn  
225 230 235 240  
Leu Arg Ala Gly Asp Val Val Cys Phe Glu Arg Ser Thr Gly Pro Asp  
245 250 255  
Arg Gln Leu Tyr Ile His Trp Lys Val Arg Ser Ser Pro Val Gln Thr  
260 265 270  
Val Val Arg Leu Phe Gly Val Asn Ile Phe Asn Val Ser Asn Glu Lys  
275 280 285  
Pro Asn Asp Val Ala Val Glu Cys Val Gly Lys Lys Arg Ser Arg Glu  
290 295 300  
Asp Asp Leu Phe Ser Leu Gly Cys Ser Lys Lys Gln Ala Ile Ile Asn  
305 310 315 320  
Ile Leu

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1351

(D) OTHER INFORMATION: / Ceres Seq. ID 1565965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

|                                              |     |
|----------------------------------------------|-----|
| aactggtaaa ccctaagaat cctccgcaat ttcgcaat    | 60  |
| tttgcgaattt tgtgaaggag ccgcgcggcta           |     |
| aatttgatgg cagaccaaag ttcggagatc gtcaatgctc  | 120 |
| tgctcgtcgga gatggaagct                       |     |
| gtttccggtt catcaactca ggcattcttct tcgtccgatg | 180 |
| gattccagat gattgaagaa                        |     |
| ggtgagaaga gatacaaaat tgtaggagat atcggtgagg  | 240 |
| aatgtatata agaggaagag                        |     |

ctaaagaatc ttcttgctaa gaaggctgct ccgatttgct acgacggott tgaaccatca 300  
ggaagaatgc acattgctca gggagtgatg aaagtcatca atgtgaacaa aatgacttca 360  
gctgggttgca gagtgaagat ttggattTgc tgattggttt gctcagttga acaacaaaat 420  
gggtgggtgac ttgaagaaaa tcagagtggg tggagaatac tttcaagaga tatggaaggc 480  
tgctgggatg gataatgaca aagtagagtt tttgtggctg toccaagaaa ttaattctaa 540  
ggcagataag tattggcctc ttgtgatgga cattgctcgc aaaaacaagc tccctagaat 600  
cttaagggtg gtgcagatta tgggacgtag tgagactgat gaactgagtg ctgccagat 660  
cctttaccca tgcattgcaat gtgcagatat ttttttctt gaggtgata tttgccagct 720  
tgggatggat caaagaaaag taaCatgtgc tagcgagaga atactgtgat gacataaaga 780  
ggaaaaacaa accgataatc ttgtcacacc atatgcttcc tgggtctcaa caaggacaag 840  
aaaagatgtc caaaagtgat ccattatctg ctatctttat ggaagatgaa gaggtgaag 900  
ttaatgtgaa gatcaagaaa gcttactgcc ctccaaaagt cgtgaagggc aatccatgcc 960  
tcgaatacat caaatacat aaatacatca ttctaccatg gtttgatgag ttcacagttg 1020  
agagaaatga agaatatggc ggtaacaaga cctacaaaag ctttgaagac attgctgctg 1080  
actatgagag cggcgagttg caccctggcg atctaaagaa aggcctgatg aacgcgttga 1140  
ataagatttt gcaacctgtt cgtgatcatt tcaaaacaga cgcacgcgcg aagaatctac 1200  
tcaaacagat caaggcttac agagtcacca gataaaatta gagagccaga atgtgtcatt 1260  
gaaagctttc tctcacttta tgaaacttat tattaccaaa aacacactgt aaaactcctg 1320  
gattttgttt atttgggtat atcagatgct c

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Met Leu Pro Gly Leu Gln Gln Gly Gln Glu Lys Met Ser Lys Ser Asp  
1 5 10 15  
Pro Leu Ser Ala Ile Phe Met Glu Asp Glu Glu Ala Glu Val Asn Val  
20 25 30  
Lys Ile Lys Lys Ala Tyr Cys Pro Pro Lys Val Val Lys Gly Asn Pro  
35 40 45  
Cys Leu Glu Tyr Ile Lys Tyr Ile Lys Tyr Ile Ile Leu Pro Trp Phe  
50 55 60  
Asp Glu Phe Thr Val Glu Arg Asn Glu Glu Tyr Gly Gly Asn Lys Thr  
65 70 75 80  
Tyr Lys Ser Phe Glu Asp Ile Ala Ala Asp Tyr Glu Ser Gly Glu Leu  
85 90 95  
His Pro Gly Asp Leu Lys Lys Gly Leu Met Asn Ala Leu Asn Lys Ile  
100 105 110  
Leu Gln Pro Val Arg Asp His Phe Lys Thr Asp Ala Arg Ala Lys Asn  
115 120 125  
Leu Leu Lys Gln Ile Lys Ala Tyr Arg Val Thr Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

1565966-1565967

Met Ser Lys Ser Asp Pro Leu Ser Ala Ile Phe Met Glu Asp Glu Glu  
1 5 10 15  
Ala Glu Val Asn Val Lys Ile Lys Lys Ala Tyr Cys Pro Pro Lys Val  
20 25 30  
Val Lys Gly Asn Pro Cys Leu Glu Tyr Ile Lys Tyr Ile Lys Tyr Ile  
35 40 45  
Ile Leu Pro Trp Phe Asp Glu Phe Thr Val Glu Arg Asn Glu Glu Tyr  
50 55 60  
Gly Gly Asn Lys Thr Tyr Lys Ser Phe Glu Asp Ile Ala Ala Asp Tyr  
65 70 75 80  
Glu Ser Gly Glu Leu His Pro Gly Asp Leu Lys Lys Gly Leu Met Asn  
85 90 95  
Ala Leu Asn Lys Ile Leu Gln Pro Val Arg Asp His Phe Lys Thr Asp  
100 105 110  
Ala Arg Ala Lys Asn Leu Leu Lys Gln Ile Lys Ala Tyr Arg Val Thr  
115 120 125  
Arg

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1565968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Met Glu Asp Glu Glu Ala Glu Val Asn Val Lys Ile Lys Lys Ala Tyr  
1 5 10 15  
Cys Pro Pro Lys Val Val Lys Gly Asn Pro Cys Leu Glu Tyr Ile Lys  
20 25 30  
Tyr Ile Lys Tyr Ile Ile Leu Pro Trp Phe Asp Glu Phe Thr Val Glu  
35 40 45  
Arg Asn Glu Glu Tyr Gly Gly Asn Lys Thr Tyr Lys Ser Phe Glu Asp  
50 55 60  
Ile Ala Ala Asp Tyr Glu Ser Gly Glu Leu His Pro Gly Asp Leu Lys  
65 70 75 80  
Lys Gly Leu Met Asn Ala Leu Asn Lys Ile Leu Gln Pro Val Arg Asp  
85 90 95  
His Phe Lys Thr Asp Ala Arg Ala Lys Asn Leu Leu Lys Gln Ile Lys  
100 105 110  
Ala Tyr Arg Val Thr Arg  
115

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1164 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1164

(D) OTHER INFORMATION: / Ceres Seq. ID 1565973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aattagctca aggagaatca aaAgcgtcgt ctcttgttcC ttccgctgcc aacaaaatgg | 60  |
| agctgtcgtc tgcgtccgcc atattaagcc actcctctc cgccgctcag cttctcagac  | 120 |
| ctaagctcgg gtttattgat ttgcttcctc gtcgagcgat gatcgtttct tctccttctt | 180 |

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| cttcgcttcc  | tcgatttttg | cggatggaat  | ctcaatctca | gcttcgcca   | tctatctctt | 240  |
| gctctgcttc  | ttcttcttct | tctatggcat  | taggtagaat | tggagaagta  | aagagagtaa | 300  |
| caaaggaaac  | gaatgtttca | gtgaagatta  | atttgatgg  | tactggagtt  | gcagatagtt | 360  |
| ctagtggaa   | tcctttcctt | gaccatatgt  | tagatcaact | tgcttcgcat  | ggcttgtttg | 420  |
| atgtgcacgt  | tagagctact | ggtgatgttc  | acattgatga | tcatcacact  | aatgaagata | 480  |
| tagctcttgc  | cattggaact | gctctattaa  | aggctcttgg | tgagcgtaaa  | gggattaacc | 540  |
| ggtttggtga  | cttcacagct | cctctagatg  | aagcgcttat | acatgtttcc  | ttggacttgt | 600  |
| ctggctgcacc | atatcttggt | tacaacttgg  | agataccaac | tcagagagtt  | ggaacatatg | 660  |
| atactcagtt  | ggtggagcac | tttttccagt  | cattggtgaa | tacttctggt  | atgactcttc | 720  |
| acatccggca  | gctcgctggt | gaaaactctc  | atcacataat | agaggcgacg  | tttaaggcgt | 780  |
| ttgccagagc  | tctacgacaa | gcaacagaga  | ctgataCacg | ccgtgggtggg | acaataccaa | 840  |
| gttcaaaagg  | agtcttatca | cggctcttgaa | agctaataca | acacacaaga  | cagttcccag | 900  |
| attcacactt  | catcgtcgag | ttcatgagcc  | atcgtcaatt | ctcttatggt  | accaaatgcc | 960  |
| aagcctgttg  | gatcttgctg | ttccattcca  | ttacagaagc | acaaagagca  | aaatgtgaaa | 1020 |
| atagattaga  | gatcacacag | ttcagaagat  | cataggctca | tctttatatt  | aatctgttgt | 1080 |
| tgcagagtgt  | attaaacctc | ttaccattgc  | tgtatcatca | tcaactgaga  | acttactgtg | 1140 |
| agttgaagtg  | actgtaattt | gctc        |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1565974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Gln | Gly | Glu | Ser | Lys | Ala | Ser | Ser | Leu | Val | Pro | Ser | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Lys | Met | Glu | Leu | Ser | Ser | Ala | Ser | Ala | Ile | Leu | Ser | His | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ala | Ala | Gln | Leu | Leu | Arg | Pro | Lys | Leu | Gly | Phe | Ile | Asp | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Arg | Arg | Ala | Met | Ile | Val | Ser | Ser | Pro | Ser | Ser | Ser | Leu | Pro | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Leu | Arg | Met | Glu | Ser | Gln | Ser | Gln | Leu | Arg | Gln | Ser | Ile | Ser | Cys |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ser | Ala | Ser | Ser | Ser | Ser | Ser | Met | Ala | Leu | Gly | Arg | Ile | Gly | Glu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Arg | Val | Thr | Lys | Glu | Thr | Asn | Val | Ser | Val | Lys | Ile | Asn | Leu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Gly | Val | Ala | Asp | Ser | Ser | Ser | Gly | Ile | Pro | Phe | Leu | Asp | His |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Met | Leu | Asp | Gln | Leu | Ala | Ser | His | Gly | Leu | Phe | Asp | Val | His | Val | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Gly | Asp | Val | His | Ile | Asp | Asp | His | His | Thr | Asn | Glu | Asp | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Leu | Ala | Ile | Gly | Thr | Ala | Leu | Leu | Lys | Ala | Leu | Gly | Glu | Arg | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ile | Asn | Arg | Phe | Gly | Asp | Phe | Thr | Ala | Pro | Leu | Asp | Glu | Ala | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ile | His | Val | Ser | Leu | Asp | Leu | Ser | Gly | Arg | Pro | Tyr | Leu | Gly | Tyr | Asn |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Glu | Ile | Pro | Thr | Gln | Arg | Val | Gly | Thr | Tyr | Asp | Thr | Gln | Leu | Val |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | His | Phe | Phe | Gln | Ser | Leu | Val | Asn | Thr | Ser | Gly | Met | Thr | Leu | His |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Arg | Gln | Leu | Ala | Gly | Glu | Asn | Ser | His | His | Ile | Ile | Glu | Ala | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Lys | Ala | Phe | Ala | Arg | Ala | Leu | Arg | Gln | Ala | Thr | Glu | Thr | Asp | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Arg | Gly | Gly | Thr | Ile | Pro | Ser | Ser | Lys | Gly | Val | Leu | Ser | Arg | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1565975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ser | Ser | Ala | Ser | Ala | Ile | Leu | Ser | His | Ser | Ser | Ser | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Gln | Leu | Leu | Arg | Pro | Lys | Leu | Gly | Phe | Ile | Asp | Leu | Leu | Pro | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Ala | Met | Ile | Val | Ser | Ser | Pro | Ser | Ser | Ser | Leu | Pro | Arg | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Met | Glu | Ser | Gln | Ser | Gln | Leu | Arg | Gln | Ser | Ile | Ser | Cys | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ser | Ser | Ser | Met | Ala | Leu | Gly | Arg | Ile | Gly | Glu | Val | Lys | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Thr | Lys | Glu | Thr | Asn | Val | Ser | Val | Lys | Ile | Asn | Leu | Asp | Gly | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Val | Ala | Asp | Ser | Ser | Ser | Gly | Ile | Pro | Phe | Leu | Asp | His | Met | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Gln | Leu | Ala | Ser | His | Gly | Leu | Phe | Asp | Val | His | Val | Arg | Ala | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Val | His | Ile | Asp | Asp | His | His | Thr | Asn | Glu | Asp | Ile | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ile | Gly | Thr | Ala | Leu | Leu | Lys | Ala | Leu | Gly | Glu | Arg | Lys | Gly | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Arg | Phe | Gly | Asp | Phe | Thr | Ala | Pro | Leu | Asp | Glu | Ala | Leu | Ile | His |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ser | Leu | Asp | Leu | Ser | Gly | Arg | Pro | Tyr | Leu | Gly | Tyr | Asn | Leu | Glu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ile | Pro | Thr | Gln | Arg | Val | Gly | Thr | Tyr | Asp | Thr | Gln | Leu | Val | Glu | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Phe | Gln | Ser | Leu | Val | Asn | Thr | Ser | Gly | Met | Thr | Leu | His | Ile | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Leu | Ala | Gly | Glu | Asn | Ser | His | His | Ile | Ile | Glu | Ala | Thr | Phe | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Phe | Ala | Arg | Ala | Leu | Arg | Gln | Ala | Thr | Glu | Thr | Asp | Pro | Arg | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Gly | Thr | Ile | Pro | Ser | Ser | Lys | Gly | Val | Leu | Ser | Arg | Ser |     |     |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     | 270 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1565976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Val | Ser | Pro | Ser | Ser | Ser | Ser | Leu | Pro | Arg | Phe | Leu | Arg | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Ser | Gln | Ser | Gln | Leu | Arg | Gln | Ser | Ile | Ser | Cys | Ser | Ala | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ser | Met | Ala | Leu | Gly | Arg | Ile | Gly | Glu | Val | Lys | Arg | Val | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Thr | Asn | Val | Ser | Val | Lys | Ile | Asn | Leu | Asp | Gly | Thr | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Asp | Ser | Ser | Ser | Gly | Ile | Pro | Phe | Leu | Asp | His | Met | Leu | Asp | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ala | Ser | His | Gly | Leu | Phe | Asp | Val | His | Val | Arg | Ala | Thr | Gly | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | His | Ile | Asp | Asp | His | His | Thr | Asn | Glu | Asp | Ile | Ala | Leu | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Ala | Leu | Leu | Lys | Ala | Leu | Gly | Glu | Arg | Lys | Gly | Ile | Asn | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Gly | Asp | Phe | Thr | Ala | Pro | Leu | Asp | Glu | Ala | Leu | Ile | His | Val | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asp | Leu | Ser | Gly | Arg | Pro | Tyr | Leu | Gly | Tyr | Asn | Leu | Glu | Ile | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Gln | Arg | Val | Gly | Thr | Tyr | Asp | Thr | Gln | Leu | Val | Glu | His | Phe | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gln | Ser | Leu | Val | Asn | Thr | Ser | Gly | Met | Thr | Leu | His | Ile | Arg | Gln | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Gly | Glu | Asn | Ser | His | His | Ile | Ile | Glu | Ala | Thr | Phe | Lys | Ala | Phe |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Arg | Ala | Leu | Arg | Gln | Ala | Thr | Glu | Thr | Asp | Pro | Arg | Arg | Gly | Gly |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Thr | Ile | Pro | Ser | Ser | Lys | Gly | Val | Leu | Ser | Arg | Ser |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1820 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1820

(D) OTHER INFORMATION: / Ceres Seq. ID 1565981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

|             |            |             |              |             |             |     |
|-------------|------------|-------------|--------------|-------------|-------------|-----|
| acaatcattt  | gattatttcc | tcctctccgt  | atctgtgtct   | ctcttctctt  | gattcttttag | 60  |
| tggtcttgct  | ttgtcgcttc | aacgcttaag  | tttgattttg   | tgtgagtctg  | cataatcatg  | 120 |
| gcgaggaaga  | tgcttggtga | tggtgagatt  | gataaggtgg   | cggctgatga  | agccaacgcg  | 180 |
| acgcactatg  | attttgattt | gtttgtcatc  | gggtgccgga   | gtggcggtgt  | tcgtgctgct  | 240 |
| aggttttcgg  | ctaatacatg | cgctaagggt  | gggtatttgt   | agcttccatt  | tcaccctatt  | 300 |
| agctctgagg  | agattggagg | cgttgggtgga | acctgtgtta   | tccgtgggtg  | tgttcctaaa  | 360 |
| aagattctcg  | tctatggagc | tacttacggt  | gggtgaacttg  | aggatgctaa  | aaattatggg  | 420 |
| tgggaaataa  | atgagaaagt | cgacttcaca  | tggaagaagc   | ttttgcaaaa  | gaagactgat  | 480 |
| gagatactaa  | gactgaataa | tatctacaag  | cggttatttg   | caaatgctgc  | gggtgaaattg | 540 |
| tatgaaggtg  | aaggaagagt | agttgggtccc | aacgaagtgg   | agggtgagaca | aatagatggc  | 600 |
| acaaaaataa  | gttataccgc | aaagcacata  | ttgattgcca   | ctggcagtcg  | ggcgcaaaag  | 660 |
| cctaataattc | ctggacatga | gctggctatt  | acatctgatg   | aagctttgag  | cttggaagaa  | 720 |
| tttcccaagc  | gtgctatagt | gcttgaggga  | gggtatatattg | ctgtggagtt  | tgcatcaata  | 780 |
| tggtgctggaa | tggttgctac | tgtagattta  | ttcttcagga   | aggaacttcc  | gctaaggggt  | 840 |
| tttgatgacg  | aaatgagggc | actagttgct  | agaaatcttg   | aaggaagggg  | cgtaaatctg  | 900 |
| catccacaaa  | caagtttgac | tcagttgaca  | aaaacagacc   | aggggatcaa  | agtcatatcg  | 960 |

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| tcccatgggg  | aggaattcgt | ggcagatgtc | gtcctatttg | ctactggcag | aagtccta    | 1020 |
| acccaaaagat | tgaatttaga | agctgttggt | gttgaacttg | atcaggctgg | agctgtgaag  | 1080 |
| gttgacgagt  | attcacgaac | taatatacct | agcatatggg | ctgtaggaga | tgccacaaac  | 1140 |
| cgaattaacc  | ttacacctgt | tcggttaatg | gaggccacct | gttttgcgaa | cactgctttt  | 1200 |
| gttggaagc   | ctactaaagc | agaatacagc | aatgtcgct  | gtgctgtatt | ttgcatacca  | 1260 |
| ccactagctg  | tagtgggtct | cagcgaagaa | gaagcagtag | aacaagcaac | cggtgatatt  | 1320 |
| ctggctcttca | cctcaggott | taatccaatg | aagaacacca | tttctggacg | ccaggaaaag  | 1380 |
| acattgatga  | agctaatagt | tgatgagaag | agtgataagg | ttattggagc | atccatgtgc  | 1440 |
| ggtcctgatg  | cagctgagat | catgcagggg | attgcaattg | cgctcaagtg | tggagcaacc  | 1500 |
| aaagcacaat  | ttgatagcac | ggbtsggatG | CGCacatcca | tcttctgcag | aggaatttgt  | 1560 |
| gacaatgcgc  | agtgtgacca | gacgcattgc | ccacaaaacc | aaacctaaga | caaactctatg | 1620 |
| aaccgcaaaa  | tataaagagc | tatatagcat | gaaaactcgg | tacacttagt | ttgatcaaag  | 1680 |
| agtcagacaa  | cgatgagttt | aatcatactc | gtgtcccaat | aaaggatttg | taatttttgt  | 1740 |
| ttgtttgtat  | gatgcttctc | ttcttactta | cttgagaaaa | catcaagggt | tcttctctta  | 1800 |
| ttgcttagtg  | gaactttatt |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1565982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Lys | Met | Leu | Val | Asp | Gly | Glu | Ile | Asp | Lys | Val | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Ala | Asn | Ala | Thr | His | Tyr | Asp | Phe | Asp | Leu | Phe | Val | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Ser | Gly | Gly | Val | Arg | Ala | Ala | Arg | Phe | Ser | Ala | Asn | His | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Lys | Val | Gly | Ile | Cys | Glu | Leu | Pro | Phe | His | Pro | Ile | Ser | Ser | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Ile | Gly | Gly | Val | Gly | Gly | Thr | Cys | Val | Ile | Arg | Gly | Cys | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Lys | Ile | Leu | Val | Tyr | Gly | Ala | Thr | Tyr | Gly | Gly | Glu | Leu | Glu | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Asn | Tyr | Gly | Trp | Glu | Ile | Asn | Glu | Lys | Val | Asp | Phe | Thr | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Lys | Leu | Leu | Gln | Lys | Lys | Thr | Asp | Glu | Ile | Leu | Arg | Leu | Asn | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Tyr | Lys | Arg | Leu | Leu | Ala | Asn | Ala | Ala | Val | Lys | Leu | Tyr | Glu | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Gly | Arg | Val | Val | Gly | Pro | Asn | Glu | Val | Glu | Val | Arg | Gln | Ile | Asp |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Thr | Lys | Ile | Ser | Tyr | Thr | Ala | Lys | His | Ile | Leu | Ile | Ala | Thr | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Arg | Ala | Gln | Lys | Pro | Asn | Ile | Pro | Gly | His | Glu | Leu | Ala | Ile | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Asp | Glu | Ala | Leu | Ser | Leu | Glu | Glu | Phe | Pro | Lys | Arg | Ala | Ile | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gly | Gly | Gly | Tyr | Ile | Ala | Val | Glu | Phe | Ala | Ser | Ile | Trp | Arg | Gly |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Gly | Ala | Thr | Val | Asp | Leu | Phe | Phe | Arg | Lys | Glu | Leu | Pro | Leu | Arg |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Phe | Asp | Asp | Glu | Met | Arg | Ala | Leu | Val | Ala | Arg | Asn | Leu | Glu | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Gly | Val | Asn | Leu | His | Pro | Gln | Thr | Ser | Leu | Thr | Gln | Leu | Thr | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Gln | Gly | Ile | Lys | Val | Ile | Ser | Ser | His | Gly | Glu | Glu | Phe | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Asp | Val | Val | Leu | Phe | Ala | Thr | Gly | Arg | Ser | Pro | Asn | Thr | Lys | Arg |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asn | Leu | Glu | Ala | Val | Gly | Val | Glu | Leu | Asp | Gln | Ala | Gly | Ala | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Val | Asp | Glu | Tyr | Ser | Arg | Thr | Asn | Ile | Pro | Ser | Ile | Trp | Ala | Val |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Asp | Ala | Thr | Asn | Arg | Ile | Asn | Leu | Thr | Pro | Val | Ala | Leu | Met | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Thr | Cys | Phe | Ala | Asn | Thr | Ala | Phe | Gly | Gly | Lys | Pro | Thr | Lys | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Tyr | Ser | Asn | Val | Ala | Cys | Ala | Val | Phe | Cys | Ile | Pro | Pro | Leu | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Val | Gly | Leu | Ser | Glu | Glu | Glu | Ala | Val | Glu | Gln | Ala | Thr | Gly | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ile | Leu | Val | Phe | Thr | Ser | Gly | Phe | Asn | Pro | Met | Lys | Asn | Thr | Ile | Ser |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gly | Arg | Gln | Glu | Lys | Thr | Leu | Met | Lys | Leu | Ile | Val | Asp | Glu | Lys | Ser |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Asp | Lys | Val | Ile | Gly | Ala | Ser | Met | Cys | Gly | Pro | Asp | Ala | Ala | Glu | Ile |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Met | Gln | Gly | Ile | Ala | Ile | Ala | Leu | Lys | Cys | Gly | Ala | Thr | Lys | Ala | Gln |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Phe | Asp | Ser | Thr | Xaa | Xaa | Met | Arg | Thr | Ser | Ile | Phe | Cys | Arg | Gly | Ile |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Cys | Asp | Asn | Ala | Gln | Cys | Asp | Gln | Thr | His | Cys | Pro | Gln | Thr | Gln | Thr |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..492
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Asp | Gly | Glu | Ile | Asp | Lys | Val | Ala | Ala | Asp | Glu | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Thr | His | Tyr | Asp | Phe | Asp | Leu | Phe | Val | Ile | Gly | Ala | Gly | Ser | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gly | Val | Arg | Ala | Ala | Arg | Phe | Ser | Ala | Asn | His | Gly | Ala | Lys | Val | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | Cys | Glu | Leu | Pro | Phe | His | Pro | Ile | Ser | Ser | Glu | Glu | Ile | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Gly | Gly | Thr | Cys | Val | Ile | Arg | Gly | Cys | Val | Pro | Lys | Lys | Ile | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Tyr | Gly | Ala | Thr | Tyr | Gly | Gly | Glu | Leu | Glu | Asp | Ala | Lys | Asn | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Trp | Glu | Ile | Asn | Glu | Lys | Val | Asp | Phe | Thr | Trp | Lys | Lys | Leu | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gln | Lys | Lys | Thr | Asp | Glu | Ile | Leu | Arg | Leu | Asn | Asn | Ile | Tyr | Lys | Arg |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Ala | Asn | Ala | Ala | Val | Lys | Leu | Tyr | Glu | Gly | Glu | Gly | Arg | Val |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Val | Gly | Pro | Asn | Glu | Val | Glu | Val | Arg | Gln | Ile | Asp | Gly | Thr | Lys | Ile |



145 150 155 160  
Ser Tyr Thr Ala Lys His Ile Leu Ile Ala Thr Gly Ser Arg Ala Gln  
165 170 175  
Lys Pro Asn Ile Pro Gly His Glu Leu Ala Ile Thr Ser Asp Glu Ala  
180 185 190  
Leu Ser Leu Glu Glu Phe Pro Lys Arg Ala Ile Val Leu Gly Gly Gly  
195 200 205  
Tyr Ile Ala Val Glu Phe Ala Ser Ile Trp Arg Gly Met Gly Ala Thr  
210 215 220  
Val Asp Leu Phe Phe Arg Lys Glu Leu Pro Leu Arg Gly Phe Asp Asp  
225 230 235 240  
Glu Met Arg Ala Leu Val Ala Arg Asn Leu Glu Gly Arg Gly Val Asn  
245 250 255  
Leu His Pro Gln Thr Ser Leu Thr Gln Leu Thr Lys Thr Asp Gln Gly  
260 265 270  
Ile Lys Val Ile Ser Ser His Gly Glu Glu Phe Val Ala Asp Val Val  
275 280 285  
Leu Phe Ala Thr Gly Arg Ser Pro Asn Thr Lys Arg Leu Asn Leu Glu  
290 295 300  
Ala Val Gly Val Glu Leu Asp Gln Ala Gly Ala Val Lys Val Asp Glu  
305 310 315 320  
Tyr Ser Arg Thr Asn Ile Pro Ser Ile Trp Ala Val Gly Asp Ala Thr  
325 330 335  
Asn Arg Ile Asn Leu Thr Pro Val Ala Leu Met Glu Ala Thr Cys Phe  
340 345 350  
Ala Asn Thr Ala Phe Gly Gly Lys Pro Thr Lys Ala Glu Tyr Ser Asn  
355 360 365  
Val Ala Cys Ala Val Phe Cys Ile Pro Pro Leu Ala Val Val Gly Leu  
370 375 380  
Ser Glu Glu Glu Ala Val Glu Gln Ala Thr Gly Asp Ile Leu Val Phe  
385 390 395 400  
Thr Ser Gly Phe Asn Pro Met Lys Asn Thr Ile Ser Gly Arg Gln Glu  
405 410 415  
Lys Thr Leu Met Lys Leu Ile Val Asp Glu Lys Ser Asp Lys Val Ile  
420 425 430  
Gly Ala Ser Met Cys Gly Pro Asp Ala Ala Glu Ile Met Gln Gly Ile  
435 440 445  
Ala Ile Ala Leu Lys Cys Gly Ala Thr Lys Ala Gln Phe Asp Ser Thr  
450 455 460  
Xaa Xaa Met Arg Thr Ser Ile Phe Cys Arg Gly Ile Cys Asp Asn Ala  
465 470 475 480  
Gln Cys Asp Gln Thr His Cys Pro Gln Thr Gln Thr  
485 490

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1565984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Gly Ala Thr Val Asp Leu Phe Phe Arg Lys Glu Leu Pro Leu Arg  
1 5 10 15  
Gly Phe Asp Asp Glu Met Arg Ala Leu Val Ala Arg Asn Leu Glu Gly  
20 25 30  
Arg Gly Val Asn Leu His Pro Gln Thr Ser Leu Thr Gln Leu Thr Lys  
35 40 45

Thr Asp Gln Gly Ile Lys Val Ile Ser Ser His Gly Glu Glu Phe Val  
50 55 60  
Ala Asp Val Val Leu Phe Ala Thr Gly Arg Ser Pro Asn Thr Lys Arg  
65 70 75 80  
Leu Asn Leu Glu Ala Val Gly Val Glu Leu Asp Gln Ala Gly Ala Val  
85 90 95  
Lys Val Asp Glu Tyr Ser Arg Thr Asn Ile Pro Ser Ile Trp Ala Val  
100 105 110  
Gly Asp Ala Thr Asn Arg Ile Asn Leu Thr Pro Val Ala Leu Met Glu  
115 120 125  
Ala Thr Cys Phe Ala Asn Thr Ala Phe Gly Gly Lys Pro Thr Lys Ala  
130 135 140  
Glu Tyr Ser Asn Val Ala Cys Ala Val Phe Cys Ile Pro Pro Leu Ala  
145 150 155 160  
Val Val Gly Leu Ser Glu Glu Glu Ala Val Glu Gln Ala Thr Gly Asp  
165 170 175  
Ile Leu Val Phe Thr Ser Gly Phe Asn Pro Met Lys Asn Thr Ile Ser  
180 185 190  
Gly Arg Gln Glu Lys Thr Leu Met Lys Leu Ile Val Asp Glu Lys Ser  
195 200 205  
Asp Lys Val Ile Gly Ala Ser Met Cys Gly Pro Asp Ala Ala Glu Ile  
210 215 220  
Met Gln Gly Ile Ala Ile Ala Leu Lys Cys Gly Ala Thr Lys Ala Gln  
225 230 235 240  
Phe Asp Ser Thr Xaa Xaa Met Arg Thr Ser Ile Phe Cys Arg Gly Ile  
245 250 255  
Cys Asp Asn Ala Gln Cys Asp Gln Thr His Cys Pro Gln Thr Gln Thr  
260 265 270

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tctctgacg gttcttttct tcttcgtcc tctcgttttt tttgtttcgt cgtctctctc    | 60   |
| tcccgctctg aaaaattcgc agaatccgtc atgtcttccg gcgtaaattc aactggctcc  | 120  |
| gccgcagcag caccggaggt tgacaagatg ttcttctgct accagtgcaa tcaaacagtc  | 180  |
| acaatctcaa tttctctcat cgtgatcct ttttgtccaa tttgtaacca agggtttctt   | 240  |
| gaagaatacg aagaccctaa cctaatacaa tccctcaatt tcaaccctaa ctcttctgat  | 300  |
| tcttttttcc ccatggccga tcttttctcc accttgctcc cgctcatatt cggctcttcc  | 360  |
| gctgccgctc ctccggcat ggacttcatg agcttattcg gtccttcgat gcaaccacag   | 420  |
| gctcgttcca ctacgcagaa tctcagttct gacgcgtttg atccgtttac gtttcttcag  | 480  |
| aatcatctcc agactttgcg atctagcggg acgcactttg agttcgtgat cgagaatcat  | 540  |
| ccttcggatc caggtaatcg tatgcctggg aatttcgggtg attacttctt tgggccaggt | 600  |
| cttgagcagt tgattcagca actagctgag aatgatccta atcgttacgg aactcctcct  | 660  |
| gcttccaaat ccgccattga tgctcttctt actgttaagg taacgaagga tatgttgaaa  | 720  |
| tcggagatga accaatgocg ggtgtgtatg gatgagtttg aggatggtag cgatgttaag  | 780  |
| cagatgcctt gtaagcacgt ctttcacatg gactgtttgc tcccttggtt ggagttgcat  | 840  |
| aattcgtgtc ctgtttgtcg attcagagttg Cctacggatg atcctgatta tgagaacagg | 900  |
| agtcaaggaa gtcaggggag tggatgatga cgaggatcgg ttgagggtca gcagacgccg  | 960  |
| aggtttagta tacaacttcc ttggccgttc aggagacaag atggctctgg ttcaggctcg  | 1020 |
| ggagcactcg gtgctggtgg aggtaatctt gagaccaggg gtgaagattt ggattgagaa  | 1080 |
| tgtgttggcc agtcattgct tggaaactgg atcagaagga tatctatccc aagttctcca  | 1140 |

(2) INFORMATION FOR SEQ ID NO:157:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1566012

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Asp | Gly | Ser | Phe | Leu | Pro | Ser | Ser | Ser | Arg | Phe | Phe | Cys | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Val | Ser | Leu | Ser | Arg | Ser | Glu | Lys | Phe | Ala | Glu | Ser | Val | Met | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Val | Asn | Ser | Thr | Gly | Ser | Ala | Ala | Ala | Ala | Pro | Glu | Val | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Met | Phe | Phe | Cys | Tyr | Gln | Cys | Asn | Gln | Thr | Val | Thr | Ile | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ser | Ala | Asp | Pro | Phe | Cys | Pro | Ile | Cys | Asn | Gln | Gly | Phe | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Glu | Tyr | Glu | Asp | Pro | Asn | Pro | Asn | Gln | Ser | Leu | Asn | Phe | Asn | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Ser | Ser | Asp | Ser | Phe | Phe | Pro | Met | Ala | Asp | Pro | Phe | Ser | Thr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Leu | Ile | Phe | Gly | Ser | Ser | Ala | Ala | Ala | Pro | Ser | Gly | Met | Asp |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Phe | Met | Ser | Leu | Phe | Gly | Pro | Ser | Met | Gln | Pro | Gln | Ala | Arg | Ser | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Gln | Asn | Pro | Gln | Ser | Asp | Ala | Phe | Asp | Pro | Phe | Thr | Phe | Leu | Gln |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Asn | His | Leu | Gln | Thr | Leu | Arg | Ser | Ser | Gly | Thr | His | Phe | Glu | Phe | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Glu | Asn | His | Pro | Ser | Asp | Pro | Gly | Asn | Arg | Met | Pro | Gly | Asn | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asp | Tyr | Phe | Phe | Gly | Pro | Gly | Leu | Glu | Gln | Leu | Ile | Gln | Gln | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Glu | Asn | Asp | Pro | Asn | Arg | Tyr | Gly | Thr | Pro | Pro | Ala | Ser | Lys | Ser |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Ile | Asp | Ala | Leu | Pro | Thr | Val | Lys | Val | Thr | Lys | Asp | Met | Leu | Lys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Glu | Met | Asn | Gln | Cys | Ala | Val | Cys | Met | Asp | Glu | Phe | Glu | Asp | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Asp | Val | Lys | Gln | Met | Pro | Cys | Lys | His | Val | Phe | His | Gln | Asp | Cys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Pro | Trp | Leu | Glu | Leu | His | Asn | Ser | Cys | Pro | Val | Cys | Arg | Phe |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Leu | Pro | Thr | Asp | Asp | Pro | Asp | Tyr | Glu | Asn | Arg | Ser | Gln | Gly | Ser |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Gly | Ser | Gly | Asp | Gly | Arg | Gly | Ser | Val | Glu | Gly | Gln | Gln | Thr | Pro |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Arg | Phe | Ser | Ile | Gln | Leu | Pro | Trp | Pro | Phe | Arg | Arg | Gln | Asp | Gly | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Ser | Gly | Ser | Gly | Ala | Pro | Gly | Ala | Gly | Gly | Gly | Asn | Leu | Glu | Thr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg | Gly | Glu | Asp | Leu | Asp |     |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..328

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEO ID NO:158:

Ser Ser Gly Val Asn Ser Thr Gly Ser Ala A

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1566014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met Phe Phe Cys Tyr Gln Cys Asn Gln Thr Val Thr Ile Ser Ile Ser  
1 5 10 15  
Ser Ser Ala Asp Pro Phe Cys Pro Ile Cys Asn Gln Gly Phe Leu Glu  
20 25 30  
Glu Tyr Glu Asp Pro Asn Pro Asn Gln Ser Leu Asn Phe Asn Pro Asn  
35 40 45  
Ser Ser Asp Ser Phe Phe Pro Met Ala Asp Pro Phe Ser Thr Leu Leu  
50 55 60  
Pro Leu Ile Phe Gly Ser Ser Ala Ala Ala Pro Ser Gly Met Asp Phe  
65 70 75 80  
Met Ser Leu Phe Gly Pro Ser Met Gln Pro Gln Ala Arg Ser Thr Gln  
85 90 95  
Gln Asn Pro Gln Ser Asp Ala Phe Asp Pro Phe Thr Phe Leu Gln Asn  
100 105 110  
His Leu Gln Thr Leu Arg Ser Ser Gly Thr His Phe Glu Phe Val Ile  
115 120 125  
Glu Asn His Pro Ser Asp Pro Gly Asn Arg Met Pro Gly Asn Phe Gly  
130 135 140  
Asp Tyr Phe Phe Gly Pro Gly Leu Glu Gln Leu Ile Gln Gln Leu Ala  
145 150 155 160  
Glu Asn Asp Pro Asn Arg Tyr Gly Thr Pro Pro Ala Ser Lys Ser Ala  
165 170 175  
Ile Asp Ala Leu Pro Thr Val Lys Val Thr Lys Asp Met Leu Lys Ser  
180 185 190  
Glu Met Asn Gln Cys Ala Val Cys Met Asp Glu Phe Glu Asp Gly Ser  
195 200 205  
Asp Val Lys Gln Met Pro Cys Lys His Val Phe His Gln Asp Cys Leu  
210 215 220  
Leu Pro Trp Leu Glu Leu His Asn Ser Cys Pro Val Cys Arg Phe Glu  
225 230 235 240  
Leu Pro Thr Asp Asp Pro Asp Tyr Glu Asn Arg Ser Gln Gly Ser Gln  
245 250 255  
Gly Ser Gly Asp Gly Arg Gly Ser Val Glu Gly Gln Gln Thr Pro Arg  
260 265 270  
Phe Ser Ile Gln Leu Pro Trp Pro Phe Arg Arg Gln Asp Gly Ser Gly  
275 280 285  
Ser Gly Ser Gly Ala Pro Gly Ala Gly Gly Gly Asn Leu Glu Thr Arg  
290 295 300  
Gly Glu Asp Leu Asp  
305

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..766

(D) OTHER INFORMATION: / Ceres Seq. ID 1566024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| acgtgtcctc agcttgaaca gataattctg cgactcttga gaaaggaaga cgaaggaagg | 60  |
| agaatagtag aagaagaaga aaggagagat cttgtgatat ctacgtagaa ggaagatggc | 120 |
| cttatctcaa gtgtctgcgt ctctgcctt ttctcttccc aattctggtg ccctaaagct  | 180 |
| agccacaatc acaaacccaa cttctacatg togggttcat gttccgcaac ttgctggaat | 240 |

ccgatccacc ttgcgttctg gttctcctct cttgccattg aagttgagta tgaccgcgtag 300  
aggaggaaac agagcagcat cagtttccat aagaagttag caaagtacag aaggaagcag 360  
tggtttggat atatggcttg gtctgtggcg catggttggg tttagcagttg ccattactgt 420  
tgaaatttcc actggaaaag gacttcttga gaattttgga gtagcaagtc cattgCctac 480  
ggttgcttta gctgtttacag cattggttgg ggttctagct gcggttttca tcttccaatc 540  
ttcttctaaa aactgatcaa caagaatctt gtttgtgatg ctgccgagga tcatttttctt 600  
gtattaagaa tcttgtatta tatatcactg taactttctac atccatcagt ggaaaaaatc 660  
ttacattctt agtttttttt ggcaacatac atgatctata catgtctttt ggccaaatct 720  
tatttttgta tttttaaaac atgatctata acatgtatta agtttg

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1566025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Met Ala Leu Ser Gln Val Ser Ala Ser Leu Ala Phe Ser Leu Pro Asn  
1 5 10 15  
Ser Gly Ala Leu Lys Leu Ala Thr Ile Thr Asn Pro Thr Ser Thr Cys  
20 25 30  
Arg Val His Val Pro Gln Leu Ala Gly Ile Arg Ser Thr Phe Ala Ser  
35 40 45  
Gly Ser Pro Leu Leu Pro Leu Lys Leu Ser Met Thr Arg Arg Gly Gly  
50 55 60  
Asn Arg Ala Ala Ser Val Ser Ile Arg Ser Glu Gln Ser Thr Glu Gly  
65 70 75 80  
Ser Ser Gly Leu Asp Ile Trp Leu Gly Arg Gly Ala Met Val Gly Phe  
85 90 95  
Ala Val Ala Ile Thr Val Glu Ile Ser Thr Gly Lys Gly Leu Leu Glu  
100 105 110  
Asn Phe Gly Val Ala Ser Pro Leu Pro Thr Val Ala Leu Ala Val Thr  
115 120 125  
Ala Leu Val Gly Val Leu Ala Ala Val Phe Ile Phe Gln Ser Ser Ser  
130 135 140  
Lys Asn  
145

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1566026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Thr Arg Arg Gly Gly Asn Arg Ala Ala Ser Val Ser Ile Arg Ser  
1 5 10 15  
Glu Gln Ser Thr Glu Gly Ser Ser Gly Leu Asp Ile Trp Leu Gly Arg  
20 25 30  
Gly Ala Met Val Gly Phe Ala Val Ala Ile Thr Val Glu Ile Ser Thr  
35 40 45  
Gly Lys Gly Leu Leu Glu Asn Phe Gly Val Ala Ser Pro Leu Pro Thr  
50 55 60

Val Ala Leu Ala Val Thr Ala Leu Val Gly Val Leu Ala Ala Val Phe  
65 70 75 80  
Ile Phe Gln Ser Ser Ser Lys Asn  
85

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1610
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| tctcttttct  | ttcactctct  | gttttgttct  | ttatcgctcg  | agaattgatg | tggatttttc  | 60   |
| atatttcagt  | taatcttagc  | taattgactt  | gaaattcaat  | gaaaagattc | aatttttggg  | 120  |
| ttaattaagc  | aagttgtgag  | atagatgaac  | gaatttggtg  | accaattgcg | ttttacagga  | 180  |
| tacgtttggt  | gctctatgaa  | gtcttataga  | ttatctgaac  | ttagttcttc | ccaagttgat  | 240  |
| agtttggaag  | cacgcccctg  | cattgacttc  | tcttctattt  | tcgccactgt | gaacccgatt  | 300  |
| atcgatgctg  | tctgtagcaa  | tggggataat  | gctgtcaaag  | aatacactga | aagatttgac  | 360  |
| aaagtccagc  | tgaataaagt  | tgtggaagat  | atgtctgagc  | tttctgttcc | tgagctcgat  | 420  |
| tccaatgtca  | aagaagcggt  | tgatgttgcg  | tatgacaaca  | tatatgcggt | tcacttagcc  | 480  |
| caaaagtcaa  | ctgagaaaag  | cgttgagaat  | atgaaagggtg | tcagatgtaa | aaggggtgtca | 540  |
| agatctattg  | gctctgtagg  | tcTttaWtk   | gcctgggtgga | acagctgttt | tgccatcaac  | 600  |
| ggctttgatg  | cttgctattc  | ctgctcaaat  | tgctgggatgt | aaaacagttg | ttcttgcaac  | 660  |
| tccaccaagt  | aaggatggaa  | gcatttgtaa  | ggaggttctg  | tattgcgcca | agagggctgg  | 720  |
| tgtaaactcac | atactcaaag  | ctgggtggagc | gcaggctata  | gctgccatgg | cctggggggac | 780  |
| agattcttgt  | ccaaagggtg  | agaagatttt  | tggtcctggg  | aaccagtatg | tcacagctgc  | 840  |
| taagatgatt  | cttcaaaaaca | gogaggcaat  | ggtctcaatc  | gatatgcctg | ctggtccttc  | 900  |
| agaagtccta  | gttattgctg  | acgaacatgc  | tagtccagtt  | tacattgcag | cagacttact  | 960  |
| ttctcaggcg  | gagcatggtc  | cagatagtca  | agttgttctt  | gtagttgtgg | gcgatagtgt  | 1020 |
| agatctcaac  | gccatcgaag  | aagaaattgc  | caagcagtg   | aaaagccttc | ctagaggaga  | 1080 |
| gtttgcttca  | aaagcactaa  | gtcacagtgt  | cacagtgttt  | gctcgagata | tgattgaggc  | 1140 |
| aatatctttc  | tcaaacttat  | atgcacccga  | acatttgatc  | atcaatgtca | aagacgctga  | 1200 |
| gaaatgggag  | ggactgattg  | agaacgcagg  | ctcggttttc  | ataggaccat | ggactccaga  | 1260 |
| gagtggtggg  | gattatgcga  | gcgggacaaa  | ccacgttctt  | ccaacatatg | gatatgcaag  | 1320 |
| aatgtacagt  | ggcgtctctc  | tcgactcttt  | cctaaagttc  | atgactgtac | aatcctttgac | 1380 |
| agaggaaggt  | ctgagaaaacc | tcggccctta  | tgtagcaact  | atggctgaaa | tcgaaggttt  | 1440 |
| agatgcacac  | aagagagccg  | ttactctcag  | actcaaggat  | atcgaagcca | aacagcttgc  | 1500 |
| ataatccaat  | tgagatttat  | attcagacaa  | aagaggcgaa  | aattcttttt | gtattgtatg  | 1560 |
| aacatatttg  | gtttcctgag  | attggataac  | aataaaataa  | gagatgttgg |             |      |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ala | Ile | Pro | Ala | Gln | Ile | Ala | Gly | Cys | Lys | Thr | Val | Val | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Thr | Pro | Pro | Ser | Lys | Asp | Gly | Ser | Ile | Cys | Lys | Glu | Val | Leu | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ala | Lys | Arg | Ala | Gly | Val | Thr | His | Ile | Leu | Lys | Ala | Gly | Gly | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

Gln Ala Ile Ala Ala Met Ala Trp Gly Thr Asp Ser Cys Pro Lys Val  
50 55 60  
Glu Lys Ile Phe Gly Pro Gly Asn Gln Tyr Val Thr Ala Ala Lys Met  
65 70 75 80  
Ile Leu Gln Asn Ser Glu Ala Met Val Ser Ile Asp Met Pro Ala Gly  
85 90 95  
Pro Ser Glu Val Leu Val Ile Ala Asp Glu His Ala Ser Pro Val Tyr  
100 105 110  
Ile Ala Ala Asp Leu Leu Ser Gln Ala Glu His Gly Pro Asp Ser Gln  
115 120 125  
Val Val Leu Val Val Val Gly Asp Ser Val Asp Leu Asn Ala Ile Glu  
130 135 140  
Glu Glu Ile Ala Lys Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe Ala  
145 150 155 160  
Ser Lys Ala Leu Ser His Ser Phe Thr Val Phe Ala Arg Asp Met Ile  
165 170 175  
Glu Ala Ile Ser Phe Ser Asn Leu Tyr Ala Pro Glu His Leu Ile Ile  
180 185 190  
Asn Val Lys Asp Ala Glu Lys Trp Glu Gly Leu Ile Glu Asn Ala Gly  
195 200 205  
Ser Val Phe Ile Gly Pro Trp Thr Pro Glu Ser Val Gly Asp Tyr Ala  
210 215 220  
Ser Gly Thr Asn His Val Leu Pro Thr Tyr Gly Tyr Ala Arg Met Tyr  
225 230 235 240  
Ser Gly Val Ser Leu Asp Ser Phe Leu Lys Phe Met Thr Val Gln Ser  
245 250 255  
Leu Thr Glu Glu Gly Leu Arg Asn Leu Gly Pro Tyr Val Ala Thr Met  
260 265 270  
Ala Glu Ile Glu Gly Leu Asp Ala His Lys Arg Ala Val Thr Leu Arg  
275 280 285  
Leu Lys Asp Ile Glu Ala Lys Gln Leu Ala  
290 295

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1566033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Met Ala Trp Gly Thr Asp Ser Cys Pro Lys Val Glu Lys Ile Phe Gly  
1 5 10 15  
Pro Gly Asn Gln Tyr Val Thr Ala Ala Lys Met Ile Leu Gln Asn Ser  
20 25 30  
Glu Ala Met Val Ser Ile Asp Met Pro Ala Gly Pro Ser Glu Val Leu  
35 40 45  
Val Ile Ala Asp Glu His Ala Ser Pro Val Tyr Ile Ala Ala Asp Leu  
50 55 60  
Leu Ser Gln Ala Glu His Gly Pro Asp Ser Gln Val Val Leu Val Val  
65 70 75 80  
Val Gly Asp Ser Val Asp Leu Asn Ala Ile Glu Glu Glu Ile Ala Lys  
85 90 95  
Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe Ala Ser Lys Ala Leu Ser  
100 105 110  
His Ser Phe Thr Val Phe Ala Arg Asp Met Ile Glu Ala Ile Ser Phe  
115 120 125  
Ser Asn Leu Tyr Ala Pro Glu His Leu Ile Ile Asn Val Lys Asp Ala

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130 135 140  
Glu Lys Trp Glu Gly Leu Ile Glu Asn Ala Gly Ser Val Phe Ile Gly  
145 150 155 160  
Pro Trp Thr Pro Glu Ser Val Gly Asp Tyr Ala Ser Gly Thr Asn His  
165 170 175  
Val Leu Pro Thr Tyr Gly Tyr Ala Arg Met Tyr Ser Gly Val Ser Leu  
180 185 190  
Asp Ser Phe Leu Lys Phe Met Thr Val Gln Ser Leu Thr Glu Glu Gly  
195 200 205  
Leu Arg Asn Leu Gly Pro Tyr Val Ala Thr Met Ala Glu Ile Glu Gly  
210 215 220  
Leu Asp Ala His Lys Arg Ala Val Thr Leu Arg Leu Lys Asp Ile Glu  
225 230 235 240  
Ala Lys Gln Leu Ala  
245

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1566034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Ile Leu Gln Asn Ser Glu Ala Met Val Ser Ile Asp Met Pro Ala  
1 5 10 15  
Gly Pro Ser Glu Val Leu Val Ile Ala Asp Glu His Ala Ser Pro Val  
20 25 30  
Tyr Ile Ala Ala Asp Leu Leu Ser Gln Ala Glu His Gly Pro Asp Ser  
35 40 45  
Gln Val Val Leu Val Val Val Gly Asp Ser Val Asp Leu Asn Ala Ile  
50 55 60  
Glu Glu Glu Ile Ala Lys Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe  
65 70 75 80  
Ala Ser Lys Ala Leu Ser His Ser Phe Thr Val Phe Ala Arg Asp Met  
85 90 95  
Ile Glu Ala Ile Ser Phe Ser Asn Leu Tyr Ala Pro Glu His Leu Ile  
100 105 110  
Ile Asn Val Lys Asp Ala Glu Lys Trp Glu Gly Leu Ile Glu Asn Ala  
115 120 125  
Gly Ser Val Phe Ile Gly Pro Trp Thr Pro Glu Ser Val Gly Asp Tyr  
130 135 140  
Ala Ser Gly Thr Asn His Val Leu Pro Thr Tyr Gly Tyr Ala Arg Met  
145 150 155 160  
Tyr Ser Gly Val Ser Leu Asp Ser Phe Leu Lys Phe Met Thr Val Gln  
165 170 175  
Ser Leu Thr Glu Glu Gly Leu Arg Asn Leu Gly Pro Tyr Val Ala Thr  
180 185 190  
Met Ala Glu Ile Glu Gly Leu Asp Ala His Lys Arg Ala Val Thr Leu  
195 200 205  
Arg Leu Lys Asp Ile Glu Ala Lys Gln Leu Ala  
210 215

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1566045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| aattcatttc | ataatcatat  | acctctctac  | atttgttact | actttcttct | aacttgtttt | 60  |
| caaagagaaa | tcacaatcta  | tctgttccaa  | gatgagtaa  | tacagccaaa | accaatcttc | 120 |
| aggagcttat | cctacgccgc  | cagtgtctac  | cggcccttac | gtggcaccgc | caccgctagg | 180 |
| ttacccaacg | aacgacacaa  | gtcatgccac  | ggtggcaacg | gtggagacaa | agtccaaggg | 240 |
| tgatggattc | ttaaaaaggct | gtcttgccgc  | catgtgttgt | tgttggtgcc | tcgacgcatg | 300 |
| cttctgaaga | cttagatggg  | ttattttgat  | tatctttgta | ttttgcttta | ccaaaatgat | 360 |
| tcgactaggt | ttatgacatt  | tgggtacttct | atttgtaa   | tcatttctat | atcactcttt | 420 |
| ctWttKgc   | at          |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1566046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ser | Phe | His | Asn | His | Thr | Pro | Leu | Tyr | Ile | Cys | Tyr | Tyr | Phe | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Thr | Cys | Phe | Gln | Arg | Glu | Ile | Thr | Ile | Tyr | Leu | Phe | Gln | Asp | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ile | Gln | Pro | Lys | Pro | Ile | Phe | Arg | Ser | Leu | Ser | Tyr | Ala | Ala | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Tyr | Arg | Pro | Leu | Arg | Gly | Thr | Ala | Thr | Ala | Arg | Leu | Pro | Asn | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Arg | His | Lys | Ser | Cys | His | Gly | Gly | Asn | Gly | Gly | Asp | Lys | Val | Gln | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1566047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Gln | Tyr | Ser | Gln | Asn | Gln | Ser | Ser | Gly | Ala | Tyr | Pro | Thr | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Val | Ser | Thr | Gly | Pro | Tyr | Val | Ala | Pro | Pro | Pro | Leu | Gly | Tyr | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Asn | Asp | Thr | Ser | His | Ala | Thr | Val | Ala | Thr | Val | Glu | Thr | Lys | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Gly | Asp | Gly | Phe | Leu | Lys | Gly | Cys | Leu | Ala | Ala | Met | Cys | Cys | Cys |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Cys | Val | Leu | Asp | Ala | Cys | Phe |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1268 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1268  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566048  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```
taggaaggat gatccaaggc tgcggcgctt agctcagact aaagttgaaa accgtgacga 60
aGttagagct gatcatcggc gtattagaca ggctgagatt atatctacgg aagaagaaga 120
atcgaggaat caagagaata gagacgagga tgatgatgaa gatgccttgg aagaaagaag 180
aagaagaatt aaggagaaga atcttagact agcacaagag gaggctgctt tacttccttt 240
agaagaagaa gatgagatac aagaggaaga agaggaggag gaggagtctg agtacgagac 300
tgattcggaa gatgatatgc ctggtattgc cttgattaag cctgtttttg taccgaaagc 360
tgagagagat acaattgcag agcgagagag gcttgaggct gaagaagaag ctcttgagga 420
attagcaaaag agaaaatttg agcaaagaaa aatagagaca aagcaaattg tggttgagga 480
agttaggaaa gatgaagaga tacggaagaa catactattg gaggaagcta atattggaga 540
tgtggaaact gatgacgaac tcaatgaagc tgaggagtat gaagtttggg agacaagaga 600
gattggtagg atcaagagag aaagagatgc aagggaagct atgctgagag agagggaga 660
aatagagaag ttgaggaata tgacagagca ggagaggaga gattgggaga ggaagaatcc 720
gaaaccttct tcagctcaac cgaaaaagaa atggaacttt atgcagaaat attaccataa 780
gggtgccttc ttccaggcag atcctgatga tgaggcaggt tctgctggaa ccgatggtat 840
atttcagcgc gacttctctg ctccaaccgg agaagatagg ttggacaaat cgattctccc 900
caaagttatg caagtcaagc acttttggtc tagtggaaga actaaatgga ctacacctgt 960
caatgaagac acaacagatt ggagtaacct gtggacttcc aatgatcctc tacgtgaaaa 1020
atacaacaag aaaatggcag gcatggatgc tccaatcgca aaaccaaag ggagcaagaa 1080
gatgaaagat tgggagactt aaaccgcacc aacatttact ttgtttgttt taaaaatcca 1140
atgatgcagc agtggtatgt ggtagtataa aaacatcgta acatcttact cagttatgtc 1200
totgagtcct ctaaatccta gtaattaaaa atattgctca aaagaatgaa gacctaacat 1260
aattcatt
```

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 366 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..366  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```
Arg Lys Asp Asp Pro Arg Leu Arg Arg Leu Ala Gln Thr Lys Val Glu
1 5 10 15
Asn Arg Asp Glu Val Arg Ala Asp His Arg Arg Ile Arg Gln Ala Glu
20 25 30
Ile Ile Ser Thr Glu Glu Glu Glu Ser Arg Asn Gln Glu Asn Arg Asp
35 40 45
Glu Asp Asp Asp Glu Asp Ala Leu Glu Glu Arg Arg Arg Arg Ile Lys
50 55 60
Glu Lys Asn Leu Arg Leu Ala Gln Glu Glu Ala Ala Leu Leu Pro Leu
65 70 75 80
Glu Glu Glu Asp Glu Ile Gln Glu Glu Glu Glu Glu Glu Glu Ser
85 90 95
Glu Tyr Glu Thr Asp Ser Glu Asp Asp Met Pro Gly Ile Ala Leu Ile
100 105 110
Lys Pro Val Phe Val Pro Lys Ala Glu Arg Asp Thr Ile Ala Glu Arg
115 120 125
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Leu | Glu | Ala | Glu | Glu | Glu | Ala | Leu | Glu | Glu | Leu | Ala | Lys | Arg |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Leu | Glu | Gln | Arg | Lys | Ile | Glu | Thr | Lys | Gln | Ile | Val | Val | Glu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Arg | Lys | Asp | Glu | Glu | Ile | Arg | Lys | Asn | Ile | Leu | Leu | Glu | Glu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Asn | Ile | Gly | Asp | Val | Glu | Thr | Asp | Asp | Glu | Leu | Asn | Glu | Ala | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Glu | Val | Trp | Lys | Thr | Arg | Glu | Ile | Gly | Arg | Ile | Lys | Arg | Glu | Arg |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Ala | Arg | Glu | Ala | Met | Leu | Arg | Glu | Arg | Glu | Glu | Ile | Glu | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Asn | Met | Thr | Glu | Gln | Glu | Arg | Arg | Asp | Trp | Glu | Arg | Lys | Asn | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Pro | Ser | Ser | Ala | Gln | Pro | Lys | Lys | Lys | Trp | Asn | Phe | Met | Gln | Lys |
|     |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |
| Tyr | Tyr | His | Lys | Gly | Ala | Phe | Phe | Gln | Ala | Asp | Pro | Asp | Asp | Glu | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Gly | Ser | Ala | Gly | Thr | Asp | Gly | Ile | Phe | Gln | Arg | Asp | Phe | Ser | Ala | Pro |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Gly | Glu | Asp | Arg | Leu | Asp | Lys | Ser | Ile | Leu | Pro | Lys | Val | Met | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Lys | His | Phe | Gly | Arg | Ser | Gly | Arg | Thr | Lys | Trp | Thr | His | Leu | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Glu | Asp | Thr | Thr | Asp | Trp | Ser | Asn | Pro | Trp | Thr | Ser | Asn | Asp | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Arg | Glu | Lys | Tyr | Asn | Lys | Lys | Met | Ala | Gly | Met | Asp | Ala | Pro | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Lys | Pro | Lys | Gly | Ser | Lys | Lys | Met | Lys | Asp | Trp | Glu | Thr |     |     |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Ile | Ala | Leu | Ile | Lys | Pro | Val | Phe | Val | Pro | Lys | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Asp | Thr | Ile | Ala | Glu | Arg | Glu | Arg | Leu | Glu | Ala | Glu | Glu | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Glu | Leu | Ala | Lys | Arg | Lys | Leu | Glu | Gln | Arg | Lys | Ile | Glu | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gln | Ile | Val | Val | Glu | Glu | Val | Arg | Lys | Asp | Glu | Glu | Ile | Arg | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Ile | Leu | Leu | Glu | Glu | Ala | Asn | Ile | Gly | Asp | Val | Glu | Thr | Asp | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Leu | Asn | Glu | Ala | Glu | Glu | Tyr | Glu | Val | Trp | Lys | Thr | Arg | Glu | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Arg | Ile | Lys | Arg | Glu | Arg | Asp | Ala | Arg | Glu | Ala | Met | Leu | Arg | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Arg | Glu | Glu | Ile | Glu | Lys | Leu | Arg | Asn | Met | Thr | Glu | Gln | Glu | Arg | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Trp | Glu | Arg | Lys | Asn | Pro | Lys | Pro | Ser | Ser | Ala | Gln | Pro | Lys | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Trp | Asn | Phe | Met | Gln | Lys | Tyr | Tyr | His | Lys | Gly | Ala | Phe | Phe | Gln |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Ala | Asp | Ile | Pro | Pro | Asn | Gln | Ser | Ile | Tyr | Ile | Lys | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Glu | Lys | Ile | Lys | Lys | Glu | Glu | Leu | Lys | Arg | Ser | Leu | Tyr | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Ser | Gln | Phe | Gly | Arg | Leu | Leu | Asp | Val | Val | Ala | Leu | Lys | Thr |

35 40 45  
Pro Lys Leu Arg Gly Gln Ala Trp Val Val Phe Thr Glu Val Thr Ala  
50 55 60  
Ala Ser Asn Ala Val Arg Gln Met Gln Asn Phe Pro Phe Tyr Asp Lys  
65 70 75 80  
Pro Met Arg Ile Gln Tyr Ala Lys Ser Lys Ser Asp Tyr Val Thr Lys  
85 90 95  
Ala Glu Gly Ser Phe Val Pro Lys Glu Lys Lys Met Lys Gln Ala Arg  
100 105 110  
Glu Ser

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1566064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Met Lys Thr Met Phe Ser Leu Pro Trp Pro Cys Arg Leu Phe Arg Val  
1 5 10 15  
Ser Arg Ser Leu Arg Arg Ile Gln Trp Ser Ser Leu Leu Pro Arg Ser  
20 25 30  
Glu Asn Gln Ser Phe Val Met Arg Met Asn Gly Asn Asp Ile Leu Ile  
35 40 45  
Ser Ser Cys Leu Lys Ala Asn Cys Leu Ile Leu Phe Gly Ser Phe Pro  
50 55 60  
Ile Ser Gly Val Asn Asp Pro Glu Ala Leu Asp Gln Asn Val Met Arg  
65 70 75 80  
Ser Lys Asn

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1566065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met Phe Ser Leu Pro Trp Pro Cys Arg Leu Phe Arg Val Ser Arg Ser  
1 5 10 15  
Leu Arg Arg Ile Gln Trp Ser Ser Leu Leu Pro Arg Ser Glu Asn Gln  
20 25 30  
Ser Phe Val Met Arg Met Asn Gly Asn Asp Ile Leu Ile Ser Ser Cys  
35 40 45  
Leu Lys Ala Asn Cys Leu Ile Leu Phe Gly Ser Phe Pro Ile Ser Gly  
50 55 60  
Val Asn Asp Pro Glu Ala Leu Asp Gln Asn Val Met Arg Ser Lys Asn  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
Met Thr Ile Arg Glu Ser Phe Glu His Ile Pro Gln Trp Leu Glu Glu
1 5 10 15
Leu Arg Val His Ala Asp Lys Asn Ile Val Ile Ile Leu Ile Gly Asn
 20 25 30
Lys Thr Asp Leu Glu Asn Gln Arg Ser Val Pro Val Glu Asp Ala Lys
 35 40 45
Glu Phe Ala Glu Lys Glu Gly Leu Phe Phe Leu Glu Thr Xaa Ala Leu
 50 55 60
Asn Ser Thr Asn Val Glu Asn Ser Phe Asn Thr Leu Leu Thr Glu Ile
65 70 75 80
Phe Asn Lys Val Asn Lys Lys Asn Leu Ala Lys Thr Thr Val Ser Cys
 85 90 95
Ser Ser Gln Val Ser Leu Leu Arg Pro Pro Cys Val Ala Ala Xaa
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..579  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
gcgtagtaca aaacaaatct tgataaatag ataaataaac atcttttctat tcgtaaggac 60
gacaagaatc tctcaggttc tgtagaattg tcagaatcat ttctaattggg aggtaaaatg 120
ggatcagtac cggagcaaaa cacagagaag cttctctggc agtcaagcga cgctcgctgat 180
agccgtgact ccaagttccg gtgttgctcg tggagggctc tctacgaggc tccggcgaag 240
ttgtacgcgc tgggacattc tgatcgctcg aaactttact tctccatcaa gatgggaatt 300
gctttggcac tctgttcttt cgtcattctt ctcaaagaac cgcttcaaga tgctagtaaa 360
ttcgcagttt gggcgattct caccgtcggt ctcatcttcg agtattacgt cggagcaact 420
ttggttaaag gattcaatag agcattaggc acaatgtag ctggaggact tgctctcggc 480
gtcgcgcagC tctctgtttt agcaggagag tttgaagaag tcatcatcgt aatctgcata 540
ttccttgca gKttttTggt gctagttatt tgaaActat
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..155  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
Met Gly Gly Lys Met Gly Ser Val Pro Glu Gln Asn Thr Glu Lys Leu
1 5 10 15
Leu Trp Gln Ser Ser Asp Val Ala Asp Ser Arg Asp Ser Lys Phe Arg
 20 25 30
Cys Cys Ser Trp Arg Ala Leu Tyr Glu Ala Pro Ala Lys Leu Tyr Ala
 35 40 45
Leu Gly His Ser Asp Arg Arg Lys Leu Tyr Phe Ser Ile Lys Met Gly
 50 55 60
Ile Ala Leu Ala Leu Cys Ser Phe Val Ile Phe Leu Lys Glu Pro Leu
```



(2) INFORMATION FOR SEO ID NO:182:

(A) LENGTH: 151 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1566105

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1566106

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ile | Ala | Leu | Ala | Leu | Cys | Ser | Phe | Val | Ile | Phe | Leu | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Gln | Asp | Ala | Ser | Lys | Phe | Ala | Val | Trp | Ala | Ile | Leu | Thr | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Ile | Phe | Glu | Tyr | Tyr | Val | Gly | Ala | Thr | Leu | Val | Lys | Gly | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Asn Arg Ala Leu Gly Thr Met Leu Ala Gly Gly Leu Ala Leu Gly Val  
50 55 60  
Ala Gln Leu Ser Val Leu Ala Gly Glu Phe Glu Glu Val Ile Ile Val  
65 70 75 80  
Ile Cys Ile Phe Leu Ala Xaa Phe Leu Val Leu Val Ile  
85 90

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..939
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ctatctctca tccacatctt agttcatgtt cgagttttctc tgcttcaatt acaaagaatg 60  
gctgcttcaa gtgctgtcac cgcaaaactac gtcctcaagc cacctccatt cgcactggat 120  
gctttggagc cgcataatgag caaacaact ctggagtttc actggggaaa acatcacaga 180  
gcttacgtgg acaacctcaa gaaacaggtt cttggaaccg agcttgaagg caagccctta 240  
gagcacatta tccacagcac ttacaacaat ggtgatctcc tccctgcttt caacaacgct 300  
gctcaggcgt ggaaccacga gttcttcttg gagtcaatga aaccaggtgg tggaggaaaa 360  
ccatcaggag agcttcttgc tttgcttgaa agagatttca cttcttatga gaagttctat 420  
gaagagtcca atgctgctgc agccactcag tttggagctg gctgggcctg gcttgcttat 480  
tcaaagtaaa aactcaaat agtgaaaact cccaatgctg tgaatcccct tgtgctcggc 540  
tctttcccCa ttgcttacca ttgatgtctg ggagcatgct tactaccttg acttccagaa 600  
ccgaagacca gattacataa agacattcat gaccaatctt gtgtcttggg aagctgtaag 660  
tgccagactt gaggcgcaca aggtcgcttc tgcttaagca aatttctgaa caatttgact 720  
tcagtgcacag tgagttctgc atcacggaag tctcttataa aatattggtc gctgtaataa 780  
ggacacagct ctcttggtgt gtatgtgtca cagagttctt cattttgctt gtgtaatgaa 840  
caattaaaca tgctcttttc tgagtgtgtg tgcgttttgt gtgtgtcaag tttttcatcg 900  
tctcctttat taaactcaaa ttggcaccta ccatcagtg

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Leu Ser Leu Ile His Ile Leu Val His Arg Val Ser Leu Leu Gln  
1 5 10 15  
Leu Gln Arg Met Ala Ala Ser Ser Ala Val Thr Ala Asn Tyr Val Leu  
20 25 30  
Lys Pro Pro Pro Phe Ala Leu Asp Ala Leu Glu Pro His Met Ser Lys  
35 40 45  
Gln Thr Leu Glu Phe His Trp Gly Lys His His Arg Ala Tyr Val Asp  
50 55 60  
Asn Leu Lys Lys Gln Val Leu Gly Thr Glu Leu Gly Lys Pro Leu  
65 70 75 80  
Glu His Ile Ile His Ser Thr Tyr Asn Asn Gly Asp Leu Leu Pro Ala  
85 90 95  
Phe Asn Asn Ala Ala Gln Ala Trp Asn His Glu Phe Phe Trp Glu Ser  
100 105 110  
Met Lys Pro Gly Gly Gly Gly Lys Pro Ser Gly Glu Leu Leu Ala Leu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Leu Glu Arg Asp Phe Thr Ser Tyr Glu Lys Phe Tyr Glu Glu Phe Asn |     |     |
| 130                                                             | 135 | 140 |
| Ala Ala Ala Ala Thr Gln Phe Gly Ala Gly Trp Ala Trp Leu Ala Tyr |     |     |
| 145                                                             | 150 | 155 |
| Ser Asn Glu Lys Leu Lys Val Val Lys Thr Pro Asn Ala Val Asn Pro |     |     |
| 165                                                             | 170 | 175 |
| Leu Val Leu Gly Ser Phe Pro Ile Ala Tyr His                     |     |     |
| 180                                                             | 185 |     |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1566117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ser | Ala | Val | Thr | Ala | Asn | Tyr | Val | Leu | Lys | Pro | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Phe | Ala | Leu | Asp | Ala | Leu | Glu | Pro | His | Met | Ser | Lys | Gln | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Glu | Phe | His | Trp | Gly | Lys | His | His | Arg | Ala | Tyr | Val | Asp | Asn | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Lys | Gln | Val | Leu | Gly | Thr | Glu | Leu | Glu | Gly | Lys | Pro | Leu | Glu | His |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Ile | His | Ser | Thr | Tyr | Asn | Asn | Gly | Asp | Leu | Leu | Pro | Ala | Phe | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ala | Gln | Ala | Trp | Asn | His | Glu | Phe | Phe | Trp | Glu | Ser | Met | Lys |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |
| Gly | Gly | Gly | Gly | Lys | Pro | Ser | Gly | Glu | Leu | Leu | Ala | Leu | Leu | Glu |
|     |     |     |     |     | 100 |     |     | 105 |     |     |     |     | 110 |     |
| Asp | Phe | Thr | Ser | Tyr | Glu | Lys | Phe | Tyr | Glu | Glu | Phe | Asn | Ala | Ala |
|     |     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |
| Ala | Thr | Gln | Phe | Gly | Ala | Gly | Trp | Ala | Trp | Leu | Ala | Tyr | Ser | Asn |
|     |     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |
| Lys | Leu | Lys | Val | Val | Lys | Thr | Pro | Asn | Ala | Val | Asn | Pro | Leu | Val |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Ser | Phe | Pro | Ile | Ala | Tyr | His |     |     |     |     |     |     |     |
|     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1566118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Gln | Thr | Leu | Glu | Phe | His | Trp | Gly | Lys | His | His | Arg |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |
| Tyr | Val | Asp | Asn | Leu | Lys | Lys | Gln | Val | Leu | Gly | Thr | Glu | Leu | Glu |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |
| Lys | Pro | Leu | Glu | His | Ile | Ile | His | Ser | Thr | Tyr | Asn | Asn | Gly | Asp |
|     |     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |

Leu Pro Ala Phe Asn Asn Ala Ala Gln Ala Trp Asn His Glu Phe Phe  
50 55 60  
Trp Glu Ser Met Lys Pro Gly Gly Gly Lys Pro Ser Gly Glu Leu  
65 70 75 80  
Leu Ala Leu Leu Glu Arg Asp Phe Thr Ser Tyr Glu Lys Phe Tyr Glu  
85 90 95  
Glu Phe Asn Ala Ala Ala Thr Gln Phe Gly Ala Gly Trp Ala Trp  
100 105 110  
Leu Ala Tyr Ser Asn Glu Lys Leu Lys Val Val Lys Thr Pro Asn Ala  
115 120 125  
Val Asn Pro Leu Val Leu Gly Ser Phe Pro Ile Ala Tyr His  
130 135 140

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ctcgaacttg tttttggttc atctctcaaa accaaaatca ctaaagagga gaagattgct 60  
aaagttagat aaaacattcc aaaatcaatg gctgatagga tcaaaggtcc atggagtcct 120  
gaagaagacg agcagcttcg taggcttggt gttaaatacg gtccaagaaa ctggacagtg 180  
attagcaaat ctattccccg tagatcgggg aaatcgtgtc gtttacggtg gtgcaaccag 240  
ctttgcggc aagttgagca tcggccggtt tcggctgagg aagacgagac gatcgcacgt 300  
gctcacgctc agttcggtaa taaatgggcg acgattgtc gtcttctcaa cggtcgtacg 360  
gacaacgccg tgaagaatca ctggaactcg acgctcaaga ggaaatgcgg cggttacgac 420  
catcggtgtt acgatgggtc ggaggatcat cggccggtta agagatcggg gagtgcggga 480  
tctccacctg ttgttactgg gctttacatg agcccaggaa gcccaactgg atctgatgtc 540  
agtgattcaa gtactatccc gatattacct tccgttgagc ttttcaagcc tgtgcctaga 600  
cctggtgctg wtgtgctacc gcytcctatc gaaacgtcgt cttcttccga tgatccaccg 660  
aMttcgttaa gcttgctact tcttggtgcc gacgtaagcg aggagtcaaa ccgtagccac 720  
gagtcaacga atatcaacaa caccacttcg agccgccaca accacaacaa tacggtgtcg 780  
tttatgccgt ttagtggtgg gtttagaggt gcgattgagg aaatggggaa gtcttttccc 840  
ggtaacggag gcgagtttat ggcggtggtg caagagatga ttaaggcgga agtgaggagt 900  
tacatgacgg agatgcaacg gaacaatggt ggcggattcg tcggaggatt cattgataat 960  
ggcatgattc cgatgagtc aattggagtt gggagaatcg agtagacaaa gtgagattat 1020  
taggaaactg tttaaattgg agaagaagaa aaatgctctg tttttttctc ctttgatta 1080  
ggcttaagaa ttttggttt taaggaaatg tatagaggaa atcgagtga caaagctcga 1140  
gagctgggga cgtagtgacg aagacgaaga tcaaatttct ctttaagctat tcaggaaaat 1200  
aaaataaatt tttattt

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Met Ala Asp Arg Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Glu Gln  
1 5 10 15  
Leu Arg Arg Leu Val Val Lys Tyr Gly Pro Arg Asn Trp Thr Val Ile  
20 25 30

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp  
35 40 45  
Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu  
50 55 60  
Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp  
65 70 75 80  
Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys  
85 90 95  
Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His  
100 105 110  
Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val  
115 120 125  
Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly  
130 135 140  
Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu  
145 150 155 160  
Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Xaa Val  
165 170 175  
Leu Pro Xaa Pro Ile Glu Thr Ser Ser Ser Asp Asp Pro Pro Xaa  
180 185 190  
Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn  
195 200 205  
Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His  
210 215 220  
Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg  
225 230 235 240  
Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu  
245 250 255  
Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr  
260 265 270  
Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe  
275 280 285  
Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile  
290 295 300  
Glu  
305

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Ser Pro Gly Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr  
1 5 10 15  
Ile Pro Ile Leu Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro  
20 25 30  
Gly Ala Xaa Val Leu Pro Xaa Pro Ile Glu Thr Ser Ser Ser Asp  
35 40 45  
Asp Pro Pro Xaa Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser  
50 55 60  
Glu Glu Ser Asn Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr  
65 70 75 80  
Ser Ser Arg His Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser  
85 90 95  
Gly Gly Phe Arg Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly

100 105 110  
Asn Gly Gly Glu Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu  
115 120 125  
Val Arg Ser Tyr Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe  
130 135 140  
Val Gly Gly Phe Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly  
145 150 155 160  
Val Gly Arg Ile Glu  
165

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

aaaactcgct ctccggtgat cgtctttcgg tcagattctt ataagcgtgc ttgattttca 60  
aatcaagttt gtttctttat ctccagagtt tatcatctct tatgtgactg tgtaaaatg 120  
aatttcttaa actcagctgc atccatttgc agaagagtta gtctgagga actcatcact 180  
gaggttcctg cttatactgg cagcagcatt tccgatggtt cttcaagtgg gttgagtttg 240  
gtcttgaagc gttgggctac taagaaaacc gctggttcta caaagaacgg tcgtgactct 300  
aatcccaagt ttcttggtgt taagaaattc ggaggagaga gtgtgatacc tggaaacatc 360  
atagttcgtc aacgtggaac tcggtttcat cctggagact atgtcgggat tggttaaggac 420  
catactctgt ttgcactgaa ggaaggacga gtcagggttc agaaaagcaa gattacagga 480  
cgcaaataga ttcatgttga tccaataggt ggtcatgttc ttcaccctat ctacacaaaa 540  
gccgcagctg caaaatcgac taagttgaac acagcttcat agcaaactcg acaatctaaa 600  
cgtgtcttgc tttcttcttt tagattatat gatctctcvt agtaaaagat gatggtatct 660  
tagaatctca aactcattt caataacagc tgctgttttg tt

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met Asn Phe Leu Asn Ser Ala Ala Ser Ile Cys Arg Arg Val Ser Leu  
1 5 10 15  
Arg Glu Leu Ile Thr Glu Val Pro Ala Tyr Thr Gly Ser Ser Ile Ser  
20 25 30  
Asp Gly Ser Ser Ser Gly Leu Ser Leu Val Leu Lys Arg Trp Ala Thr  
35 40 45  
Lys Lys Thr Ala Gly Ser Thr Lys Asn Gly Arg Asp Ser Asn Pro Lys  
50 55 60  
Phe Leu Gly Val Lys Lys Phe Gly Gly Glu Ser Val Ile Pro Gly Asn  
65 70 75 80  
Ile Ile Val Arg Gln Arg Gly Thr Arg Phe His Pro Gly Asp Tyr Val  
85 90 95  
Gly Ile Gly Lys Asp His Thr Leu Phe Ala Leu Lys Glu Gly Arg Val  
100 105 110  
Arg Phe Glu Lys Ser Lys Ile Thr Gly Arg Lys Trp Ile His Val Asp  
115 120 125

Pro Ile Gly Gly His Val Leu His Pro Ile Tyr Thr Lys Ala Ala Ala  
130 135 140  
Ala Lys Ser Thr Lys Leu Asn Thr Ala Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

atcgagtgtc tcgcccagct tcttcagtct tcaccacata atattaataa aaagcatttt 60  
cttcttttga ttgcttcaga ttggtcagct cactctttcc tctccagaag aaaccctaga 120  
catctcatcg ccaaaatggt cagatctatg ctggtccgat cttctgcctc cgcgaaagCag 180  
gcggctatcc gccgtagctt ctctctccgt tccgtccccg agcgtaaagt cgccatcctt 240  
ggtgccgccc gtggaattgg tcagcctctt gctctcctca tgaagcttaa tcctcttgct 300  
tcttctctct cctctacaga tatcgctaac actcccggag ttgctgctga tgtcgggtcac 360  
atcaacacca gatctgaggt tgttggtatc atgggcgatg ataacttggc caaagctcta 420  
gaaggagctg atctcggtat cattccagct ggtgtgccaa ggaagcctgg tatgaccctg 480  
gacgatcttt tcaacattaa tgctggaatt gtcaagaacc tttgactgc catcgccaag 540  
tactgcccac atgcgcttat taatatgac agcaaccctg tgaactctac tgttccaatt 600  
gcagctgaga tatttaagaa ggctggatg tacgatgaaa agaaattggt tgggtgtacc 660  
actcttgacg tcgtcagggc caggactttc tatgctggaa aggcaaagt cccagttgca 720  
gaagttaatg ttccggtgat tgggtggtcat gctgggggta ctattctccc tctcttctct 780  
caggcaactc ctcaagccaa cttgtcaagt gacatactta ccgcccttac taagcgatcc 840  
caagatggag gtacagaagt cgtggaggca aaagcaggaa aagggttcagc tacattgtcc 900  
atggcctatg ccggagcatt gttcgctgat gcatgcttga aaggactcaa cgggtgttcca 960  
gatgtcatag aatgctcata cgtgcaatct acaatcacgc agcttccttt ctttgccctcg 1020  
aagggtgaggt tggggaagaa tgggtgtggag gaggttcttg acttgggacc actctcagac 1080  
tttgagaagg aaggcttggg agcattgaag ccagaactca agtcctccat agaaaaggga 1140  
gtcaagtttg ccaaccagtg attaaaccga gtttactcgg taatttttcc aatttkccag 1200  
ctagagttgc cacctcctcc ttcacggtg tgtatcaat

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ile Glu Cys Leu Ala Gln Leu Leu Gln Ser Ser Pro His Asn Ile Asn  
1 5 10 15  
Lys Lys His Phe Leu Leu Ser Ile Ala Ser Asp Ser Ser Ala His Ser  
20 25 30  
Phe Leu Ser Arg Arg Asn Pro Arg His Leu Ile Ala Lys Met Phe Arg  
35 40 45  
Ser Met Leu Val Arg Ser Ser Ala Ser Ala Lys Gln Ala Ala Ile Arg  
50 55 60  
Arg Ser Phe Ser Ser Gly Ser Val Pro Glu Arg Lys Val Ala Ile Leu  
65 70 75 80  
Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu Met Lys Leu  
85 90 95

```

Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala Asn Thr Pro
 100 105 110
Gly Val Ala Asp Val Gly His Ile Asn Thr Arg Ser Glu Val Val
 115 120 125
Gly Tyr Met Gly Asp Asp Asn Leu Ala Lys Ala Leu Glu Gly Ala Asp
 130 135 140
Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg
 145 150 155 160
Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys Asn Leu Cys Thr
 165 170 175
Ala Ile Ala Lys Tyr Cys Pro His Ala Leu Ile Asn Met Ile Ser Asn
 180 185 190
Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Phe Lys Lys Ala
 195 200 205
Gly Met Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val
 210 215 220
Val Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Ala
 225 230 235 240
Glu Val Asn Val Pro Val Ile Gly Gly His Ala Gly Val Thr Ile Leu
 245 250 255
Pro Leu Phe Ser Gln Ala Thr Pro Gln Ala Asn Leu Ser Ser Asp Ile
 260 265 270
Leu Thr Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu Val Val
 275 280 285
Glu Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala
 290 295 300
Gly Ala Leu Phe Ala Asp Ala Cys Leu Lys Gly Leu Asn Gly Val Pro
 305 310 315 320
Asp Val Ile Glu Cys Ser Tyr Val Gln Ser Thr Ile Thr Glu Leu Pro
 325 330 335
Phe Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu Glu Val
 340 345 350
Leu Asp Leu Gly Pro Leu Ser Asp Phe Glu Lys Glu Gly Leu Glu Ala
 355 360 365
Leu Lys Pro Glu Leu Lys Ser Ser Ile Glu Lys Gly Val Lys Phe Ala
 370 375 380
Asn Gln
 385

```

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..341

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

```

Met Phe Arg Ser Met Leu Val Arg Ser Ser Ala Ser Ala Lys Gln Ala
1 5 10 15
Ala Ile Arg Arg Ser Phe Ser Ser Gly Ser Val Pro Glu Arg Lys Val
 20 25 30
Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu
 35 40 45
Met Lys Leu Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala
 50 55 60
Asn Thr Pro Gly Val Ala Ala Asp Val Gly His Ile Asn Thr Arg Ser
 65 70 75 80
Glu Val Val Gly Tyr Met Gly Asp Asp Asn Leu Ala Lys Ala Leu Glu

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Arg | Ser | Ser | Ala | Ser | Ala | Lys | Gln | Ala | Ala | Ile | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Ser | Ser | Gly | Ser | Val | Pro | Glu | Arg | Lys | Val | Ala | Ile | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Gly | Gly | Ile | Gly | Gln | Pro | Leu | Ala | Leu | Leu | Met | Lys | Leu | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Val | Ser | Ser | Leu | Ser | Leu | Tyr | Asp | Ile | Ala | Asn | Thr | Pro | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Ala | Asp | Val | Gly | His | Ile | Asn | Thr | Arg | Ser | Glu | Val | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Met | Gly | Asp | Asp | Asn | Leu | Ala | Lys | Ala | Leu | Glu | Gly | Ala | Asp | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ile | Ile | Pro | Ala | Gly | Val | Pro | Arg | Lys | Pro | Gly | Met | Thr | Arg | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Phe | Asn | Ile | Asn | Ala | Gly | Ile | Val | Lys | Asn | Leu | Cys | Thr | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ile Ala Lys Tyr Cys Pro His Ala Leu Ile Asn Met Ile Ser Asn Pro  
130 135 140  
Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Phe Lys Lys Ala Gly  
145 150 155 160  
Met Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val Val  
165 170 175  
Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Ala Glu  
180 185 190  
Val Asn Val Pro Val Ile Gly Gly His Ala Gly Val Thr Ile Leu Pro  
195 200 205  
Leu Phe Ser Gln Ala Thr Pro Gln Ala Asn Leu Ser Ser Asp Ile Leu  
210 215 220  
Thr Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu Val Val Glu  
225 230 235 240  
Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Gly  
245 250 255  
Ala Leu Phe Ala Asp Ala Cys Leu Lys Gly Leu Asn Gly Val Pro Asp  
260 265 270  
Val Ile Glu Cys Ser Tyr Val Gln Ser Thr Ile Thr Glu Leu Pro Phe  
275 280 285  
Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu Glu Val Leu  
290 295 300  
Asp Leu Gly Pro Leu Ser Asp Phe Glu Lys Glu Gly Leu Glu Ala Leu  
305 310 315 320  
Lys Pro Glu Leu Lys Ser Ser Ile Glu Lys Gly Val Lys Phe Ala Asn  
325 330 335  
Gln

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1844
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ttcaatctca ttaaagagaa aagaaacgat tagagaaaga gaagagggta gagacttctt  | 60   |
| ttctttgttt ctgtagaggc ttttcttctt cttctctgtc tctgtctctg tctctgtctc  | 120  |
| tctgtaatct tctgtgctct ccacaaattt gtctctcctc tctctcgccg actccacaaa  | 180  |
| ttttgagctt ctttttttga agttcttgag aacaagtga agagcttaat atccacaaga   | 240  |
| ctcttgtttc tttcttaaat ggctaaagtt tattggcctt atttcgatcc tgaatatgag  | 300  |
| aacttgagct ccagaatcaa tcttccaagt gtttctatag ataacactag ctgcaaagaa  | 360  |
| tgcactcttg tcaagggtga cagtatgaac aaacctggaa tactacttga agttgtgcaa  | 420  |
| gtcctaaccg atctcgatct cactatcact aaagcttata tctcttctga tgggtgatgg  | 480  |
| ttcatggacg tattccatgt caccgatcaa caaggaaaca aggttactga tagcaaaacc  | 540  |
| atcgattaca tcgagaaggt gttaggacca aagggtcatg cttcggcttc acaaaacact  | 600  |
| tggcctggtg aaagagtcgg tgtoCattca ttaggcgacc acacatcgat agagattatt  | 660  |
| gctcgtgatc gtctggcct cttgtcggag gtttcagccg tactagcaga cctcaacatt   | 720  |
| aatgtggtgg cagctgaagc atggactcac aaccgtagga ttgcgtgtgt cctctatgtg  | 780  |
| aatgacaatg caacttctag agccgttgat gatccagaaa gattgtcttc catggaagaa  | 840  |
| cagcttaaca atgtgctgcg tgggtgcgaa gaacaagatg agaaatttgc tcggacgagt  | 900  |
| ctctccattg ggtcgactca cgttgatoga aggttcatc agatgttttt cgctgataga   | 960  |
| gactacgaag cagtgaactaa gcttgatgat tctgcttctt gcggattcga gcccaaaatc | 1020 |
| acggttgagc attgtgaaga gaaaggttac tccgtgataa acgtgagctg cgaggatcga  | 1080 |
| ccaaagctca tgtttgacat tgtatgcacg cttacggata tgcaatacat tgtgtttcac  | 1140 |
| gccacgattt catcaagcgg ctctcatgct tctcaggagt atttcatcag acacaaagac  | 1200 |
| ggttgactc ttgacacaga aggagagaaa gagagagdtg tcaaattgtct agaagctgca  | 1260 |

```
atccatagac gagtcagcga gggttggagt ttggagctct gcgcaaagga cagagttgga 1320
ttactgtcgg aagtgacaag gattctgaga gagcacgggc tatcagtgtc gagagctggg 1380
gtgacaacag taggagaaca agccgtcaac gttttctatg tgaaagatgc ttcagggaat 1440
ccagtggatg tgaagacgat tgaggcgtta cgcggagaga ttggacacag tatgatgatt 1500
gacttcaaga ataaagtcc gagcagaaaa tggaaagaag aaggtcaagc cggaacagga 1560
ggaggatggg ccaaaaccag tttcttcttt gggaatttgc tggagaagtt actgccttga 1620
gagaaaaggt aactatgtgt ggataaaacg tactgtaaaa tgtgtattat gtatgatcta 1680
gagggcctta gtgtgatgta tgacttggtc agggattttg gtggtttgcc cgaagtcaaa 1740
ccgaaccaa actggttttc ggttacttta gactttagtc atagtataat gaacatgtct 1800
ataaatgaat aatagcaac tcttccaatt ggtaggcttg cttt
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1566151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```
Met Ala Lys Val Tyr Trp Pro Tyr Phe Asp Pro Glu Tyr Glu Asn Leu
1 5 10 15
Ser Ser Arg Ile Asn Pro Pro Ser Val Ser Ile Asp Asn Thr Ser Cys
 20 25 30
Lys Glu Cys Thr Leu Val Lys Val Asp Ser Met Asn Lys Pro Gly Ile
 35 40 45
Leu Leu Glu Val Val Gln Val Leu Thr Asp Leu Asp Leu Thr Ile Thr
 50 55 60
Lys Ala Tyr Ile Ser Ser Asp Gly Gly Trp Phe Met Asp Val Phe His
65 70 75 80
Val Thr Asp Gln Gln Gly Asn Lys Val Thr Asp Ser Lys Thr Ile Asp
 85 90 95
Tyr Ile Glu Lys Val Leu Gly Pro Lys Gly His Ala Ser Ala Ser Gln
 100 105 110
Asn Thr Trp Pro Gly Lys Arg Val Gly Val His Ser Leu Gly Asp His
 115 120 125
Thr Ser Ile Glu Ile Ile Ala Arg Asp Arg Pro Gly Leu Leu Ser Glu
 130 135 140
Val Ser Ala Val Leu Ala Asp Leu Asn Ile Asn Val Val Ala Ala Glu
145 150 155 160
Ala Trp Thr His Asn Arg Arg Ile Ala Cys Val Leu Tyr Val Asn Asp
 165 170 175
Asn Ala Thr Ser Arg Ala Val Asp Asp Pro Glu Arg Leu Ser Ser Met
 180 185 190
Glu Glu Gln Leu Asn Asn Val Leu Arg Gly Cys Glu Glu Gln Asp Glu
 195 200 205
Lys Phe Ala Arg Thr Ser Leu Ser Ile Gly Ser Thr His Val Asp Arg
210 215 220
Arg Leu His Gln Met Phe Phe Ala Asp Arg Asp Tyr Glu Ala Val Thr
225 230 235 240
Lys Leu Asp Asp Ser Ala Ser Cys Gly Phe Glu Pro Lys Ile Thr Val
 245 250 255
Glu His Cys Glu Lys Gly Tyr Ser Val Ile Asn Val Ser Cys Glu
 260 265 270
Asp Arg Pro Lys Leu Met Phe Asp Ile Val Cys Thr Leu Thr Asp Met
275 280 285
Gln Tyr Ile Val Phe His Ala Thr Ile Ser Ser Ser Gly Ser His Ala
290 295 300
Ser Gln Glu Tyr Phe Ile Arg His Lys Asp Gly Cys Thr Leu Asp Thr
```

2025 RELEASE UNDER E.O. 14176

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Gly | Glu | Lys | Glu | Arg | Xaa | Val | Lys | Cys | Leu | Glu | Ala | Ala | Ile | His |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |
| Arg | Arg | Val | Ser | Glu | Gly | Trp | Ser | Leu | Glu | Leu | Cys | Ala | Lys | Asp | Arg |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |
| Val | Gly | Leu | Leu | Ser | Glu | Val | Thr | Arg | Ile | Leu | Arg | Glu | His | Gly | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Val | Ser | Arg | Ala | Gly | Val | Thr | Thr | Val | Gly | Glu | Gln | Ala | Val | Asn |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Phe | Tyr | Val | Lys | Asp | Ala | Ser | Gly | Asn | Pro | Val | Asp | Val | Lys | Thr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ile | Glu | Ala | Leu | Arg | Gly | Glu | Ile | Gly | His | Ser | Met | Met | Ile | Asp | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Asn | Lys | Val | Pro | Ser | Arg | Lys | Trp | Lys | Glu | Glu | Gly | Gln | Ala | Gly |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Thr | Gly | Gly | Gly | Trp | Ala | Lys | Thr | Ser | Phe | Phe | Phe | Gly | Asn | Leu | Leu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Lys | Leu | Leu | Pro |     |     |     |     |     |     |     |     |     |     |     |
| 450 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1566152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Pro | Gly | Ile | Leu | Leu | Glu | Val | Val | Gln | Val | Leu | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Asp | Leu | Thr | Ile | Thr | Lys | Ala | Tyr | Ile | Ser | Ser | Asp | Gly | Gly | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Met | Asp | Val | Phe | His | Val | Thr | Asp | Gln | Gln | Gly | Asn | Lys | Val | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | Lys | Thr | Ile | Asp | Tyr | Ile | Glu | Lys | Val | Leu | Gly | Pro | Lys | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| His | Ala | Ser | Ala | Ser | Gln | Asn | Thr | Trp | Pro | Gly | Lys | Arg | Val | Gly | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Ser | Leu | Gly | Asp | His | Thr | Ser | Ile | Glu | Ile | Ile | Ala | Arg | Asp | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Leu | Leu | Ser | Glu | Val | Ser | Ala | Val | Leu | Ala | Asp | Leu | Asn | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Val | Val | Ala | Ala | Glu | Ala | Trp | Thr | His | Asn | Arg | Arg | Ile | Ala | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Leu | Tyr | Val | Asn | Asp | Asn | Ala | Thr | Ser | Arg | Ala | Val | Asp | Asp | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Arg | Leu | Ser | Ser | Met | Glu | Glu | Gln | Leu | Asn | Asn | Val | Leu | Arg | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Cys | Glu | Glu | Gln | Asp | Glu | Lys | Phe | Ala | Arg | Thr | Ser | Leu | Ser | Ile | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Thr | His | Val | Asp | Arg | Arg | Leu | His | Gln | Met | Phe | Phe | Ala | Asp | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Tyr | Glu | Ala | Val | Thr | Lys | Leu | Asp | Asp | Ser | Ala | Ser | Cys | Gly | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Pro | Lys | Ile | Thr | Val | Glu | His | Cys | Glu | Glu | Lys | Gly | Tyr | Ser | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Asn | Val | Ser | Cys | Glu | Asp | Arg | Pro | Lys | Leu | Met | Phe | Asp | Ile | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Cys Thr Leu Thr Asp Met Gln Tyr Ile Val Phe His Ala Thr Ile Ser  
245 250 255  
Ser Ser Gly Ser His Ala Ser Gln Glu Tyr Phe Ile Arg His Lys Asp  
260 270  
Gly Cys Thr Leu Asp Thr Glu Gly Glu Lys Glu Arg Xaa Val Lys Cys  
275 280 285  
Leu Glu Ala Ala Ile His Arg Arg Val Ser Glu Gly Trp Ser Leu Glu  
290 295 300  
Leu Cys Ala Lys Asp Arg Val Gly Leu Leu Ser Glu Val Thr Arg Ile  
305 310 315 320  
Leu Arg Glu His Gly Leu Ser Val Ser Arg Ala Gly Val Thr Thr Val  
325 330 335  
Gly Glu Gln Ala Val Asn Val Phe Tyr Val Lys Asp Ala Ser Gly Asn  
340 345 350  
Pro Val Asp Val Lys Thr Ile Glu Ala Leu Arg Gly Glu Ile Gly His  
355 360 365  
Ser Met Met Ile Asp Phe Lys Asn Lys Val Pro Ser Arg Lys Trp Lys  
370 375 380  
Glu Glu Gly Gln Ala Gly Thr Gly Gly Gly Trp Ala Lys Thr Ser Phe  
385 390 395 400  
Phe Phe Gly Asn Leu Glu Lys Leu Leu Pro  
405 410

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met Asp Val Phe His Val Thr Asp Gln Gln Gly Asn Lys Val Thr Asp  
1 5 10 15  
Ser Lys Thr Ile Asp Tyr Ile Glu Lys Val Leu Gly Pro Lys Gly His  
20 25 30  
Ala Ser Ala Ser Gln Asn Thr Trp Pro Gly Lys Arg Val Gly Val His  
35 40 45  
Ser Leu Gly Asp His Thr Ser Ile Glu Ile Ile Ala Arg Asp Arg Pro  
50 55 60  
Gly Leu Leu Ser Glu Val Ser Ala Val Leu Ala Asp Leu Asn Ile Asn  
65 70 75 80  
Val Val Ala Ala Glu Ala Trp Thr His Asn Arg Arg Ile Ala Cys Val  
85 90 95  
Leu Tyr Val Asn Asp Asn Ala Thr Ser Arg Ala Val Asp Asp Pro Glu  
100 105 110  
Arg Leu Ser Ser Met Glu Glu Gln Leu Asn Asn Val Leu Arg Gly Cys  
115 120 125  
Glu Glu Gln Asp Glu Lys Phe Ala Arg Thr Ser Leu Ser Ile Gly Ser  
130 135 140  
Thr His Val Asp Arg Arg Leu His Gln Met Phe Phe Ala Asp Arg Asp  
145 150 155 160  
Tyr Glu Ala Val Thr Lys Leu Asp Asp Ser Ala Ser Cys Gly Phe Glu  
165 170 175  
Pro Lys Ile Thr Val Glu His Cys Glu Glu Lys Gly Tyr Ser Val Ile  
180 185 190  
Asn Val Ser Cys Glu Asp Arg Pro Lys Leu Met Phe Asp Ile Val Cys  
195 200 205  
Thr Leu Thr Asp Met Gln Tyr Ile Val Phe His Ala Thr Ile Ser Ser

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210 215 220  
Ser Gly Ser His Ala Ser Gln Glu Tyr Phe Ile Arg His Lys Asp Gly  
225 230 235 240  
Cys Thr Leu Asp Thr Glu Gly Glu Lys Glu Arg Xaa Val Lys Cys Leu  
245 250 255  
Glu Ala Ala Ile His Arg Arg Val Ser Glu Gly Trp Ser Leu Glu Leu  
260 265 270  
Cys Ala Lys Asp Arg Val Gly Leu Leu Ser Glu Val Thr Arg Ile Leu  
275 280 285  
Arg Glu His Gly Leu Ser Val Ser Arg Ala Gly Val Thr Thr Val Gly  
290 295 300  
Glu Gln Ala Val Asn Val Phe Tyr Val Lys Asp Ala Ser Gly Asn Pro  
305 310 315 320  
Val Asp Val Lys Thr Ile Glu Ala Leu Arg Gly Glu Ile Gly His Ser  
325 330 335  
Met Met Ile Asp Phe Lys Asn Lys Val Pro Ser Arg Lys Trp Lys Glu  
340 345 350  
Glu Gly Gln Ala Gly Thr Gly Gly Gly Trp Ala Lys Thr Ser Phe Phe  
355 360 365  
Phe Gly Asn Leu Leu Glu Lys Leu Leu Pro  
370 375

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| acataagtct  | ctctcttaca  | ttttgaaacc | ctaatttctc | aaaaaaaaatg | tctgaagttg | 60  |
| agtaccggtg  | ctttgtcggc  | ggccttgcc  | gggccaccaa | tgatgaagat  | cttcaaagga | 120 |
| cgttctcaca  | gttcggcgac  | ggtatcgatt | ctaagatcat | taacgaccgc  | gagagtggaa | 180 |
| gatcaagggg  | attcggattc  | gtcaccttca | aggacgagaa | agccatgagg  | gatgcgattg | 240 |
| aagagatgaa  | cggtaaagag  | ctcgatggac | gtgtcatcac | cgtgaacgag  | gctcagtcga | 300 |
| gaggtagcgg  | cgggtggcggc | ggatactcag | gaggaggcgg | tggtgggttac | gagagacgta | 360 |
| gcggagggtta | cggatctggt  | ggargcggg  | gtggccgagg | atacgggtgt  | ggtggacgcc | 420 |
| gtgagggagg  | tggctacgga  | ggcggtgatg | gtggaagtta | cggcggcggt  | ggtggcggt  | 480 |
| ggtaatcaaa  | gatagagttg  | tttgcggtgt | gctgctctgt | ttttggttta  | gatttggGat | 540 |
| ttgtgtcacc  | acttctggtt  | tggttatcgt | tcgttkggtt | tacttttttg  | atgaaacagt | 600 |
| ttcgtttaag  | tcttctttgt  | ctggatcgaa | atgttaattc | gcgtgttggt  | tactaaattt | 660 |
| ataacgtttc  | cttttc      |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Val | Glu | Tyr | Arg | Cys | Phe | Val | Gly | Gly | Leu | Ala | Trp | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Thr | Asn | Asp | Glu | Asp | Leu | Gln | Arg | Thr | Phe | Ser | Gln | Phe | Gly | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Ser Gly Arg Ser Arg Gly  
35 40 45  
Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Arg Asp Ala Ile  
50 55 60  
Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn  
65 70 75 80  
Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly Tyr Ser Gly Gly  
85 90 95  
Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly  
100 105 110  
Xaa Gly Gly Gly Arg Gly Tyr Gly Gly Gly Arg Arg Glu Gly Gly  
115 120 125  
Gly Tyr Gly Gly Gly Asp Gly Gly Ser Tyr Gly Gly Gly Gly Gly  
130 135 140

Trp  
145

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Met Arg Asp Ala Ile Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg  
1 5 10 15  
Val Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly  
20 25 30  
Gly Tyr Ser Gly Gly Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly Gly  
35 40 45  
Tyr Gly Ser Gly Gly Xaa Gly Gly Gly Arg Gly Tyr Gly Gly Gly Gly  
50 55 60  
Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Asp Gly Gly Ser Tyr Gly  
65 70 75 80  
Gly Gly Gly Gly Gly Trp  
85

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn Glu Ala  
1 5 10 15  
Gln Ser Arg Gly Ser Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly  
20 25 30  
Gly Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly Xaa Gly  
35 40 45  
Gly Gly Arg Gly Tyr Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr  
50 55 60  
Gly Gly Gly Asp Gly Gly Ser Tyr Gly Gly Gly Gly Gly Trp

65

70

75

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1415
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| atgttcatag  | tgaattgtt   | agttggttt   | aattctttt  | taagacaaca | tataatgtca | 60   |
| attgtatgta  | cgtttttctt  | gtttctctta  | aacacttctt | ttgcgtttgc | atttgcgatt | 120  |
| cctaaaccgc  | caatagtaag  | gagactatca  | acgacagtga | catcaaattc | aacagcgctc | 180  |
| tcttgctcag  | ccaatggaaa  | tccaatcgat  | gagtgttga  | gatgcgacga | aaactggaag | 240  |
| gacaaccgca  | aaaacctcgc  | ggattgcgcg  | gttggtattc | gacgcgactc | aattggcggg | 300  |
| agagccgggg  | agttctacac  | ggtagactgat | tcaggagacg | acaatcctct | aaatccaact | 360  |
| ccaggtagat  | tacggtagcg  | tgcgacacaa  | gatcaacctc | tatggatcat | ttttgatcga | 420  |
| gacatggtaa  | tacaactaaa  | acaagatctt  | caagtagctt | catacaaaac | cattgatggt | 480  |
| agaggaaata  | acgtacaaat  | agcttatgga  | ccgtgtttta | ctttatataa | agttagtaac | 540  |
| attattataa  | acaatcttta  | tattcacgat  | tgtgttcccg | cgaaacggaa | tgctttatcg | 600  |
| tcgttgggag  | gatactcgga  | tggagatgga  | atatcgatat | tcgagtctcg | agatatttgg | 660  |
| attgatcatt  | gtacgttaga  | gaaatgttac  | gatgggctta | ttgatgcggg | gaatggatcc | 720  |
| acggatataa  | cgatttcgaa  | tagttacatg  | ttgaatcata | atgaagtcac | gcttttgggc | 780  |
| catagtgatg  | agtattccgg  | tgatcgggat  | atgcgagtta | cgatcgcggt | taactatttt | 840  |
| ggtgaaggac  | ttgtccaaag  | aatgccaaag  | tgtaggcatg | gatattttca | catagtgaat | 900  |
| aacattttata | gagaactggaa | gatgtatgct  | attggtggaa | gtgctaatac | aacgatcttt | 960  |
| agccaaggaa  | atgttttcat  | agcttccaat  | aatcagttca | ccaaggaggt | tacaaagcga | 1020 |
| gagagtgcag  | atggagacga  | agaatggaag  | gaatggaact | ggaaatcaga | aggagacgaa | 1080 |
| atgggttaacg | gagctttctt  | tacaccgtca  | gggaaagagg | attctccgag | Ctacgcgaaa | 1140 |
| ttttcgagta  | tggtagctcg  | accagcttca  | cttctcaaga | ccacacatcc | atcagtaggt | 1200 |
| gttcttagtt  | gcgaaattga  | ccaagcttgt  | taaaaacaca | aacataagct | tgtgaccaa  | 1260 |
| tctagtgttt  | gtccttcttt  | ttcttttttg  | ctcttctact | tggtgtgggt | attgttatcg | 1320 |
| taaataggat  | ttgtactgaa  | tgtgatgatg  | atcatagacc | caaacaacaa | ttgttcattg | 1380 |
| tcaatttctt  | tacaaaaaaa  | tttcttttac  | gagtc      |            |            |      |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ile | Val | Lys | Leu | Leu | Val | Gly | Phe | Asn | Leu | Phe | Leu | Arg | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ile | Met | Ser | Ile | Val | Cys | Thr | Phe | Phe | Leu | Phe | Leu | Leu | Asn | Thr |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Phe | Ala | Phe | Ala | Phe | Ala | Ile | Pro | Lys | Pro | Pro | Ile | Val | Arg | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Leu | Ser | Thr | Thr | Val | Thr | Ser | Asn | Ser | Thr | Ala | Ser | Ser | Cys | Ser | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Asn | Gly | Asn | Pro | Ile | Asp | Glu | Cys | Trp | Arg | Cys | Asp | Glu | Asn | Trp | Lys |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  | 80  |
| Asp | Asn | Arg | Lys | Asn | Leu | Ala | Asp | Cys | Ala | Val | Gly | Phe | Gly | Arg | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |



Ser Ile Gly Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly  
100 105 110  
Asp Asp Asn Pro Leu Asn Pro Thr Pro Gly Thr Leu Arg Tyr Ala Ala  
115 120 125  
Thr Gln Asp Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile  
130 135 140  
Gln Leu Lys Gln Asp Leu Gln Val Ala Ser Tyr Lys Thr Ile Asp Gly  
145 150 155 160  
Arg Gly Asn Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Thr Leu Tyr  
165 170 175  
Lys Val Ser Asn Ile Ile Ile Asn Asn Leu Tyr Ile His Asp Cys Val  
180 185 190  
Pro Ala Lys Arg Asn Ala Leu Ser Ser Leu Gly Gly Tyr Ser Asp Gly  
195 200 205  
Asp Gly Ile Ser Ile Phe Glu Ser Arg Asp Ile Trp Ile Asp His Cys  
210 215 220  
Thr Leu Glu Lys Cys Tyr Asp Gly Leu Ile Asp Ala Val Asn Gly Ser  
225 230 235 240  
Thr Asp Ile Thr Ile Ser Asn Ser Tyr Met Leu Asn His Asn Glu Val  
245 250 255  
Met Leu Leu Gly His Ser Asp Glu Tyr Ser Gly Asp Arg Asp Met Arg  
260 265 270  
Val Thr Ile Ala Phe Asn Tyr Phe Gly Glu Gly Leu Val Gln Arg Met  
275 280 285  
Pro Arg Cys Arg His Gly Tyr Phe His Ile Val Asn Asn Ile Tyr Arg  
290 295 300  
Asp Trp Lys Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Phe  
305 310 315 320  
Ser Gln Gly Asn Val Phe Ile Ala Ser Asn Asn Gln Phe Thr Lys Glu  
325 330 335  
Val Thr Lys Arg Glu Ser Ala Asp Gly Asp Glu Glu Trp Lys Glu Trp  
340 345 350  
Asn Trp Lys Ser Glu Gly Asp Glu Met Val Asn Gly Ala Phe Phe Thr  
355 360 365  
Pro Ser Gly Lys Glu Asp Ser Pro Ser Tyr Ala Lys Phe Ser Ser Met  
370 375 380  
Val Ala Arg Pro Ala Ser Leu Leu Lys Thr Thr His Pro Ser Val Gly  
385 390 395 400  
Val Leu Ser Cys Glu Ile Asp Gln Ala Cys  
405 410

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1566173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Ser Ile Val Cys Thr Phe Phe Leu Phe Leu Leu Asn Thr Ser Phe  
1 5 10 15  
Ala Phe Ala Phe Ala Ile Pro Lys Pro Pro Ile Val Arg Arg Leu Ser  
20 25 30  
Thr Thr Val Thr Ser Asn Ser Thr Ala Ser Ser Cys Ser Ala Asn Gly  
35 40 45  
Asn Pro Ile Asp Glu Cys Trp Arg Cys Asp Glu Asn Trp Lys Asp Asn  
50 55 60  
Arg Lys Asn Leu Ala Asp Cys Ala Val Gly Phe Gly Arg Asp Ser Ile

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Gly | Gly | Arg | Ala | Gly | Glu | Phe | Tyr | Thr | Val | Thr | Asp | Ser | Gly | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| Asn | Pro | Leu | Asn | Pro | Thr | Pro | Gly | Thr | Leu | Arg | Tyr | Ala | Ala | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Gln |
| Asp | Gln | Pro | Leu | Trp | Ile | Ile | Phe | Asp | Arg | Asp | Met | Val | Ile | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     | Leu |
| Lys | Gln | Asp | Leu | Gln | Val | Ala | Ser | Tyr | Lys | Thr | Ile | Asp | Gly | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     | Gly |
| Asn | Asn | Val | Gln | Ile | Ala | Tyr | Gly | Pro | Cys | Leu | Thr | Leu | Tyr | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | Val |
| Ser | Asn | Ile | Ile | Ile | Asn | Asn | Leu | Tyr | Ile | His | Asp | Cys | Val | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | Ala |
| Lys | Arg | Asn | Ala | Leu | Ser | Ser | Leu | Gly | Gly | Tyr | Ser | Asp | Gly | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Gly |
| Ile | Ser | Ile | Phe | Glu | Ser | Arg | Asp | Ile | Trp | Ile | Asp | His | Cys | Thr |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     | Leu |
| Glu | Lys | Cys | Tyr | Asp | Gly | Leu | Ile | Asp | Ala | Val | Asn | Gly | Ser | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     | Asp |
| Ile | Thr | Ile | Ser | Asn | Ser | Tyr | Met | Leu | Asn | His | Asn | Glu | Val | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | Leu |
| Leu | Gly | His | Ser | Asp | Glu | Tyr | Ser | Gly | Asp | Arg | Asp | Met | Arg | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | Thr |
| Ile | Ala | Phe | Asn | Tyr | Phe | Gly | Glu | Gly | Leu | Val | Gln | Arg | Met | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 | Arg |
| Cys | Arg | His | Gly | Tyr | Phe | His | Ile | Val | Asn | Asn | Ile | Tyr | Arg | Asp |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 | Trp |
| Lys | Met | Tyr | Ala | Ile | Gly | Gly | Ser | Ala | Asn | Pro | Thr | Ile | Phe | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     | Gln |
| Gly | Asn | Val | Phe | Ile | Ala | Ser | Asn | Asn | Gln | Phe | Thr | Lys | Glu | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | Thr |
| Lys | Arg | Glu | Ser | Ala | Asp | Gly | Asp | Glu | Glu | Trp | Lys | Glu | Trp | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | Trp |
| Lys | Ser | Glu | Gly | Asp | Glu | Met | Val | Asn | Gly | Ala | Phe | Phe | Thr | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 | Ser |
| Gly | Lys | Glu | Asp | Ser | Pro | Ser | Tyr | Ala | Lys | Phe | Ser | Ser | Met | Val |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     | Ala |
| Arg | Pro | Ala | Ser | Leu | Leu | Lys | Thr | Thr | His | Pro | Ser | Val | Gly | Val |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     | Leu |
| Ser | Cys | Glu | Ile | Asp | Gln | Ala | Cys |     |     |     |     |     |     |     |
| 385 |     |     |     |     | 390 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..731
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| agtttttgggt | tgtttttgggt | gttgcgaggtt | tgtgactata | aaacctctcc  | cacttggttc | 60  |
| ttcactctca  | ctgtttctca  | tctcttcgct  | ttctccgctt | ccttcaatct  | cactccgatc | 120 |
| tctctacgat  | tcattcggtt  | tatggcttcc  | attgctgctt | ctgcttctat  | ttcccttcaa | 180 |
| gctcgtcttc  | gccaaactggc | gatcgcggtt  | aggcaagtta | aaagcttttag | caatggaaga | 240 |
| agaagcagtc  | tttcttttaa  | tctccgccag  | cttcctaccc | gcttgactgt  | ttcctgcgct | 300 |
| gcaaaacctg  | agacagtggg  | caaggtgtgt  | gcagttgtca | gaaagcaact  | ctcacttaaa | 360 |
| gaggctgacg  | aaattactgc  | tgccacaaaa  | tttgctgcac | ttggtgctga  | ttcccttgat | 420 |
| acggtggaga  | ttgtgatggg  | actagaggaa  | gagttcggga | ttgaaatggc  | ggaggagaaa | 480 |

```
gcacagtcaa tcgccacagt tgagcaagca Gctgcgctca ttgaggagct cttgtttgaa 540
aaggccaagt agaatatctt tattacatta gcaaaaacga aaaaaatcaa aacccaaacc 600
actatcttat tgtttcggtta gctagagagc aattgtgtct gttgaaagat tttatgttat 660
tttggggaaa ttattacaag gcttgtatct gacttttatc tttcttctaa aacattttac 720
tttcagcctc c
```

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
Ser Phe Cys Leu Phe Trp Leu Leu Arg Val Cys Asp Tyr Lys Thr Ser
1 5 10 15
Pro Thr Trp Phe Phe Thr Leu Thr Val Ser His Leu Phe Val Phe Ser
20 25 30
Ala Ser Phe Asn Leu Thr Pro Ile Ser Leu Arg Phe Ile Arg Ser Met
35 40 45
Ala Ser Ile Ala Ala Ser Ala Ser Ile Ser Leu Gln Ala Arg Pro Arg
50 55 60
Gln Leu Ala Ile Ala Ala Arg Gln Val Lys Ser Phe Ser Asn Gly Arg
65 70 75 80
Arg Ser Ser Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu Thr
85 90 95
Val Ser Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala Val
100 105 110
Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala Ala
115 120 125
Thr Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu Ile
130 135 140
Val Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Glu Glu Lys
145 150 155 160
Ala Gln Ser Ile Ala Thr Val Glu Gln Ala Ala Ala Leu Ile Glu Glu
165 170 175
Leu Leu Phe Glu Lys Ala Lys
180
```

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```
Val Phe Val Cys Phe Gly Cys Cys Glu Phe Val Thr Ile Lys Pro Leu
1 5 10 15
Pro Leu Gly Ser Ser Leu Ser Leu Phe Leu Ile Ser Ser Ser Pro
20 25 30
Pro Pro Ser Ile Ser Leu Arg Ser Leu Tyr Asp Ser Phe Val Leu Trp
35 40 45
Leu Pro Leu Leu Leu Leu Leu Phe Pro Phe Lys Leu Val Leu Ala
50 55 60
```

Asn Trp Arg Ser Arg Leu Gly Lys Leu Lys Ala Leu Ala Met Glu Glu  
65 70 75 80  
Glu Ala Val Phe Leu Ile Ser Ala Ser Phe Leu Pro Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Met Ala Ser Ile Ala Ala Ser Ala Ser Ile Ser Leu Gln Ala Arg Pro  
1 5 10 15  
Arg Gln Leu Ala Ile Ala Ala Arg Gln Val Lys Ser Phe Ser Asn Gly  
20 25 30  
Arg Arg Ser Ser Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu  
35 40 45  
Thr Val Ser Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala  
50 55 60  
Val Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala  
65 70 75 80  
Ala Thr Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu  
85 90 95  
Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Glu Glu  
100 105 110  
Lys Ala Gln Ser Ile Ala Thr Val Glu Gln Ala Ala Ala Leu Ile Glu  
115 120 125  
Glu Leu Leu Phe Glu Lys Ala Lys  
130 135

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| gaagaacaaa  | cacaaaaaatg | gcgacggtac | cattgttcac  | ccagtttccc  | tgcaaaaccc | 60  |
| taaatccaag  | ctcatcaaac  | actaaacacc | aatcgaaatc  | tccgataccta | ctaccgatta | 120 |
| actcaataaaa | tccgatcggag | attggagtct | ctgttcacgc  | gccagatttc  | aaaatccgag | 180 |
| cgacggacat  | cgacgcagaa  | tggggtcaag | atggagtggg  | gagagtattt  | gcctcatctt | 240 |
| caaccgtatc  | ggtagcagat  | aaagcaatcg | aatccgtgga  | ggagacggag  | aggctaaaga | 300 |
| gatcaactagc | ggattcggtg  | tacggaacag | atcgagggtt  | aagcgtatcg  | agtgatacga | 360 |
| gagctgagat  | cagcgcagctc | atcacacagc | tccgagtctaa | gaaccctact  | ccagctccta | 420 |
| acgaagctct  | gtttctcctc  | aacggcaaat | ggatcctcgc  | ctacacgtcg  | ttcgtggggg | 480 |
| tgttcccatt  | gctctcacga  | agaattgaac | cgttggttaa  | agtggatgag  | atctcacaaa | 540 |
| ccattgattc  | cgatagcttc  | accgttcaaa | actctgtccg  | gttcgctggg  | ccgttttcca | 600 |
| caacgtcgtt  | tagcaccaac  | gctaagtttg | aaatccgaag  | tcctaaacgt  | gtccagatta | 660 |
| agttcgagca  | aggtgttata  | ggRactcctc | agctaacgga  | ttcgattgaa  | ataccggaat | 720 |
| ccgtggagggt | tcttggtcag  | aaaatcgatc | tcaatcccat  | taaagggtta  | cttacatcag | 780 |
| tccaagacac  | tgcttcttca  | gtggctagaa | ccatttcaaa  | ccaaccacca  | ttgaagtttt | 840 |
| ctctgcctag  | tgacaacacg  | cagtcgtggc | tgctcacaac  | ttatctcgac  | aaggacCttc | 900 |

ggatctcgag aggcgatggt ggaagcgtct atgtgctcat caaagaagga agctctctct 960  
taaaccctta aatcatcata actctcatca catccatagt aacatatata caagtataga 1020  
cccattgtgc tatgtttact agtggtgtaa ctgttatata gcttctttac ctgttgagaga 1080  
gttataaact tataatggat gttactcttg gtatactgta ctacaataca tatacataac 1140  
tacataacttg aacaggcc

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Arg Thr Asn Thr Lys Met Ala Thr Val Pro Leu Phe Thr Gln Phe Pro  
1 5 10 15  
Cys Lys Thr Leu Asn Pro Ser Ser Ser Asn Thr Lys His Gln Ser Lys  
20 25 30  
Ser Pro Ile Leu Leu Pro Ile Asn Ser Ile Asn Arg Ser Glu Ile Gly  
35 40 45  
Val Ser Val His Arg Pro Asp Phe Lys Ile Arg Ala Thr Asp Ile Asp  
50 55 60  
Asp Glu Trp Gly Gln Asp Gly Val Glu Arg Val Phe Ala Ser Ser Ser  
65 70 75 80  
Thr Val Ser Val Ala Asp Lys Ala Ile Glu Ser Val Glu Glu Thr Glu  
85 90 95  
Arg Leu Lys Arg Ser Leu Ala Asp Ser Leu Tyr Gly Thr Asp Arg Gly  
100 105 110  
Leu Ser Val Ser Ser Asp Thr Arg Ala Glu Ile Ser Glu Leu Ile Thr  
115 120 125  
Gln Leu Glu Ser Lys Asn Pro Thr Pro Ala Pro Asn Glu Ala Leu Phe  
130 135 140  
Leu Leu Asn Gly Lys Trp Ile Leu Ala Tyr Thr Ser Phe Val Gly Leu  
145 150 155 160  
Phe Pro Leu Leu Ser Arg Arg Ile Glu Pro Leu Val Lys Val Asp Glu  
165 170 175  
Ile Ser Gln Thr Ile Asp Ser Asp Ser Phe Thr Val Gln Asn Ser Val  
180 185 190  
Arg Phe Ala Gly Pro Phe Ser Thr Thr Ser Phe Ser Thr Asn Ala Lys  
195 200 205  
Phe Glu Ile Arg Ser Pro Lys Arg Val Gln Ile Lys Phe Glu Gln Gly  
210 215 220  
Val Ile Xaa Thr Pro Gln Leu Thr Asp Ser Ile Glu Ile Pro Glu Ser  
225 230 235 240  
Val Glu Val Leu Gly Gln Lys Ile Asp Leu Asn Pro Ile Lys Gly Leu  
245 250 255  
Leu Thr Ser Val Gln Asp Thr Ala Ser Ser Val Ala Arg Thr Ile Ser  
260 265 270  
Asn Gln Pro Pro Leu Lys Phe Ser Leu Pro Ser Asp Asn Thr Gln Ser  
275 280 285  
Trp Leu Leu Thr Thr Tyr Leu Asp Lys Asp Leu Arg Ile Ser Arg Gly  
290 295 300  
Asp Gly Gly Ser Val Tyr Val Leu Ile Lys Glu Gly Ser Ser Leu Leu  
305 310 315 320  
Asn Pro

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..317
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1566187
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Ala Thr Val Pro Leu Phe Thr Gln Phe Pro Cys Lys Thr Leu Asn  
1 5 10 15  
Pro Ser Ser Ser Asn Thr Lys His Gln Ser Lys Ser Pro Ile Leu Leu  
20 25 30  
Pro Ile Asn Ser Ile Asn Arg Ser Glu Ile Gly Val Ser Val His Arg  
35 40 45  
Pro Asp Phe Lys Ile Arg Ala Thr Asp Ile Asp Asp Glu Trp Gly Gln  
50 55 60  
Asp Gly Val Glu Arg Val Phe Ala Ser Ser Ser Thr Val Ser Val Ala  
65 70 75 80  
Asp Lys Ala Ile Glu Ser Val Glu Glu Thr Glu Arg Leu Lys Arg Ser  
85 90 95  
Leu Ala Asp Ser Leu Tyr Gly Thr Asp Arg Gly Leu Ser Val Ser Ser  
100 105 110  
Asp Thr Arg Ala Glu Ile Ser Glu Leu Ile Thr Gln Leu Glu Ser Lys  
115 120 125  
Asn Pro Thr Pro Ala Pro Asn Glu Ala Leu Phe Leu Leu Asn Gly Lys  
130 135 140  
Trp Ile Leu Ala Tyr Thr Ser Phe Val Gly Leu Phe Pro Leu Leu Ser  
145 150 155 160  
Arg Arg Ile Glu Pro Leu Val Lys Val Asp Glu Ile Ser Gln Thr Ile  
165 170 175  
Asp Ser Asp Ser Phe Thr Val Gln Asn Ser Val Arg Phe Ala Gly Pro  
180 185 190  
Phe Ser Thr Thr Ser Phe Ser Thr Asn Ala Lys Phe Glu Ile Arg Ser  
195 200 205  
Pro Lys Arg Val Gln Ile Lys Phe Glu Gln Gly Val Ile Xaa Thr Pro  
210 215 220  
Gln Leu Thr Asp Ser Ile Glu Ile Pro Glu Ser Val Glu Val Leu Gly  
225 230 235 240  
Gln Lys Ile Asp Leu Asn Pro Ile Lys Gly Leu Leu Thr Ser Val Gln  
245 250 255  
Asp Thr Ala Ser Ser Val Ala Arg Thr Ile Ser Asn Gln Pro Pro Leu  
260 265 270  
Lys Phe Ser Leu Pro Ser Asp Asn Thr Gln Ser Trp Leu Leu Thr Thr  
275 280 285  
Tyr Leu Asp Lys Asp Leu Arg Ile Ser Arg Gly Asp Gly Gly Ser Val  
290 295 300  
Tyr Val Leu Ile Lys Glu Gly Ser Ser Leu Leu Asn Pro  
305 310 315

- (2) INFORMATION FOR SEQ ID NO:215:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 655 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..655
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1566214

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aatggttact | tttacttcct  | cttcttctct | tcttgttcca | tctttcatgt  | gaaagagaga | 60  |
| gttgaatttt | gcagatgagt  | atgagaagaa | gcaaagcgga | aggggaagagg | agcttacgag | 120 |
| aactgagtga | ggaagaggaa  | gaagaagaag | aaactgaaga | tgaagatact  | tttgaagaag | 180 |
| aagaggcttt | ggagaagaag  | cagaaaggta | aagctacaag | tagtagtgga  | gtttgtcagg | 240 |
| tcgagagttg | taccgcggat  | ataagcaaag | ccaaacagta | ccacaaacga  | cacaaagtct | 300 |
| gccagtttca | tgccaaagct  | cctcatgttc | ggatctctgg | tcttcaccaa  | cgtttctgcc | 360 |
| aacaatgcag | caggtttcac  | gcgctcagtg | agtttgatga | agccaagcgg  | agttgcagga | 420 |
| gacgcttagc | tggaacacaac | gagagaaggc | ggaaaagcac | aactgactaa  | agacggtgaa | 480 |
| acgtgtgaga | tccCggtttg  | aaggttaatg | aaacaggGct | ttgGcttact  | ctcttctgtc | 540 |
| agtctctttt | agctccttgt  | aatcctctgt | gtctctgtct | gttccccata  | ttacctgtaa | 600 |
| tcaaagctat | ctgctaaacc  | tacgacatgg | ttaaataaat | gcattgagac  | ttagc      |     |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Met | Arg | Arg | Ser | Lys | Ala | Glu | Gly | Lys | Arg | Ser | Leu | Arg | Glu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Ser | Glu | Glu | Glu | Glu | Glu | Glu | Glu | Glu | Thr | Glu | Asp | Glu | Asp | Thr |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Glu | Glu | Glu | Glu | Ala | Leu | Glu | Lys | Lys | Gln | Lys | Gly | Lys | Ala | Thr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Ser | Ser | Gly | Val | Cys | Gln | Val | Glu | Ser | Cys | Thr | Ala | Asp | Ile | Ser |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Ala | Lys | Gln | Tyr | His | Lys | Arg | His | Lys | Val | Cys | Gln | Phe | His | Ala |  |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Ala | Pro | His | Val | Arg | Ile | Ser | Gly | Leu | His | Gln | Arg | Phe | Cys | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gln | Cys | Ser | Arg | Phe | His | Ala | Leu | Ser | Glu | Phe | Asp | Glu | Ala | Lys | Arg |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Cys | Arg | Arg | Arg | Leu | Ala | Gly | His | Asn | Glu | Arg | Arg | Arg | Lys | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Thr | Thr | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Arg | Ser | Lys | Ala | Glu | Gly | Lys | Arg | Ser | Leu | Arg | Glu | Leu | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Glu | Glu | Glu | Glu | Glu | Glu | Glu | Glu | Thr | Glu | Asp | Glu | Asp | Thr | Phe | Glu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Glu | Glu | Ala | Leu | Glu | Lys | Lys | Gln | Lys | Gly | Lys | Ala | Thr | Ser | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Gly | Val | Cys | Gln | Val | Glu | Ser | Cys | Thr | Ala | Asp | Ile | Ser | Lys | Ala |  |

(2) INFORMATION FOR SEQ ID NO:218:

(A) LENGTH: 631 base pairs

(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1566220

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| atatttatat  | tttccaataa | tctcaaaaaa  | aaActctctg | attcgaaaag | tgaaatttga  | 60  |
| ttttgacaaa  | aaaaaaatga | gctacgacag  | agtcacacag | gaatcgtatc | ctcctccagg  | 120 |
| ataccaatct  | cactatccac | ctccgggtta  | tccatcagca | ccgccaccgc | cgggatatcc  | 180 |
| ttctctccg   | tgcatacag  | aaggatatcc  | tccacctcag | ccttacggag | gatatccacc  | 240 |
| accgtcttca  | cgtocttaag | aaggcgggtta | tcaaggctac | ttcgccggag | gagggttatcc | 300 |
| tcatcagcat  | cacggaccac | cacctcctcc  | tccgcgcaa  | aattacgacc | actgccatca  | 360 |
| tgatcatcac  | cattaccaag | attctgactc  | tggttgcttc | tctttcatcc | gtggtgtct   | 420 |
| tgctgctctt  | tgctgttgct | gtttgtttgga | ggaatgctgc | ttctgagaat | gccgccagtc  | 480 |
| tctgtggatc  | tcgtcgttta | ctctcagcat  | tatgtgtcta | atcgaagaca | tatgccataa  | 540 |
| cactctatgt  | cttatatgta | tccatcaaaa  | taaaccatgg | tgagtttgta | atgcagttcc  | 600 |
| ttcagaaaatg | tgtggaataa | tgtttcacaa  | t          |            |             |     |

(2) INFORMATION FOR SEQ ID NO:219:

(A) LENGTH: 154 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1566221

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Leu | Tyr | Phe | Pro | Ile | Ile | Ser | Lys | Lys | Asn | Ser | Leu | Ile | Arg | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Lys | Phe | Asp | Phe | Asp | Lys | Lys | Lys | Met | Ser | Tyr | Asp | Arg | Val | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Glu | Ser | Tyr | Pro | Pro | Pro | Gly | Tyr | Gln | Ser | His | Tyr | Pro | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Tyr | Pro | Ser | Ala | Pro | Pro | Pro | Pro | Gly | Tyr | Pro | Ser | Pro | Pro | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| His | His | Glu | Gly | Tyr | Pro | Pro | Pro | Gln | Pro | Tyr | Gly | Gly | Tyr | Pro | Pro |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Ser | Ser | Arg | Pro | Tyr | Glu | Gly | Gly | Tyr | Gln | Gly | Tyr | Phe | Ala | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Gly | Tyr | Pro | His | Gln | His | His | Gly | Pro | Pro | Pro | Pro | Pro | Pro | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gln | Asn | Tyr | Asp | His | Cys | His | His | Asp | His | His | His | Tyr | Gln | Asp | Ser |



115 120 125  
Asp Ser Gly Cys Phe Ser Phe Ile Arg Gly Cys Leu Ala Ala Leu Cys  
130 135 140  
Cys Cys Cys Leu Leu Glu Glu Cys Cys Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met Ser Tyr Asp Arg Val Pro Pro Glu Ser Tyr Pro Pro Pro Gly Tyr  
1 5 10 15  
Gln Ser His Tyr Pro Pro Pro Gly Tyr Pro Ser Ala Pro Pro Pro  
20 25 30  
Gly Tyr Pro Ser Pro Pro Ser His Glu Gly Tyr Pro Pro Pro Gln  
35 40 45  
Pro Tyr Gly Gly Tyr Pro Pro Pro Ser Ser Arg Pro Tyr Glu Gly Gly  
50 55 60  
Tyr Gln Gly Tyr Phe Ala Gly Gly Gly Tyr Pro His Gln His His Gly  
65 70 75 80  
Pro Pro Pro Pro Pro Pro Gln Asn Tyr Asp His Cys His His Asp  
85 90 95  
His His His Tyr Gln Asp Ser Asp Ser Gly Cys Phe Ser Phe Ile Arg  
100 105 110  
Gly Cys Leu Ala Ala Leu Cys Cys Cys Cys Leu Leu Glu Glu Cys Cys  
115 120 125  
Phe

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..771
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

aaaaaattag ttogtcgaag catcgtgaaa atgatcgtac tttctgttg ttccgcttct 60  
tcattctccga tgcgtcgtcgt cttttccgctc gcgcttcttc tgttctactt ctctgaaact 120  
tctctaggag ctccttgctcc catcaatggc ttgccaatcg tgaggaatat tagtgacctt 180  
cctcaggata actatggaag accaggtctt tcccacatga ctgttgctgg ctccgtattg 240  
catggaatga aagaggttga aatatggctt cagacatttg ctccagggtc agagacacca 300  
attcacaggc actcctgtga agaggttttt gttctcctaa agggcagtgg tactctgtat 360  
ctcgtcgaaa cacatggaaa tttccctggg aaaccaatcg aatttccaat ctttgccaac 420  
agtacaattc atattccgat caatgatgct catcagggtca aaaacaccgg tcatgaggac 480  
ctgcagggtg tggttatcat atctcggcgg cctattaaaa tcttcattta cgaagactgg 540  
tttatgccac accagtctgc aaggctgaag ttCcttact attgggatga gcaatgcatt 600  
caagaatcac aaaaagacga gctttaaagc aaagtccgag gctaaaagca agcacaacct 660  
ttagatagta aaatcatagt tgagggttttg tgacActacg tagatactgg taaattggca 720  
aggattttac atgaatgttg ttgttaccag aaagtaaata aatgttcaag c

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 208 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..208  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566224  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Lys Lys Leu Val Arg Arg Ser Ile Val Lys Met Ile Val Leu Ser Val  
1                    5                    10                    15  
Gly Ser Ala Ser Ser Ser Pro Ile Val Val Val Phe Ser Val Ala Leu  
                    20                    25                    30  
Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu Gly Ala Pro Cys Pro Ile  
                    35                    40                    45  
Asn Gly Leu Pro Ile Val Arg Asn Ile Ser Asp Leu Pro Gln Asp Asn  
50                    55                    60  
Tyr Gly Arg Pro Gly Leu Ser His Met Thr Val Ala Gly Ser Val Leu  
65                    70                    75                    80  
His Gly Met Lys Glu Val Glu Ile Trp Leu Gln Thr Phe Ala Pro Gly  
                    85                    90                    95  
Ser Glu Thr Pro Ile His Arg His Ser Cys Glu Glu Val Phe Val Leu  
                    100                    105                    110  
Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala Glu Thr His Gly Asn Phe  
115                    120                    125  
Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe Ala Asn Ser Thr Ile His  
130                    135                    140  
Ile Pro Ile Asn Asp Ala His Gln Val Lys Asn Thr Gly His Glu Asp  
145                    150                    155                    160  
Leu Gln Val Leu Val Ile Ile Ser Arg Pro Pro Ile Lys Ile Phe Ile  
                    165                    170                    175  
Tyr Glu Asp Trp Phe Met Pro His Thr Ala Ala Arg Leu Lys Phe Pro  
180                    185                    190  
Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu Ser Gln Lys Asp Glu Leu  
195                    200                    205

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 198 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..198  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566225  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val Val  
1                    5                    10                    15  
Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu  
20                    25                    30  
Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser  
35                    40                    45  
Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr  
50                    55                    60  
Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu  
65                    70                    75                    80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys  
85 90 95  
Glu Glu Val Phe Val Leu Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala  
100 105 110  
Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe  
115 120 125  
Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys  
130 135 140  
Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro  
145 150 155 160  
Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala  
165 170 175  
Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu  
180 185 190  
Ser Gln Lys Asp Glu Leu  
195

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1566226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile  
1 5 10 15  
Trp Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His  
20 25 30  
Ser Cys Glu Glu Val Phe Val Leu Leu Lys Gly Ser Gly Thr Leu Tyr  
35 40 45  
Leu Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro  
50 55 60  
Ile Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln  
65 70 75 80  
Val Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser  
85 90 95  
Arg Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His  
100 105 110  
Thr Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile  
115 120 125  
Gln Glu Ser Gln Lys Asp Glu Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1256

(D) OTHER INFORMATION: / Ceres Seq. ID 1566234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaacaaaaca caggtttggt cggagaaggc tttattaatc cacttgcct cctctcagac  | 60  |
| tctacaaagt caaagttgtt cactttacct ataaaaacgc tttcttttca atggcttctt | 120 |
| cttcttgttt ccttcgctcg attctcttct cttctcctac taaccttcgt tcaaatcacc | 180 |

```
atctccccac tttcttcccc aagaatcatc tcatttgctc tcattccact tcttctcgct 240
tcgaatcgct ctcggtttca tcgatcggaa ctggatctac caagaaatca tccgatactc 300
ggagaaaagg aaagagcatg gctacgacaa atataaggaa ggaggagaag aaaagagtcg 360
agatttatga tctcgaagAg aattttagcga ttgatttggc taaattcaca gcagatctct 420
ccgataagtt ttgtaaagag agaggcgctt tcaccgctcg tgtctccggt ggctctctca 480
tcaaactact ccggaaatta gtagaatctc cttacgttga ttctatagat tgggcaaggt 540
ggcatttttt ctgggttgac gagagagttg ttcccaagaa tcacgatgat agcaactata 600
aactcgctta tgatagtttt ctatccaagg taccaattcc gcctggaaat gtatatgcaa 660
tcaacgaagc cctctccgct gaggctgcag cggatgatta cgagacctgc ctcaaacatt 720
tggccaacac caacattctc cgtgtatctg aatcaactgg ctttcccaaa tttgatctca 780
tgcttctagg tatgggacct gatggtcatg tggcatcatt attccctggg catggtctct 840
gcaacgagag caagaaatgg gtagtttcaa tctctgactc tccaaaacca ccgtctgaga 900
gaatcacctt cacgttcccg gtcatacaat catctgcaca tgtagctcta gttgtttgcg 960
gttctgggaa agctgaagct gtggaggcag ctttaaagaa gactgggaat gtaccacctg 1020
ctggttctgt ttctgtgtaa gacgagttgg tttggttctt ggacaaacca gcatcttcca 1080
agctctaaaa acaggtggta tgcttcccat tccagtgaac ttaccaatgt gactagtccg 1140
gtttagtttt tggattttga ctctttgggt ctctccattt atgttgtggg aagagactgt 1200
tgtgataaaa gcgtgtactt tacatggaaa taatgaacta atcaatgggt tctctg
```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```
Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
1 5 10 15
Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
20 25 30
His Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser
35 40 45
Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
50 55 60
Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
65 70 75 80
Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Ala Ile Asp Leu
85 90 95
Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly
100 105 110
Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg
115 120 125
Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp
130 135 140
His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp
145 150 155 160
Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile
165 170 175
Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala
180 185 190
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn
195 200 205
Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met
210 215 220
Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly
225 230 235 240
His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp
```

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245 250 255  
Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile  
260 265 270  
Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala  
275 280 285  
Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala  
290 295 300  
Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro  
305 310 315 320  
Ala Ser Ser Lys Leu  
325

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys Lys Arg Val Glu Ile  
1 5 10 15  
Tyr Asp Leu Glu Glu Asn Leu Ala Ile Asp Leu Ala Lys Phe Thr Ala  
20 25 30  
Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly Ala Phe Thr Val Val  
35 40 45  
Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg Lys Leu Val Glu Ser  
50 55 60  
Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp His Phe Phe Trp Val  
65 70 75 80  
Asp Glu Arg Val Val Pro Lys Asn His Asp Asp Ser Asn Tyr Lys Leu  
85 90 95  
Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile Pro Pro Gly Asn Val  
100 105 110  
Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala Ala Asp Asp Tyr  
115 120 125  
Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn Ile Leu Arg Val Ser  
130 135 140  
Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met Leu Leu Gly Met Gly  
145 150 155 160  
Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly His Gly Leu Cys Asn  
165 170 175  
Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp Ser Pro Lys Pro Pro  
180 185 190  
Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile Asn Ser Ser Ala His  
195 200 205  
Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala Glu Ala Val Glu Ala  
210 215 220  
Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala Gly Ser Val Ser Ala  
225 230 235 240  
Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro Ala Ser Ser Lys Leu  
245 250 255

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..640
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1566237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aactaccacc aattcaatcc attgctcaaa ctctcttatac atctctaaca caccaccct | 60  |
| acctacctcc atctctctct ctgcaacaga gcacaaaaat ggattctgca tcgtccaaca | 120 |
| ccaaagctat agacctcca cttcacatgt tgggtttcga gttcgatgaa ttatctccga  | 180 |
| cacgtatcac aggtcgctt cctgtttctc ccgtctgctg ccagccttc aaggtgttac   | 240 |
| acggtggtgt atctgctttg atagccgagt ctttagcaag tatgggagct cacatggctt | 300 |
| ctggtttcaa aagggtcgt ggaattcaac tctcaatcaa ccatttgaag agtgctgac   | 360 |
| ttggagacct tgtcttcgcc gaagcaactc ctgtaagcac agggaagact attcaggtt  | 420 |
| gggaagtcaa gttatggaaa acaacacaga aagataaagc taacaaaatc Tttaatatct | 480 |
| tcctctagag ttacacttat ctgtaatcta cctatccctg ataacgcaa agatgcagca  | 540 |
| aacatgctca aaatggtcgc aaagttgtag atttcttcag gctttttgt tttacttgta  | 600 |
| ttgtatgtaa tgaccatct tctcgaaatt gataataagc                        |     |

- (2) INFORMATION FOR SEQ ID NO:229:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 161 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..161
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1566238
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Pro | Ile | Gln | Ser | Ile | Ala | Gln | Thr | Leu | Leu | Ser | Ser | Leu | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Pro | Pro | Tyr | Leu | Pro | Pro | Ser | Leu | Ser | Leu | Gln | Gln | Ser | Thr | Lys |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Met | Asp | Ser | Ala | Ser | Ser | Asn | Thr | Lys | Ala | Ile | Asp | Pro | Pro | Leu | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Leu | Gly | Phe | Glu | Phe | Asp | Glu | Leu | Ser | Pro | Thr | Arg | Ile | Thr | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Pro | Val | Ser | Pro | Val | Cys | Cys | Gln | Pro | Phe | Lys | Val | Leu | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Gly | Val | Ser | Ala | Leu | Ile | Ala | Glu | Ser | Leu | Ala | Ser | Met | Gly | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| His | Met | Ala | Ser | Gly | Phe | Lys | Arg | Val | Ala | Gly | Ile | Gln | Leu | Ser | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | His | Leu | Lys | Ser | Ala | Asp | Leu | Gly | Asp | Leu | Val | Phe | Ala | Glu | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Pro | Val | Ser | Thr | Gly | Lys | Thr | Ile | Gln | Val | Trp | Glu | Val | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Lys | Thr | Thr | Gln | Lys | Asp | Lys | Ala | Asn | Lys | Ile | Phe | Asn | Ile | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:230:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 129 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met Asp Ser Ala Ser Ser Asn Thr Lys Ala Ile Asp Pro Pro Leu His  
1 5 10 15  
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly  
20 25 30  
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His  
35 40 45  
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala  
50 55 60  
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile  
65 70 75 80  
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala  
85 90 95  
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu  
100 105 110  
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe  
115 120 125  
Leu

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly  
1 5 10 15  
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His  
20 25 30  
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala  
35 40 45  
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile  
50 55 60  
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala  
65 70 75 80  
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu  
85 90 95  
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe  
100 105 110  
Leu

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1090
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| actctttctt | cttctttctg | tcgtcgtttg | tcacttttaga | gctactttctt | cttctttctct | 60   |
| gctaagcggt | tcctctcgac | ttgatacttt | tctccagtaa  | gggtttgcaa  | agatgaagct  | 120  |
| tgatactagt | gggttcgaga | cttccatgcc | tatgattgga  | tttggtcga   | gcagtgatat  | 180  |
| gcttgatgag | ctttcttctg | tacctcgtt  | tgatctaccc  | cgtactaaag  | agtttgatgg  | 240  |
| atctcagaaa | aaagctaaag | acatgttgaa | gcatgcaaaa  | ggaacaacca  | ctctcgcttt  | 300  |
| tatcttcaaa | ggtggtgtta | tggtcgtgc  | tgattctcgg  | gctagcatgg  | gaggatatat  | 360  |
| ctcctcacia | tctgtgaaga | agattattga | aatcaatcct  | tatatgctcg  | gtacaatggc  | 420  |
| tggaggagct | gctgattgcc | aattctggca | cagaaatctt  | ggaattaagt  | gccgtctaca  | 480  |
| tgagctggca | aacaagagga | gaatctctgt | ttccggagct  | tcgaaacttc  | ttgccaacat  | 540  |
| gctctattca | taccgtggaa | tgggactttc | tggttggtaca | atgattgctg  | gatgggacga  | 600  |
| aactggtccc | ggactatact | atgtcgacaa | cgaaggagga  | cggctcaagg  | gagacaggtt  | 660  |
| ttcagtcggt | tctggttcac | catatgctta | cgggtgtgctg | gacagcgggt  | acaaatatga  | 720  |
| tatgtcagtt | gaagaagctt | ccgagttaga | ggagatcaat  | ctaccatgcg  | acattccgtg  | 780  |
| atggagccag | tggtggagtt | gctagCgtgt | accacgttgg  | tcccgaagga  | tggacgaaac  | 840  |
| tatcaggaga | tgatgttggg | gagctacact | accattacta  | ccccgtggca  | ccagctaccg  | 900  |
| cagaacaagt | catggaggaa | gcaacagccg | aataaaaatc  | ctgttttagtt | ttctaatcgt  | 960  |
| tcactccctt | tcttgttggt | gcattttgtg | gtagtatata  | ctgagttgtc  | tctagctgaa  | 1020 |
| gctttggtat | tctattttac | tgatctgaaa | tggtgctcgc  | ggattattct  | ctataagatt  | 1080 |
| ctctttttct |            |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Leu | Asp | Thr | Ser | Gly | Phe | Glu | Thr | Ser | Met | Pro | Met | Ile | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Gly | Ser | Ser | Ser | Asp | Met | Leu | Asp | Glu | Leu | Ser | Ser | Val | Pro | Ser |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |  |
| Phe | Asp | Leu | Pro | Arg | Thr | Lys | Glu | Phe | Asp | Gly | Phe | Gln | Lys | Lys | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Asp | Met | Leu | Lys | His | Ala | Lys | Gly | Thr | Thr | Thr | Leu | Ala | Phe | Ile |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Lys | Gly | Gly | Val | Met | Val | Ala | Ala | Asp | Ser | Arg | Ala | Ser | Met | Gly |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Tyr | Ile | Ser | Ser | Gln | Ser | Val | Lys | Lys | Ile | Ile | Glu | Ile | Asn | Pro |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Tyr | Met | Leu | Gly | Thr | Met | Ala | Gly | Gly | Ala | Ala | Asp | Cys | Gln | Phe | Trp |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| His | Arg | Asn | Leu | Gly | Ile | Lys | Cys | Arg | Leu | His | Glu | Leu | Ala | Asn | Lys |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Arg | Arg | Ile | Ser | Val | Ser | Gly | Ala | Ser | Lys | Leu | Leu | Ala | Asn | Met | Leu |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Tyr | Ser | Tyr | Arg | Gly | Met | Gly | Leu | Ser | Val | Gly | Thr | Met | Ile | Ala | Gly |  |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Trp | Asp | Glu | Thr | Gly | Pro | Gly | Leu | Tyr | Tyr | Val | Asp | Asn | Glu | Gly | Gly |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Arg | Leu | Lys | Gly | Asp | Arg | Phe | Ser | Val | Gly | Ser | Gly | Ser | Pro | Tyr | Ala |  |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |  |
| Tyr | Gly | Val | Leu | Asp | Ser | Gly | Tyr | Lys | Tyr | Asp | Met | Ser | Val | Glu | Glu |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| Ala | Ser | Glu | Leu | Glu | Glu | Ile | Asn | Leu | Pro | Cys | Asp | Ile | Pro |     |     |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:234:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 211 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..211  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566243  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met Pro Met Ile Gly Phe Gly Ser Ser Ser Asp Met Leu Asp Glu Leu  
1                  5                  10                  15  
Ser Ser Val Pro Ser Phe Asp Leu Pro Arg Thr Lys Glu Phe Asp Gly  
                  20                  25                  30  
Phe Gln Lys Lys Ala Lys Asp Met Leu Lys His Ala Lys Gly Thr Thr  
                  35                  40                  45  
Thr Leu Ala Phe Ile Phe Lys Gly Gly Val Met Val Ala Ala Asp Ser  
50                  55                  60  
Arg Ala Ser Met Gly Gly Tyr Ile Ser Ser Gln Ser Val Lys Lys Ile  
65                  70                  75                  80  
Ile Glu Ile Asn Pro Tyr Met Leu Gly Thr Met Ala Gly Gly Ala Ala  
                  85                  90                  95  
Asp Cys Gln Phe Trp His Arg Asn Leu Gly Ile Lys Cys Arg Leu His  
                  100                  105                  110  
Glu Leu Ala Asn Lys Arg Arg Ile Ser Val Ser Gly Ala Ser Lys Leu  
                  115                  120                  125  
Leu Ala Asn Met Leu Tyr Ser Tyr Arg Gly Met Gly Leu Ser Val Gly  
130                  135                  140  
Thr Met Ile Ala Gly Trp Asp Glu Thr Gly Pro Gly Leu Tyr Tyr Val  
145                  150                  155                  160  
Asp Asn Glu Gly Gly Arg Leu Lys Gly Asp Arg Phe Ser Val Gly Ser  
                  165                  170                  175  
Gly Ser Pro Tyr Ala Tyr Gly Val Leu Asp Ser Gly Tyr Lys Tyr Asp  
                  180                  185                  190  
Met Ser Val Glu Glu Ala Ser Glu Leu Glu Glu Ile Asn Leu Pro Cys  
195                  200                  205  
Asp Ile Pro  
210

- (2) INFORMATION FOR SEQ ID NO:235:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 209 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..209  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1566244  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Met Ile Gly Phe Gly Ser Ser Ser Asp Met Leu Asp Glu Leu Ser Ser  
1                  5                  10                  15  
Val Pro Ser Phe Asp Leu Pro Arg Thr Lys Glu Phe Asp Gly Phe Gln  
                  20                  25                  30  
Lys Lys Ala Lys Asp Met Leu Lys His Ala Lys Gly Thr Thr Thr Leu  
                  35                  40                  45  
Ala Phe Ile Phe Lys Gly Gly Val Met Val Ala Ala Asp Ser Arg Ala  
50                  55                  60  
Ser Met Gly Gly Tyr Ile Ser Ser Gln Ser Val Lys Lys Ile Ile Glu  
65                  70                  75                  80

Ile Asn Pro Tyr Met Leu Gly Thr Met Ala Gly Gly Ala Ala Asp Cys  
85 90 95  
Gln Phe Trp His Arg Asn Leu Gly Ile Lys Cys Arg Leu His Glu Leu  
100 105 110  
Ala Asn Lys Arg Arg Ile Ser Val Ser Gly Ala Ser Lys Leu Leu Ala  
115 120 125  
Asn Met Leu Tyr Ser Tyr Arg Gly Met Gly Leu Ser Val Gly Thr Met  
130 135 140  
Ile Ala Gly Trp Asp Glu Thr Gly Pro Gly Leu Tyr Tyr Val Asp Asn  
145 150 155 160  
Glu Gly Gly Arg Leu Lys Gly Asp Arg Phe Ser Val Gly Ser Gly Ser  
165 170 175  
Pro Tyr Ala Tyr Gly Val Leu Asp Ser Gly Tyr Lys Tyr Asp Met Ser  
180 185 190  
Val Glu Glu Ala Ser Glu Leu Glu Glu Ile Asn Leu Pro Cys Asp Ile  
195 200 205  
Pro

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aggaagaaga gaaacctgat tctattcttg aggaacctga agattctaac atcaaagctg  | 60   |
| ttactttctgg tgacacacca tatacatcag caagtagatt tgaagacttg aacttgtcac | 120  |
| ctgaattgat gaaaggcttg tacgttgaga tgaaattcga aaagcctagc aagatccaag  | 180  |
| ctattagttt gcctatgata atgacgccgc cacacaagca tctgattgcc caggctcata  | 240  |
| acggatctgg aaagacgact tgtttcgttc ttggaatgtt gagtcgtgtt gatcccacat  | 300  |
| tgagagagcc tcaagctctc tgtatttgtc ccactagaga attagcta at cagaatatgg | 360  |
| aagttcttca gaagatgggg aagtttactg ggatcaactgc tgagttggct gtgCctgact | 420  |
| caacgagagg tgcaccggcg gcaacaagag gagctcctgt ttctgctcat gttgtgattg  | 480  |
| gcacccttgg aacgcttaag aaatggatgg catttaagag actagggtcta aatcatttga | 540  |
| agattctggg ttttgatgag gctgaccata tgcttgctac ggatggggtt agggatgatt  | 600  |
| ccttgaagat aatgaaagac attgggagag ttaatcccaa tttccagggt cttcttttct  | 660  |
| cggcaacttt taacgaaact gtcaaagatt ttgttgccgc gacagtcaaa gatcccaacc  | 720  |
| aattgtttgt caaaagagag gatctggctt tcgactcggg gaagcagtat aaagttgttt  | 780  |
| gcccgaagga gcaaaacaag atcgaagtca tcaaggatca gattatggag cttggggata  | 840  |
| ttgggcaaac cattatcttt gtgaaaacaa aagcgTtctg ctcaaaaggt gcacaaagcc  | 900  |
| cttgcgga aa tgggatatga cgttaccagt gtccatggta atctgactga atcggacagg | 960  |
| gataagatag ttaaagagtt taaagaatgc cttactcaag tgctcattgc taccgatgtc  | 1020 |
| attgcaagag gttttgacca acagcgggtg aatttggttg tcaattataa tcttccact   | 1080 |
| aaatatgaaa ctggagagcc agattatgag gtgtaccttc acagggttgg gagagctggc  | 1140 |
| cggtttggtc gcaaaggagc ggttttcaac ttgctgcttg atgatggctg ggataaagag  | 1200 |
| gtgatggaga agatcgagaa gtattttgaa gcaaagtgtt aggagatcaa gtcgtggaac  | 1260 |
| tcagaggaag agtataagag tgcattaaag gaagctggcc tgctggacga gtgaggaaga  | 1320 |
| gagacagcat gtgttcaaac catcttaaaa gactatgtcg tctgttttct tgagattgtt  | 1380 |
| ttaagaaaga aacttgtata cctctttgag gttttcttgt aatcttttta tctgattgct  | 1440 |
| gagattttca gactttgtag attttttgtt aagggaaaag gaaaacattt tttatgtc    |      |

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1566254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Glu | Lys | Pro | Asp | Ser | Ile | Leu | Glu | Glu | Pro | Glu | Asp | Ser | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Lys | Ala | Val | Thr | Ser | Gly | Asp | Thr | Pro | Tyr | Thr | Ser | Ala | Ser | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Glu | Asp | Leu | Asn | Leu | Ser | Pro | Glu | Leu | Met | Lys | Gly | Leu | Tyr | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Met | Lys | Phe | Glu | Lys | Pro | Ser | Lys | Ile | Gln | Ala | Ile | Ser | Leu | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Ile | Met | Thr | Pro | Pro | His | Lys | His | Leu | Ile | Ala | Gln | Ala | His | Asn |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ser | Gly | Lys | Thr | Thr | Cys | Phe | Val | Leu | Gly | Met | Leu | Ser | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Pro | Thr | Leu | Arg | Glu | Pro | Gln | Ala | Leu | Cys | Ile | Cys | Pro | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Leu | Ala | Asn | Gln | Asn | Met | Glu | Val | Leu | Gln | Lys | Met | Gly | Lys | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Gly | Ile | Thr | Ala | Glu | Leu | Ala | Val | Pro | Asp | Ser | Thr | Arg | Gly | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Ala | Ala | Thr | Arg | Gly | Ala | Pro | Val | Ser | Ala | His | Val | Val | Ile | Gly |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Pro | Gly | Thr | Leu | Lys | Lys | Trp | Met | Ala | Phe | Lys | Arg | Leu | Gly | Leu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | His | Leu | Lys | Ile | Leu | Val | Phe | Asp | Glu | Ala | Asp | His | Met | Leu | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Asp | Gly | Phe | Arg | Asp | Asp | Ser | Leu | Lys | Ile | Met | Lys | Asp | Ile | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Val | Asn | Pro | Asn | Phe | Gln | Val | Leu | Leu | Phe | Ser | Ala | Thr | Phe | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Thr | Val | Lys | Asp | Phe | Val | Ala | Arg | Thr | Val | Lys | Asp | Pro | Asn | Gln |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Phe | Val | Lys | Arg | Glu | Asp | Leu | Ala | Phe | Asp | Ser | Val | Lys | Gln | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Val | Val | Cys | Pro | Lys | Glu | Gln | Asn | Lys | Ile | Glu | Val | Ile | Lys | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Ile | Met | Glu | Leu | Gly | Asp | Ile | Gly | Gln | Thr | Ile | Ile | Phe | Val | Lys |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Thr | Lys | Ala | Phe | Cys | Ser | Lys | Gly | Ala | Gln | Ser | Pro | Cys | Gly | Asn | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

Ile

305

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1566255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gly | Leu | Tyr | Val | Glu | Met | Lys | Phe | Glu | Lys | Pro | Ser | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Gln | Ala | Ile | Ser | Leu | Pro | Met | Ile | Met | Thr | Pro | Pro | His | Lys | His | Leu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ile | Ala | Gln | Ala | His | Asn | Gly | Ser | Gly | Lys | Thr | Thr | Cys | Phe | Val | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Met | Leu | Ser | Arg | Val | Asp | Pro | Thr | Leu | Arg | Glu | Pro | Gln | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Ile | Cys | Pro | Thr | Arg | Glu | Leu | Ala | Asn | Gln | Asn | Met | Glu | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Lys | Met | Gly | Lys | Phe | Thr | Gly | Ile | Thr | Ala | Glu | Leu | Ala | Val | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ser | Thr | Arg | Gly | Ala | Pro | Ala | Ala | Thr | Arg | Gly | Ala | Pro | Val | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | His | Val | Val | Ile | Gly | Thr | Pro | Gly | Thr | Leu | Lys | Lys | Trp | Met | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Lys | Arg | Leu | Gly | Leu | Asn | His | Leu | Lys | Ile | Leu | Val | Phe | Asp | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Asp | His | Met | Leu | Ala | Thr | Asp | Gly | Phe | Arg | Asp | Asp | Ser | Leu | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Met | Lys | Asp | Ile | Gly | Arg | Val | Asn | Pro | Asn | Phe | Gln | Val | Leu | Leu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Ser | Ala | Thr | Phe | Asn | Glu | Thr | Val | Lys | Asp | Phe | Val | Ala | Arg | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Lys | Asp | Pro | Asn | Gln | Leu | Phe | Val | Lys | Arg | Glu | Asp | Leu | Ala | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Ser | Val | Lys | Gln | Tyr | Lys | Val | Val | Cys | Pro | Lys | Glu | Gln | Asn | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Glu | Val | Ile | Lys | Asp | Gln | Ile | Met | Glu | Leu | Gly | Asp | Ile | Gly | Gln |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Ile | Ile | Phe | Val | Lys | Thr | Lys | Ala | Phe | Cys | Ser | Lys | Gly | Ala | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Pro | Cys | Gly | Asn | Gly | Ile |     |     |     |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Glu | Lys | Pro | Ser | Lys | Ile | Gln | Ala | Ile | Ser | Leu | Pro | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Thr | Pro | Pro | His | Lys | His | Leu | Ile | Ala | Gln | Ala | His | Asn | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Lys | Thr | Thr | Cys | Phe | Val | Leu | Gly | Met | Leu | Ser | Arg | Val | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Thr | Leu | Arg | Glu | Pro | Gln | Ala | Leu | Cys | Ile | Cys | Pro | Thr | Arg | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Asn | Gln | Asn | Met | Glu | Val | Leu | Gln | Lys | Met | Gly | Lys | Phe | Thr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ile | Thr | Ala | Glu | Leu | Ala | Val | Pro | Asp | Ser | Thr | Arg | Gly | Ala | Pro |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Ala | Thr | Arg | Gly | Ala | Pro | Val | Ser | Ala | His | Val | Val | Ile | Gly | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Gly | Thr | Leu | Lys | Lys | Trp | Met | Ala | Phe | Lys | Arg | Leu | Gly | Leu | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Leu | Lys | Ile | Leu | Val | Phe | Asp | Glu | Ala | Asp | His | Met | Leu | Ala | Thr |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

Asp Gly Phe Arg Asp Asp Ser Leu Lys Ile Met Lys Asp Ile Gly Arg  
145 150 155 160  
Val Asn Pro Asn Phe Gln Val Leu Leu Phe Ser Ala Thr Phe Asn Glu  
165 170 175  
Thr Val Lys Asp Phe Val Ala Arg Thr Val Lys Asp Pro Asn Gln Leu  
180 185 190  
Phe Val Lys Arg Glu Asp Leu Ala Phe Asp Ser Val Lys Gln Tyr Lys  
195 200 205  
Val Val Cys Pro Lys Glu Gln Asn Lys Ile Glu Val Ile Lys Asp Gln  
210 215 220  
Ile Met Glu Leu Gly Asp Ile Gly Gln Thr Ile Ile Phe Val Lys Thr  
225 230 235 240  
Lys Ala Phe Cys Ser Lys Gly Ala Gln Ser Pro Cys Gly Asn Gly Ile  
245 250 255

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..637
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acgataccca aaatatcaaa ctcttcttct tttcccttct cttctcttct tctcttcttc  | 60  |
| cacgtttacg cgtatacaca tctctataca tacattaatc ttgatccttc tttatctctt  | 120 |
| tgcttccaat aaactccaaa gaacagctct tcttttttct cattcttact atcatcatta  | 180 |
| atggagagag aagacttgta cgctgtcttg gatttgaaca acgaatgtac acaaggagat  | 240 |
| ctcagacttt cttacaagaa ccttggtctg aaatggcctc cagatcgggt tcttgaagaa  | 300 |
| atagagaaag atgaagctaa gatgaaattt cagtccattc aacgagccta ttctgttttg  | 360 |
| tcggattcca acaagaggct tttgtatgac gtcgggtgctt atgatagtga tgacgacgaa | 420 |
| actggaatgg ctgatttcat aaatgagatg gtgacgctta tggctcaaac tcaatctacg  | 480 |
| ggggacgaaa atttagagga atttgaagag ttatttcaag aattgttgaa ggatgatgtg  | 540 |
| aatcaattca aaactcgttc atcTttcgtc ttcattgttcg caatttagtg gcacgtcgcg | 600 |
| tttggttccat tgcgatgatt tatcaaattc aaatgat                          |     |

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Glu Arg Glu Asp Leu Tyr Ala Val Leu Asp Leu Asn Asn Glu Cys  
1 5 10 15  
Thr Gln Gly Asp Leu Arg Leu Ser Tyr Lys Asn Leu Val Leu Lys Trp  
20 25 30  
His Pro Asp Arg Phe Leu Glu Glu Ile Glu Lys Asp Glu Ala Lys Met  
35 40 45  
Lys Phe Gln Ser Ile Gln Arg Ala Tyr Ser Val Leu Ser Asp Ser Asn  
50 55 60  
Lys Arg Leu Leu Tyr Asp Val Gly Ala Tyr Asp Ser Asp Asp Asp Glu  
65 70 75 80

Thr Gly Met Ala Asp Phe Ile Asn Glu Met Val Thr Leu Met Ala Gln  
85 90 95  
Thr Gln Ser Thr Gly Asp Glu Asn Leu Glu Glu Phe Glu Glu Leu Phe  
100 105 110  
Gln Glu Leu Leu Lys Asp Asp Val Asn Gln Phe Lys Thr Arg Ser Ser  
115 120 125  
Phe Val Phe Met Phe Ala Ile  
130 135

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1566259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met Lys Phe Gln Ser Ile Gln Arg Ala Tyr Ser Val Leu Ser Asp Ser  
1 5 10 15  
Asn Lys Arg Leu Leu Tyr Asp Val Gly Ala Tyr Asp Ser Asp Asp  
20 25 30  
Glu Thr Gly Met Ala Asp Phe Ile Asn Glu Met Val Thr Leu Met Ala  
35 40 45  
Gln Thr Gln Ser Thr Gly Asp Glu Asn Leu Glu Glu Phe Glu Glu Leu  
50 55 60  
Phe Gln Glu Leu Leu Lys Asp Asp Val Asn Gln Phe Lys Thr Arg Ser  
65 70 75 80  
Ser Phe Val Phe Met Phe Ala Ile  
85

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

ccggttgccg caccgtGctt cgtttctctc tctcgtctc tactcaggac tcgtttactc 60  
tttcaaagct aagctttcaa gatgcaaaac gaagagggtc aagtcactga gctttacatt 120  
cctaggaaat gttctgtctac taaccgggttg atcacatcca aggatcatgc ctctgttcag 180  
ctcaacattg gtcatttaga tgctaattggc ttgtacacog gacagttcac aacctttgct 240  
ctctgcggtt ttgtccgtgc tcaggggagac gctgacagtg gtgtcgacag gttgtggcag 300  
aagaagaagg ttgaagccaa acaaaaactaa gagcttaatc tgtcttggtt tttgtcgaat 360  
cttggttttt tttttccgaa agattgcctc atactgaagt aatgattttg gctttgggtc 420  
gtggaactta acttaaatac ttttgtgcac catgtcttct aatttttcac cagttcg

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

2025-11-11 14:55:50

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1566269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Gln Asn Glu Gly Gln Val Thr Glu Leu Tyr Ile Pro Arg Lys  
1 5 10 15  
Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val  
20 25 30  
Gln Leu Asn Ile Gly His Leu Asp Ala Asn Gly Leu Tyr Thr Gly Gln  
35 40 45  
Phe Thr Thr Phe Ala Leu Cys Gly Phe Val Arg Ala Gln Gly Asp Ala  
50 55 60  
Asp Ser Gly Val Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Ala Lys  
65 70 75 80  
Gln Asn

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1566270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met Leu Met Ala Cys Thr Pro Asp Ser Ser Gln Pro Leu Leu Ser Ala  
1 5 10 15  
Val Leu Ser Val Leu Arg Glu Thr Leu Thr Val Val Ser Thr Gly Cys  
20 25 30  
Gly Arg Arg Arg Arg Leu Lys Pro Asn Lys Thr Lys Ser Leu Ile Cys  
35 40 45  
Leu Val Phe Cys Arg Ile Leu Phe Phe Phe Phe Arg Lys Ile Ala Ser  
50 55 60  
Tyr  
65

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Ala Cys Thr Pro Asp Ser Ser Gln Pro Leu Leu Ser Ala Val Leu  
1 5 10 15  
Ser Val Leu Arg Glu Thr Leu Thr Val Val Ser Thr Gly Cys Gly Arg  
20 25 30  
Arg Arg Arg Leu Lys Pro Asn Lys Thr Lys Ser Leu Ile Cys Leu Val  
35 40 45  
Phe Cys Arg Ile Leu Phe Phe Phe Phe Arg Lys Ile Ala Ser Tyr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..988  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566276  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aaaagaagac | ttttgtaagg | aaataaacac | acaactaaag  | agatgtcgtc | aaccttgagc | 60  |
| aacgaagagt | caggactcgg | tgattcaaat | cgttcgacgg  | aagtagatag | cggcgacgga | 120 |
| ggaaacttca | cggttacga  | gtctcgattc | cagtcgcagc  | ggtttgactc | ttccttctct | 180 |
| aattttgact | cccaaccgga | gaaagagtca | gacttaccag  | gcggcgattc | atctcctcga | 240 |
| cccgaaactc | aatctccgcc | gtcgataaat | agtttcgatg  | atacaaacgg | ttcgatcttg | 300 |
| ccgccaccat | cggccatgga | gaaagaggaa | ggtttcgctc  | ttagagagtg | gcgaaggcta | 360 |
| aatgctctga | gattggaaga | gaaagaaaag | gaagagaaaag | aaatggttca | acaaattcta | 420 |
| gaagcagcag | agcaatataa | ggctgagttc | tatagcaagc  | gtaacgttac | tattgaaaac | 480 |
| aacaagaaac | taaaccgcga | gaaagagaag | tttttttttg  | agaatcaaga | aaagttttac | 540 |
| gctgaagctg | acaaaaacaa | ttggaaggcg | attgcagaac  | tcattcctcg | tgaagtgcca | 600 |
| gttatagaga | atagagggaa | caagaagaaa | acagcaacca  | taactgtaat | ccagggacca | 660 |
| aagccaggga | agcccactga | tctgtGctcg | tatgcgtcaa  | gtgctcacga | aactcaagca | 720 |
| caatccgcc  | actcatatga | agccaaaaat | gccctcacca  | tctggagctg | acccgaatgt | 780 |
| gagtggtgag | gaacaggtca | cagttacaga | gaagttgtag  | ttgtgtatgt | gacaagttaa | 840 |
| cttcttcttg | attgatgtta | aaccgtcttt | actttgttag  | cttccctcat | gttcagtctc | 900 |
| gactattggt | tgttttgatt | tctgtctttg | tcttaccatt  | gttggtttcc | cacacagttt | 960 |
| tctactttga | tgtatatata | atatattc   |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 242 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..242  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566277  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Thr | Leu | Ser | Asn | Glu | Glu | Ser | Gly | Leu | Gly | Asp | Ser | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Ser | Thr | Glu | Val | Asp | Ser | Gly | Asp | Gly | Gly | Asn | Phe | Thr | Ala | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ser | Arg | Phe | Gln | Ser | Gln | Arg | Phe | Asp | Ser | Ser | Phe | Ser | Asn | Phe |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Ser | Gln | Pro | Glu | Lys | Glu | Ser | Asp | Leu | Pro | Gly | Gly | Asp | Ser | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Pro | Arg | Pro | Glu | Thr | Gln | Ser | Pro | Pro | Ser | Ile | Asn | Ser | Phe | Asp | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Asn | Gly | Ser | Ile | Leu | Pro | Pro | Pro | Ser | Ala | Met | Glu | Lys | Glu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Phe | Ala | Leu | Arg | Glu | Trp | Arg | Arg | Leu | Asn | Ala | Leu | Arg | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | Glu | Lys | Glu | Glu | Lys | Glu | Met | Val | Gln | Gln | Ile | Leu | Glu | Ala |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ala | Glu | Gln | Tyr | Lys | Ala | Glu | Phe | Tyr | Ser | Lys | Arg | Asn | Val | Thr | Ile |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Glu | Asn | Asn | Lys | Lys | Leu | Asn | Arg | Glu | Lys | Glu | Lys | Phe | Phe | Leu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Gln | Glu | Lys | Phe | Tyr | Ala | Glu | Ala | Asp | Lys | Asn | Asn | Trp | Lys | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ala | Glu | Leu | Ile | Pro | Arg | Glu | Val | Pro | Val | Ile | Glu | Asn | Arg | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |



Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile Gln Gly Pro Lys Pro  
195 200 205  
Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser Ser Ala His Glu Thr  
210 215 220  
Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys Thr Ala Leu Thr Ile  
225 230 235 240  
Trp Ser

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1566278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Glu Lys Glu Glu Gly Phe Ala Leu Arg Glu Trp Arg Arg Leu Asn  
1 5 10 15  
Ala Leu Arg Leu Glu Glu Lys Glu Lys Glu Lys Glu Met Val Gln  
20 25 30  
Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe Tyr Ser Lys  
35 40 45  
Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg Glu Lys Glu  
50 55 60  
Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu Ala Asp Lys  
65 70 75 80  
Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu Val Pro Val  
85 90 95  
Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile  
100 105 110  
Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser  
115 120 125  
Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys  
130 135 140  
Thr Ala Leu Thr Ile Trp Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1566279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Val Gln Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe  
1 5 10 15  
Tyr Ser Lys Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg  
20 25 30  
Glu Lys Glu Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu  
35 40 45  
Ala Asp Lys Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu  
50 55 60  
Val Pro Val Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile

Lys Lys Arg Pro Tyr Ser His Arg Ser Ser Leu Arg Ser Ser Ser Ser  
1 5 10 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Thr | Met | Met | Asp | Thr | Asp | Glu | Gly | Lys | Thr | Val | Met | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Asp | Pro | Glu | Gly | Thr | His | Leu | Gly | Ser | Ala | Met | Tyr | Ile | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Lys | Ala | Gly | Pro | Leu | Gln | Leu | Thr | Gln | Leu | Val | Asn | Arg | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Asn | Glu | Glu | Met | Leu | Pro | Tyr | Ser | Phe | Tyr | Val | Ser | Asp | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Leu | Val | Pro | Val | Gly | Thr | Tyr | Leu | Glu | Lys | Asn | Lys | Val | Ser | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Val | Leu | Thr | Ile | Val | Tyr | Gln | Gln | Gln | Ala | Val | Phe | Arg | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Val | Asn | Arg | Cys | Ser | Gln | Thr | Ile | Ala | Gly | His | Ala | Glu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Leu | Cys | Val | Ser | Phe | Ser | Pro | Asp | Gly | Lys | Gln | Leu | Ala | Ser | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gly | Asp | Thr | Thr | Val | Arg | Leu | Trp | Asp | Leu | Tyr | Thr | Glu | Thr | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Phe | Thr | Cys | Lys | Gly | His | Lys | Asn | Trp | Val | Leu | Thr | Val | Ala | Trp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Pro | Asp | Gly | Lys | His | Leu | Val | Ser | Gly | Ser | Lys | Ser | Gly | Glu | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Cys | Cys | Trp | Asn | Pro | Lys | Lys | Gly | Glu | Leu | Glu | Gly | Ser | Pro | Leu | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | His | Lys | Lys | Trp | Ile | Thr | Gly | Ile | Ser | Trp | Glu | Pro | Val | His | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ser | Pro | Cys | Arg | Arg | Phe | Val | Thr | Ser | Ser | Lys | Asp | Gly | Asp | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Ile | Trp | Asp | Ile | Thr | Leu | Lys | Lys | Ser | Ile | Ile | Cys | Leu | Ser | Gly |
|     |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |
| His | Thr | Leu | Ala | Val | Thr | Cys | Val | Lys | Trp | Gly | Gly | Asp | Gly | Ile | Ile |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Thr | Gly | Ser | Gln | Asp | Cys | Thr | Ile | Lys | Met | Trp | Glu | Thr | Thr | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Lys | Leu | Ile | Arg | Glu | Leu | Lys | Gly | His | Gly | His | Trp | Ile | Asn | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Ala | Leu | Ser | Thr | Glu | Tyr | Val | Leu | Arg | Thr | Gly | Ala | Phe | Asp | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Gly | Arg | Gln | Tyr | Pro | Pro | Asn | Glu | Glu | Lys | Gln | Lys | Ala | Leu | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Tyr | Asn | Lys | Thr | Lys | Gly | Asp | Ser | Pro | Glu | Arg | Leu | Val | Ser | Gly |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Asp | Asp | Phe | Thr | Met | Phe | Leu | Trp | Glu | Pro | Ser | Val | Ser | Lys | Gln |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Pro | Lys | Lys | Arg | Leu | Thr | Gly | His | Gln | Gln | Leu | Val | Asn | His | Val | Tyr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Phe | Ser | Pro | Asp | Gly | Lys | Trp | Ile | Ala | Ser | Ala | Ser | Phe | Asp | Lys | Ser |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Arg | Leu | Trp | Asn | Gly | Ile | Thr | Gly | Gln | Phe | Val | Thr | Val | Phe | Arg |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gly | His | Val | Gly | Pro | Val | Tyr | Gln | Val | Ser | Trp | Ser | Ala | Asp | Ser | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Leu | Leu | Ser | Gly | Ser | Lys | Asp | Ser | Thr | Leu | Lys | Ile | Trp | Glu | Ile |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Arg | Thr | Lys | Lys | Leu | Lys | Gln | Asp | Leu | Pro | Gly | His | Ala | Asp | Glu | Val |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Phe | Ala | Val | Asp | Trp | Ser | Pro | Asp | Gly | Glu | Lys | Val | Val | Ser | Gly | Gly |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Lys | Asp | Arg | Val | Leu | Lys | Leu | Trp | Lys | Gly |     |     |     |     |     |     |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 473 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:  
 (A) NAME/KEY: peptide  
 (B) LOCATION: 1..473  
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566292  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Met | Met | Asp | Thr | Asp | Glu | Gly | Lys | Thr | Val | Met | Cys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asp | Pro | Glu | Gly | Thr | His | Leu | Gly | Ser | Ala | Met | Tyr | Ile | Pro | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ala | Gly | Pro | Leu | Gln | Leu | Thr | Gln | Leu | Val | Asn | Arg | Phe | Leu | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Glu | Glu | Met | Leu | Pro | Tyr | Ser | Phe | Tyr | Val | Ser | Asp | Glu | Glu | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Pro | Val | Gly | Thr | Tyr | Leu | Glu | Lys | Asn | Lys | Val | Ser | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Val | Leu | Thr | Ile | Val | Tyr | Gln | Gln | Gln | Ala | Val | Phe | Arg | Ile | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Val | Asn | Arg | Cys | Ser | Gln | Thr | Ile | Ala | Gly | His | Ala | Glu | Ala | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Cys | Val | Ser | Phe | Ser | Pro | Asp | Gly | Lys | Gln | Leu | Ala | Ser | Gly | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Thr | Thr | Val | Arg | Leu | Trp | Asp | Leu | Tyr | Thr | Glu | Thr | Pro | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Thr | Cys | Lys | Gly | His | Lys | Asn | Trp | Val | Leu | Thr | Val | Ala | Trp | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Asp | Gly | Lys | His | Leu | Val | Ser | Gly | Ser | Lys | Ser | Gly | Glu | Ile | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Trp | Asn | Pro | Lys | Lys | Gly | Glu | Leu | Glu | Gly | Ser | Pro | Leu | Thr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Lys | Lys | Trp | Ile | Thr | Gly | Ile | Ser | Trp | Glu | Pro | Val | His | Leu | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Pro | Cys | Arg | Arg | Phe | Val | Thr | Ser | Ser | Lys | Asp | Gly | Asp | Ala | Arg |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Trp | Asp | Ile | Thr | Leu | Lys | Lys | Ser | Ile | Ile | Cys | Leu | Ser | Gly | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Leu | Ala | Val | Thr | Cys | Val | Lys | Trp | Gly | Gly | Asp | Gly | Ile | Ile | Tyr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Gly | Ser | Gln | Asp | Cys | Thr | Ile | Lys | Met | Trp | Glu | Thr | Thr | Gln | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Leu | Ile | Arg | Glu | Leu | Lys | Gly | His | Gly | His | Trp | Ile | Asn | Ser | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Ala | Leu | Ser | Thr | Glu | Tyr | Val | Leu | Arg | Thr | Gly | Ala | Phe | Asp | His | Thr |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Arg | Gln | Tyr | Pro | Pro | Asn | Glu | Glu | Lys | Gln | Lys | Ala | Leu | Glu | Arg |
| 305 |     |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Asn | Lys | Thr | Lys | Gly | Asp | Ser | Pro | Glu | Arg | Leu | Val | Ser | Gly | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Asp | Phe | Thr | Met | Phe | Leu | Trp | Glu | Pro | Ser | Val | Ser | Lys | Gln | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Lys | Arg | Leu | Thr | Gly | His | Gln | Leu | Val | Asn | His | Val | Tyr | Phe |     |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Pro | Asp | Gly | Lys | Trp | Ile | Ala | Ser | Ala | Ser | Phe | Asp | Lys | Ser | Val |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Arg | Leu | Trp | Asn | Gly | Ile | Thr | Gly | Gln | Phe | Val | Thr | Val | Phe | Arg | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

His Val Gly Pro Val Tyr Gln Val Ser Trp Ser Ala Asp Ser Arg Leu  
405 410 415  
Leu Leu Ser Gly Ser Lys Asp Ser Thr Leu Lys Ile Trp Glu Ile Arg  
420 425 430  
Thr Lys Lys Leu Lys Gln Asp Leu Pro Gly His Ala Asp Glu Val Phe  
435 440 445  
Ala Val Asp Trp Ser Pro Asp Gly Glu Lys Val Val Ser Gly Gly Lys  
450 455 460  
Asp Arg Val Leu Lys Leu Trp Lys Gly  
465 470

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1566293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Met Asp Thr Asp Glu Gly Lys Thr Val Met Cys Leu Leu Thr Asp  
1 5 10 15  
Pro Glu Gly Thr His Leu Gly Ser Ala Met Tyr Ile Pro Gln Lys Ala  
20 25 30  
Gly Pro Leu Gln Leu Thr Gln Leu Val Asn Arg Phe Leu Asp Asn Glu  
35 40 45  
Glu Met Leu Pro Tyr Ser Phe Tyr Val Ser Asp Glu Leu Leu Val  
50 55 60  
Pro Val Gly Thr Tyr Leu Glu Lys Asn Lys Val Ser Val Glu Lys Val  
65 70 75 80  
Leu Thr Ile Val Tyr Gln Gln Gln Ala Val Phe Arg Ile Arg Pro Val  
85 90 95  
Asn Arg Cys Ser Gln Thr Ile Ala Gly His Ala Glu Ala Val Leu Cys  
100 105 110  
Val Ser Phe Ser Pro Asp Gly Lys Gln Leu Ala Ser Gly Ser Gly Asp  
115 120 125  
Thr Thr Val Arg Leu Trp Asp Leu Tyr Thr Glu Thr Pro Leu Phe Thr  
130 135 140  
Cys Lys Gly His Lys Asn Trp Val Leu Thr Val Ala Trp Ser Pro Asp  
145 150 155 160  
Gly Lys His Leu Val Ser Gly Ser Lys Ser Gly Glu Ile Cys Cys Trp  
165 170 175  
Asn Pro Lys Lys Gly Glu Leu Glu Gly Ser Pro Leu Thr Gly His Lys  
180 185 190  
Lys Trp Ile Thr Gly Ile Ser Trp Glu Pro Val His Leu Ser Ser Pro  
195 200 205  
Cys Arg Arg Phe Val Thr Ser Ser Lys Asp Gly Asp Ala Arg Ile Trp  
210 215 220  
Asp Ile Thr Leu Lys Lys Ser Ile Ile Cys Leu Ser Gly His Thr Leu  
225 230 235 240  
Ala Val Thr Cys Val Lys Trp Gly Gly Asp Gly Ile Ile Tyr Thr Gly  
245 250 255  
Ser Gln Asp Cys Thr Ile Lys Met Trp Glu Thr Thr Gln Gly Lys Leu  
260 265 270  
Ile Arg Glu Leu Lys Gly His Gly His Trp Ile Asn Ser Leu Ala Leu  
275 280 285  
Ser Thr Glu Tyr Val Leu Arg Thr Gly Ala Phe Asp His Thr Gly Arg  
290 295 300  
Gln Tyr Pro Pro Asn Glu Glu Lys Gln Lys Ala Leu Glu Arg Tyr Asn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Glu Lys Glu Gly Leu Gly Leu Glu Ile Thr Glu Leu Arg Leu Gly  
1 5 10 15  
Leu Pro Gly Arg Asp Val Ala Glu Lys Met Met Lys Lys Arg Ala Phe  
20 25 30  
Thr Glu Met Asn Met Thr Ser Ser Gly Ser Asn Ser Asp Gln Cys Glu  
35 40 45  
Ser Gly Val Val Ser Ser Gly Gly Asp Ala Glu Lys Val Asn Asp Ser  
50 55 60  
Pro Ala Ala Lys Ser Gln Val Val Gly Trp Pro Pro Val Cys Ser Tyr  
65 70 75 80  
Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser Thr Thr Lys Val Xaa Leu  
85 90 95  
Gly Tyr Val Lys Val Ser Met Asp Gly Val Pro Tyr Leu Arg Lys Met  
100 105 110  
Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp Leu Ala Phe Ser Leu Asp  
115 120 125  
Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp  
130 135 140  
Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met  
145 150 155 160  
Leu Ala Gly Asp Xaa Pro Trp Gly Met Cys Ser Arg Val Met Gln Glu  
165 170 175  
Val Glu Asn Asn Glu Lys Ile Gly Cys Tyr Arg Val Trp Ala Ala Ala  
180 185 190

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1566299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Met Met Lys Lys Arg Ala Phe Thr Glu Met Asn Met Thr Ser Ser Gly  
1 5 10 15  
Ser Asn Ser Asp Gln Cys Glu Ser Gly Val Val Ser Ser Gly Gly Asp  
20 25 30  
Ala Glu Lys Val Asn Asp Ser Pro Ala Ala Lys Ser Gln Val Val Gly  
35 40 45  
Trp Pro Pro Val Cys Ser Tyr Arg Lys Lys Asn Ser Cys Lys Glu Ala  
50 55 60  
Ser Thr Thr Lys Val Xaa Leu Gly Tyr Val Lys Val Ser Met Asp Gly  
65 70 75 80  
Val Pro Tyr Leu Arg Lys Met Asp Leu Gly Ser Ser Gln Gly Tyr Asp  
85 90 95  
Asp Leu Ala Phe Ser Leu Asp Lys Leu Phe Gly Phe Arg Gly Ile Gly  
100 105 110  
Val Ala Leu Lys Asp Gly Asp Asn Cys Glu Tyr Val Thr Ile Tyr Glu  
115 120 125  
Asp Lys Asp Gly Asp Trp Met Leu Ala Gly Asp Xaa Pro Trp Gly Met  
130 135 140  
Cys Ser Arg Val Met Gln Glu Val Glu Asn Asn Glu Lys Ile Gly Cys  
145 150 155 160  
Tyr Arg Val Trp Ala Ala Ala  
165

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 166 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..166  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566300  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Arg | Ala | Phe | Thr | Glu | Met | Asn | Met | Thr | Ser | Ser | Gly | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Ser | Asp | Gln | Cys | Glu | Ser | Gly | Val | Val | Ser | Ser | Gly | Gly | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Glu | Lys | Val | Asn | Asp | Ser | Pro | Ala | Ala | Lys | Ser | Gln | Val | Val | Gly | Trp |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Pro | Pro | Val | Cys | Ser | Tyr | Arg | Lys | Lys | Asn | Ser | Cys | Lys | Glu | Ala | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Thr | Thr | Lys | Val | Xaa | Leu | Gly | Tyr | Val | Lys | Val | Ser | Met | Asp | Gly | Val |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Pro | Tyr | Leu | Arg | Lys | Met | Asp | Leu | Gly | Ser | Ser | Gln | Gly | Tyr | Asp | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Ala | Phe | Ser | Leu | Asp | Lys | Leu | Phe | Gly | Phe | Arg | Gly | Ile | Gly | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Leu | Lys | Asp | Gly | Asp | Asn | Cys | Glu | Tyr | Val | Thr | Ile | Tyr | Glu | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Asp | Gly | Asp | Trp | Met | Leu | Ala | Gly | Asp | Xaa | Pro | Trp | Gly | Met | Cys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Arg | Val | Met | Gln | Glu | Val | Glu | Asn | Asn | Glu | Lys | Ile | Gly | Cys | Tyr |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Val | Trp | Ala | Ala | Ala |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 2363 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..2363  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566353  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| actcaaacgc | tgcattctcat | gcagaaccgt  | actacccttc | ctttaaagat | gtcaaaattg  | 60  |
| ttgtccccga | aattttcttgt | gaaacagaat  | gttcgaagaa | gtttcagaat | cttaattggt  | 120 |
| ctcacgagct | aagaactacc  | acagctacgg  | aggatcaatt | gccgggtgta | tctaattgatg | 180 |
| ctaaacagga | cogtgggtcta | gagttattga  | cccataacat | ggacaacggt | ggaaaaaacc  | 240 |
| aagcacttca | acaagattttt | caaagttcag  | taagattaag | tgatcaacct | tttttgtcaa  | 300 |
| actcggacac | agatccagaa  | gctcaaaactt | tgatcacgga | tgaggaaatg | tgtagggttc  | 360 |
| tttttccaga | taacatgaaa  | gatagcagta  | catcttctgg | tgagcaagg  | cggaaatag   | 420 |
| ttgacctca  | aaacggcaaaa | ggatctcttt  | gttctcaggc | tgagaaaacc | catgctcatg  | 480 |
| aaactggaaa | agttccagct  | ttaccgtggc  | atccttcaag | ttctgagggc | ctggcgggtc  | 540 |
| ataattgtgt | ccctttgttg  | gattcagact  | tgaaggactc | acttttacct | cgtaatgatt  | 600 |
| ccaacgctcc | tatacaagg   | tgtcgccttt  | ttggagctac | cgaattagaa | tgtaaagctg  | 660 |
| atacaaatga | cggtttctatc | gatacttacg  | gacatgtaac | ttcccatggc | aatgatgata  | 720 |
| atggtggttt | cccagaacaa  | caggggctgt  | catatattcc | caaggattct | ttgaagctag  | 780 |
| tacctttgaa | tagtttttct  | tctccttcta  | gagtgaacaa | gatttatttt | cctattgacg  | 840 |
| ataagccggc | tgaaaaagac  | aaaggagctc  | tttgttatga | acctccacgt | tttccaagtg  | 900 |
| cagatattcc | tttcttcagc  | tgtgatcttg  | taccatcaaa | tagtgactta | cggcaagagt  | 960 |



acagtccctt tggatatccgt cagttgatga tttcttcaat gaattgtaca actccgttaa 1020  
ggttatggga ttcaccgtgt cagcatagga gccctgatgt catgcttaat gatactgcca 1080  
aaagtttttag tgggtgcacca tccatcttaa agaagcggca tgcgagacttg ctttcacctg 1140  
tgcttgatag aagaaaagac aaaaagctta aaaggcgtgc gacttcctcc ttggctaagt 1200  
atttttcgcg cttagatgta atgcttgatg aaggagatga ttgcatgacc tctcgtccgt 1260  
cagagtctcc tgaagataaa aatatatgtg cctccccctc catagccaga gataacagaa 1320  
attgtgcata atctcgggta tatcaagaaa tgattccgat agatgaggaa ccaaaggaaa 1380  
ccttagaatc aggtggagtg acttctatgc aaaatgaaaa tggatgtaat gacggtggtg 1440  
cttcagctaa aaatgaccaa gaaacttctg gaagtttttt tgagttacga ctgtgttctc 1500  
ctggatatgac tgcagctaga ccagataaca aagttaatgc aagtgcgaaa gatctatcaa 1560  
accagcacia aatatcatta ggtgattttc caacagaaga aatgtcatca gaacctctat 1620  
gcacagtgga ctctatttct ttatctgcaa tcgataaaac taacactgca gagaccagct 1680  
ttgatattga aaacttcaac atatttgatg gaactccgtt cagaaaactc cttgataccc 1740  
catcaccttg gaaatctcct ttactctttg gttctttctt gcaaagtcca aagttgcctc 1800  
cagaaatcac atttgaggat attgggtggt ttatgagtcc cggcgagaga agttatgatg 1860  
ccataggact gatgaagcat ttgagtgaac actcagctac ggcataatgca gatgccttgg 1920  
aagttctggg taatgacaca cctgaatcga tactcaagaa gagacagctg aacaagtcca 1980  
ttcaagggaa agaaaatcag caccagcctc atgatcagct tgggaaccga tcccacgtgg 2040  
agtgtcgcgc cttagacttc agcgattgtg ggacaccagg gaaagctaag gtacCttcgg 2100  
cttctccggg aggcactact agcccatcat cttacctttt gaagagttgc agatagagaa 2160  
gggtgggttt gttcatagag ttctgaaggg agtctcgcct tcaatttttt gatcccatat 2220  
gtgtatgtct tttttattcc ctccctgtcc aattttcttg tttctaattt ttttaaatgt 2280  
gtagatctct caactctgga catcatacca ttgattaaat agcgaaaaag taacttgttc 2340  
tcaagtaatt aacttgtaac tcc

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..717
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Ser Asn Ala Ala Ser His Ala Glu Pro Tyr Tyr Pro Ser Phe Lys Asp  
1 5 10 15  
Val Lys Ile Val Val Pro Glu Ile Ser Cys Glu Thr Glu Cys Ser Lys  
20 25 30  
Lys Phe Gln Asn Leu Asn Cys Ser His Glu Leu Arg Thr Thr Thr Ala  
35 40 45  
Thr Glu Asp Gln Leu Pro Gly Val Ser Asn Asp Ala Lys Gln Asp Arg  
50 55 60  
Gly Leu Glu Leu Leu Thr His Asn Met Asp Asn Gly Gly Lys Asn Gln  
65 70 75 80  
Ala Leu Gln Gln Asp Phe Gln Ser Ser Val Arg Leu Ser Asp Gln Pro  
85 90 95  
Phe Leu Ser Asn Ser Asp Thr Asp Pro Glu Ala Gln Thr Leu Ile Thr  
100 105 110  
Asp Glu Glu Cys Cys Arg Val Leu Phe Pro Asp Asn Met Lys Asp Ser  
115 120 125  
Ser Thr Ser Ser Gly Glu Gln Gly Arg Asn Met Val Asp Pro Gln Asn  
130 135 140  
Gly Lys Gly Ser Leu Cys Ser Gln Ala Ala Glu Thr His Ala His Glu  
145 150 155 160  
Thr Gly Lys Val Pro Ala Leu Pro Trp His Pro Ser Ser Ser Glu Gly  
165 170 175  
Leu Ala Gly His Asn Cys Val Pro Leu Leu Asp Ser Asp Leu Lys Asp  
180 185 190  
Ser Leu Leu Pro Arg Asn Asp Ser Asn Ala Pro Ile Gln Gly Cys Arg

|                         |                         |                 |
|-------------------------|-------------------------|-----------------|
| 195                     | 200                     | 205             |
| Leu Phe Gly Ala Thr Glu | Leu Glu Cys Lys Thr Asp | Thr Asn Asp Gly |
| 210                     | 215                     | 220             |
| Phe Ile Asp Thr Tyr Gly | His Val Thr Ser His Gly | Asn Asp Asp Asn |
| 225                     | 230                     | 235             |
| Gly Gly Phe Pro Glu Gln | Gln Gly Leu Ser Tyr Ile | Pro Lys Asp Ser |
| 245                     | 250                     | 255             |
| Leu Lys Leu Val Pro Leu | Asn Ser Phe Ser Ser Pro | Ser Arg Val Asn |
| 260                     | 265                     | 270             |
| Lys Ile Tyr Phe Pro Ile | Asp Asp Lys Pro Ala Glu | Lys Asp Lys Gly |
| 275                     | 280                     | 285             |
| Ala Leu Cys Tyr Glu Pro | Pro Arg Phe Pro Ser Ala | Asp Ile Pro Phe |
| 290                     | 295                     | 300             |
| Phe Ser Cys Asp Leu Val | Pro Ser Asn Ser Asp Leu | Arg Gln Glu Tyr |
| 305                     | 310                     | 315             |
| Ser Pro Phe Gly Ile Arg | Gln Leu Met Ile Ser Ser | Met Asn Cys Thr |
| 325                     | 330                     | 335             |
| Thr Pro Leu Arg Leu Trp | Asp Ser Pro Cys His Asp | Arg Ser Pro Asp |
| 340                     | 345                     | 350             |
| Val Met Leu Asn Asp Thr | Ala Lys Ser Phe Ser Gly | Ala Pro Ser Ile |
| 355                     | 360                     | 365             |
| Leu Lys Lys Arg His Arg | Asp Leu Leu Ser Pro Val | Leu Asp Arg Arg |
| 370                     | 375                     | 380             |
| Lys Asp Lys Lys Leu Lys | Arg Ala Ala Thr Ser Ser | Leu Ala Asn Asp |
| 385                     | 390                     | 395             |
| Phe Ser Arg Leu Asp Val | Met Leu Asp Glu Gly Asp | Asp Cys Met Thr |
| 405                     | 410                     | 415             |
| Ser Arg Pro Ser Glu Ser | Pro Glu Asp Lys Asn Ile | Cys Ala Ser Pro |
| 420                     | 425                     | 430             |
| Ser Ile Ala Arg Asp Asn | Arg Asn Cys Ala Ser Ser | Arg Leu Tyr Gln |
| 435                     | 440                     | 445             |
| Glu Met Ile Pro Ile Asp | Glu Glu Pro Lys Glu Thr | Leu Glu Ser Gly |
| 450                     | 455                     | 460             |
| Gly Val Thr Ser Met Gln | Asn Glu Asn Gly Cys Asn | Asp Gly Gly Ala |
| 465                     | 470                     | 475             |
| Ser Ala Lys Asn Asp Gln | Glu Thr Ser Gly Ser Phe | Phe Glu Leu Arg |
| 485                     | 490                     | 495             |
| Leu Cys Ser Pro Gly Met | Thr Arg Ala Arg Pro Asp | Asn Lys Val Asn |
| 500                     | 505                     | 510             |
| Ala Ser Ala Lys Asp Leu | Ser Asn Gln His Lys Ile | Ser Leu Gly Asp |
| 515                     | 520                     | 525             |
| Phe Pro Thr Glu Glu Met | Ser Ser Glu Pro Leu Cys | Thr Val Asp Ser |
| 530                     | 535                     | 540             |
| Ile Pro Leu Ser Ala Ile | Asp Lys Thr Asn Thr Ala | Glu Thr Ser Phe |
| 545                     | 550                     | 555             |
| Asp Ile Glu Asn Phe Asn | Ile Phe Asp Gly Thr Pro | Phe Arg Lys Leu |
| 565                     | 570                     | 575             |
| Leu Asp Thr Pro Ser Pro | Trp Lys Ser Pro Leu Leu | Phe Gly Ser Phe |
| 580                     | 585                     | 590             |
| Leu Gln Ser Pro Lys Leu | Pro Pro Glu Ile Thr Phe | Glu Asp Ile Gly |
| 595                     | 600                     | 605             |
| Cys Phe Met Ser Pro Gly | Glu Arg Ser Tyr Asp Ala | Ile Gly Leu Met |
| 610                     | 615                     | 620             |
| Lys His Leu Ser Glu His | Ser Ala Thr Ala Tyr Ala | Asp Ala Leu Glu |
| 625                     | 630                     | 635             |
| Val Leu Gly Asn Asp Thr | Pro Glu Ser Ile Leu Lys | Lys Arg Gln Leu |
| 645                     | 650                     | 655             |
| Asn Lys Ser Ile Gln Gly | Lys Glu Asn Gln His Gln | Pro His Asp Gln |
| 660                     | 665                     | 670             |
| Leu Gly Asn Arg Ser His | Val Glu Cys Arg Ala Leu | Asp Phe Ser Asp |
| 675                     | 680                     | 685             |

Cys Gly Thr Pro Gly Lys Ala Lys Val Pro Ser Ala Ser Pro Gly Gly  
690 695 700  
Tyr Ser Ser Pro Ser Ser Tyr Leu Leu Lys Ser Cys Arg  
705 710 715

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..645

(D) OTHER INFORMATION: / Ceres Seq. ID 1566355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Asp Asn Gly Gly Lys Asn Gln Ala Leu Gln Gln Asp Phe Gln Ser  
1 5 10 15  
Ser Val Arg Leu Ser Asp Gln Pro Phe Leu Ser Asn Ser Asp Thr Asp  
20 25 30  
Pro Glu Ala Gln Thr Leu Ile Thr Asp Glu Glu Cys Cys Arg Val Leu  
35 40 45  
Phe Pro Asp Asn Met Lys Asp Ser Ser Thr Ser Ser Gly Glu Gln Gly  
50 55 60  
Arg Asn Met Val Asp Pro Gln Asn Gly Lys Gly Ser Leu Cys Ser Gln  
65 70 75 80  
Ala Ala Glu Thr His Ala His Glu Thr Gly Lys Val Pro Ala Leu Pro  
85 90 95  
Trp His Pro Ser Ser Glu Gly Leu Ala Gly His Asn Cys Val Pro  
100 105 110  
Leu Leu Asp Ser Asp Leu Lys Asp Ser Leu Leu Pro Arg Asn Asp Ser  
115 120 125  
Asn Ala Pro Ile Gln Gly Cys Arg Leu Phe Gly Ala Thr Glu Leu Glu  
130 135 140  
Cys Lys Thr Asp Thr Asn Asp Gly Phe Ile Asp Thr Tyr Gly His Val  
145 150 155 160  
Thr Ser His Gly Asn Asp Asp Asn Gly Gly Phe Pro Glu Gln Gln Gly  
165 170 175  
Leu Ser Tyr Ile Pro Lys Asp Ser Leu Lys Leu Val Pro Leu Asn Ser  
180 185 190  
Phe Ser Ser Pro Ser Arg Val Asn Lys Ile Tyr Phe Pro Ile Asp Asp  
195 200 205  
Lys Pro Ala Glu Lys Asp Lys Gly Ala Leu Cys Tyr Glu Pro Pro Arg  
210 215 220  
Phe Pro Ser Ala Asp Ile Pro Phe Phe Ser Cys Asp Leu Val Pro Ser  
225 230 235 240  
Asn Ser Asp Leu Arg Gln Glu Tyr Ser Pro Phe Gly Ile Arg Gln Leu  
245 250 255  
Met Ile Ser Ser Met Asn Cys Thr Thr Pro Leu Arg Leu Trp Asp Ser  
260 265 270  
Pro Cys His Asp Arg Ser Pro Asp Val Met Leu Asn Asp Thr Ala Lys  
275 280 285  
Ser Phe Ser Gly Ala Pro Ser Ile Leu Lys Lys Arg His Arg Asp Leu  
290 295 300  
Leu Ser Pro Val Leu Asp Arg Arg Lys Asp Lys Lys Leu Lys Arg Ala  
305 310 315 320  
Ala Thr Ser Ser Leu Ala Asn Asp Phe Ser Arg Leu Asp Val Met Leu  
325 330 335  
Asp Glu Gly Asp Asp Cys Met Thr Ser Arg Pro Ser Glu Ser Pro Glu  
340 345 350  
Asp Lys Asn Ile Cys Ala Ser Pro Ser Ile Ala Arg Asp Asn Arg Asn

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 355                                                             | 360 | 365 |
| Cys Ala Ser Ser Arg Leu Tyr Gln Glu Met Ile Pro Ile Asp Glu Glu |     |     |
| 370                                                             | 375 | 380 |
| Pro Lys Glu Thr Leu Glu Ser Gly Gly Val Thr Ser Met Gln Asn Glu |     |     |
| 385                                                             | 390 | 395 |
| Asn Gly Cys Asn Asp Gly Gly Ala Ser Ala Lys Asn Asp Gln Glu Thr |     | 400 |
|                                                                 | 405 | 410 |
|                                                                 |     | 415 |
| Ser Gly Ser Phe Phe Glu Leu Arg Leu Cys Ser Pro Gly Met Thr Arg |     |     |
|                                                                 | 420 | 425 |
|                                                                 |     | 430 |
| Ala Arg Pro Asp Asn Lys Val Asn Ala Ser Ala Lys Asp Leu Ser Asn |     |     |
|                                                                 | 435 | 440 |
|                                                                 |     | 445 |
| Gln His Lys Ile Ser Leu Gly Asp Phe Pro Thr Glu Glu Met Ser Ser |     |     |
|                                                                 | 450 | 455 |
|                                                                 |     | 460 |
| Glu Pro Leu Cys Thr Val Asp Ser Ile Pro Leu Ser Ala Ile Asp Lys |     |     |
| 465                                                             | 470 | 475 |
|                                                                 |     | 480 |
| Thr Asn Thr Ala Glu Thr Ser Phe Asp Ile Glu Asn Phe Asn Ile Phe |     |     |
|                                                                 | 485 | 490 |
|                                                                 |     | 495 |
| Asp Gly Thr Pro Phe Arg Lys Leu Leu Asp Thr Pro Ser Pro Trp Lys |     |     |
|                                                                 | 500 | 505 |
|                                                                 |     | 510 |
| Ser Pro Leu Leu Phe Gly Ser Phe Leu Gln Ser Pro Lys Leu Pro Pro |     |     |
|                                                                 | 515 | 520 |
|                                                                 |     | 525 |
| Glu Ile Thr Phe Glu Asp Ile Gly Cys Phe Met Ser Pro Gly Glu Arg |     |     |
|                                                                 | 530 | 535 |
|                                                                 |     | 540 |
| Ser Tyr Asp Ala Ile Gly Leu Met Lys His Leu Ser Glu His Ser Ala |     |     |
| 545                                                             | 550 | 555 |
|                                                                 |     | 560 |
| Thr Ala Tyr Ala Asp Ala Leu Glu Val Leu Gly Asn Asp Thr Pro Glu |     |     |
|                                                                 | 565 | 570 |
|                                                                 |     | 575 |
| Ser Ile Leu Lys Lys Arg Gln Leu Asn Lys Ser Ile Gln Gly Lys Glu |     |     |
|                                                                 | 580 | 585 |
|                                                                 |     | 590 |
| Asn Gln His Gln Pro His Asp Gln Leu Gly Asn Arg Ser His Val Glu |     |     |
|                                                                 | 595 | 600 |
|                                                                 |     | 605 |
| Cys Arg Ala Leu Asp Phe Ser Asp Cys Gly Thr Pro Gly Lys Ala Lys |     |     |
|                                                                 | 610 | 615 |
|                                                                 |     | 620 |
| Val Pro Ser Ala Ser Pro Gly Gly Tyr Ser Ser Pro Ser Ser Tyr Leu |     |     |
| 625                                                             | 630 | 635 |
|                                                                 |     | 640 |
| Leu Lys Ser Cys Arg                                             |     |     |
|                                                                 | 645 |     |

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..593
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Lys Asp Ser Ser Thr Ser Ser Gly Glu Gln Gly Arg Asn Met Val |    |
| 1                                                               | 15 |
| Asp Pro Gln Asn Gly Lys Gly Ser Leu Cys Ser Gln Ala Ala Glu Thr |    |
|                                                                 | 20 |
|                                                                 | 25 |
|                                                                 | 30 |
| His Ala His Glu Thr Gly Lys Val Pro Ala Leu Pro Trp His Pro Ser |    |
|                                                                 | 35 |
|                                                                 | 40 |
|                                                                 | 45 |
| Ser Ser Glu Gly Leu Ala Gly His Asn Cys Val Pro Leu Leu Asp Ser |    |
|                                                                 | 50 |
|                                                                 | 55 |
|                                                                 | 60 |
| Asp Leu Lys Asp Ser Leu Leu Pro Arg Asn Asp Ser Asn Ala Pro Ile |    |
| 65                                                              | 70 |
|                                                                 | 75 |
|                                                                 | 80 |
| Gln Gly Cys Arg Leu Phe Gly Ala Thr Glu Leu Glu Cys Lys Thr Asp |    |
|                                                                 | 85 |
|                                                                 | 90 |
|                                                                 | 95 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Asn | Asp | Gly | Phe | Ile | Asp | Thr | Tyr | Gly | His | Val | Thr | Ser | His | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Asp | Asp | Asn | Gly | Gly | Phe | Pro | Glu | Gln | Gln | Gly | Leu | Ser | Tyr | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Pro | Lys | Asp | Ser | Leu | Lys | Leu | Val | Pro | Leu | Asn | Ser | Phe | Ser | Ser | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Arg | Val | Asn | Lys | Ile | Tyr | Phe | Pro | Ile | Asp | Asp | Lys | Pro | Ala | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Lys | Asp | Lys | Gly | Ala | Leu | Cys | Tyr | Glu | Pro | Pro | Arg | Phe | Pro | Ser | Ala |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Asp | Ile | Pro | Phe | Phe | Ser | Cys | Asp | Leu | Val | Pro | Ser | Asn | Ser | Asp | Leu |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg | Gln | Glu | Tyr | Ser | Pro | Phe | Gly | Ile | Arg | Gln | Leu | Met | Ile | Ser | Ser |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Met | Asn | Cys | Thr | Thr | Pro | Leu | Arg | Leu | Trp | Asp | Ser | Pro | Cys | His | Asp |  |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |  |
| Arg | Ser | Pro | Asp | Val | Met | Leu | Asn | Asp | Thr | Ala | Lys | Ser | Phe | Ser | Gly |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ala | Pro | Ser | Ile | Leu | Lys | Lys | Arg | His | Arg | Asp | Leu | Leu | Ser | Pro | Val |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Leu | Asp | Arg | Arg | Lys | Asp | Lys | Lys | Leu | Lys | Arg | Ala | Ala | Thr | Ser | Ser |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Ala | Asn | Asp | Phe | Ser | Arg | Leu | Asp | Val | Met | Leu | Asp | Glu | Gly | Asp |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Asp | Cys | Met | Thr | Ser | Arg | Pro | Ser | Glu | Ser | Pro | Glu | Asp | Lys | Asn | Ile |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Cys | Ala | Ser | Pro | Ser | Ile | Ala | Arg | Asp | Asn | Arg | Asn | Cys | Ala | Ser | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Arg | Leu | Tyr | Gln | Glu | Met | Ile | Pro | Ile | Asp | Glu | Glu | Pro | Lys | Glu | Thr |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Leu | Glu | Ser | Gly | Gly | Val | Thr | Ser | Met | Gln | Asn | Glu | Asn | Gly | Cys | Asn |  |
|     | 340 |     |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Asp | Gly | Gly | Ala | Ser | Ala | Lys | Asn | Asp | Gln | Glu | Thr | Ser | Gly | Ser | Phe |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Phe | Glu | Leu | Arg | Leu | Cys | Ser | Pro | Gly | Met | Thr | Arg | Ala | Arg | Pro | Asp |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Asn | Lys | Val | Asn | Ala | Ser | Ala | Lys | Asp | Leu | Ser | Asn | Gln | His | Lys | Ile |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Ser | Leu | Gly | Asp | Phe | Pro | Thr | Glu | Glu | Met | Ser | Ser | Glu | Pro | Leu | Cys |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Thr | Val | Asp | Ser | Ile | Pro | Leu | Ser | Ala | Ile | Asp | Lys | Thr | Asn | Thr | Ala |  |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Glu | Thr | Ser | Phe | Asp | Ile | Glu | Asn | Phe | Asn | Ile | Phe | Asp | Gly | Thr | Pro |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Phe | Arg | Lys | Leu | Leu | Asp | Thr | Pro | Ser | Pro | Trp | Lys | Ser | Pro | Leu | Leu |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| Phe | Gly | Ser | Phe | Leu | Gln | Ser | Pro | Lys | Leu | Pro | Pro | Glu | Ile | Thr | Phe |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Glu | Asp | Ile | Gly | Cys | Phe | Met | Ser | Pro | Gly | Glu | Arg | Ser | Tyr | Asp | Ala |  |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |  |
| Ile | Gly | Leu | Met | Lys | His | Leu | Ser | Glu | His | Ser | Ala | Thr | Ala | Tyr | Ala |  |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |
| Asp | Ala | Leu | Glu | Val | Leu | Gly | Asn | Asp | Thr | Pro | Glu | Ser | Ile | Leu | Lys |  |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |
| Lys | Arg | Gln | Leu | Asn | Lys | Ser | Ile | Gln | Gly | Lys | Glu | Asn | Gln | His | Gln |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |
| Pro | His | Asp | Gln | Leu | Gly | Asn | Arg | Ser | His | Val | Glu | Cys | Arg | Ala | Leu |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |
| Asp | Phe | Ser | Asp | Cys | Gly | Thr | Pro | Gly | Lys | Ala | Lys | Val | Pro | Ser | Ala |  |
|     |     |     | 565 |     |     |     |     |     | 570 |     |     |     |     | 575 |     |  |
| Ser | Pro | Gly | Gly | Tyr | Ser | Ser | Pro | Ser | Ser | Tyr | Leu | Leu | Lys | Ser | Cys |  |

2025 RELEASE UNDER E.O. 14176

Arg 580 585 590

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..574
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| actagaaatt ttgtctctct cgccgccttg cgaaaagcat ttctgatctt actcttagga    | 60  |
| taaaaaaatg tcgacagttg gagagcttgc tNtGCagcta cgctggtatg atcctcgagg    | 120 |
| acgagggtat cgctatcacg gctgacaaaa tcgcgacott ggtgaaagct gctggtgtta    | 180 |
| gtattgagtc atactggcca atgctattcg ccaagatggc tgagaaacgt aacgtgactg    | 240 |
| atctcatcat gaacgttggg gctggtgggt gaggtgggtgc tccggttgca gctgctgctc   | 300 |
| cagctgctgg cggtggtgcg gcaGctgctc ctgctgctga ggagaagaag aaggatgagc    | 360 |
| cagcagaaga gagtgcgga gatttgggtt tcggtttgtt tgactaaacg caGtcacttg     | 420 |
| tctttcttct ttgtagtggg atattggaga ctatatatttgc tctgtatgagt tattattact | 480 |
| tgtttgatct ggctaaagga ctattagtgg gtttatgatg cgtatgttgt ataactcaag    | 540 |
| tttctagca aaccaatcgg ctcgggcttt tggt                                 |     |

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ile Leu Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala |  |
| 1 5 10 15                                                       |  |
| Thr Leu Val Lys Ala Ala Gly Val Ser Ile Glu Ser Tyr Trp Pro Met |  |
| 20 25 30                                                        |  |
| Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met |  |
| 35 40 45                                                        |  |
| Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Ala     |  |
| 50 55 60                                                        |  |
| Pro Ala Ala Gly Gly Gly Ala Ala Ala Pro Ala Ala Glu Glu Lys     |  |
| 65 70 75 80                                                     |  |
| Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly |  |
| 85 90 95                                                        |  |
| Leu Phe Asp                                                     |  |

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1566366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Met Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile  
1 5 10 15  
Met Asn Val Gly Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala  
20 25 30  
Ala Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu  
35 40 45  
Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe  
50 55 60  
Gly Leu Phe Asp  
65

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly Ala  
1 5 10 15  
Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Ala Pro Ala Ala Gly  
20 25 30  
Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu Lys Lys Lys Asp Glu  
35 40 45  
Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly Leu Phe Asp  
50 55 60

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1582

(D) OTHER INFORMATION: / Ceres Seq. ID 1566379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| tgagaaaaatg cctgagagaa atgcagtgtc atggagtgtc atgatcactg ggctttgtca | 60   |
| gaacggtgaa gtggatcgcg cggttgtgtt gtttcggaaa atgcctgtga aggattcgtc  | 120  |
| tcctctatgt gcacttgtgg ctggtcttat taaaaacgag agactttcag aagctgcgtg  | 180  |
| ggttttgggt cagtatggga gtttagtttc aggaagggaa gatttggtgt atgcttataa  | 240  |
| cactttgatt gttggatatg gacagcgagg acaagtagaa gcagctcgat gtctgtttga  | 300  |
| tcagattcct gatctctgtg gtgatgatca tgggtggagag tttagagaga ggttctgtaa | 360  |
| aaatgttggtg tcatggaatt ctatgatcaa agcttacttg aaagtgggtg atgtggtctc | 420  |
| tgctagggtg ctatttgatc agatgaaaga ccgcgataca atttcttgga acacaatgat  | 480  |
| tgatggatac gtacatgttt ccaggatgga agatgctttt gctctgtttt cggaaatgcc  | 540  |
| gaaccgtgat gcacattcgt ggaacatgat ggtctcgggt tatgctagtgt ttggcaatgt | 600  |
| agagcttgct cgccactact ttgaaaaaac acctgagaaa catacagtct cgtggaactc  | 660  |
| gataaatagca gcttatgaga aaaacaagga ctacaaagaa gctgttgatt tgtttatccg | 720  |
| gatgaacatt gaaggagaga agcctgaccc acatacttta acttctcttc tcagtgcatac | 780  |
| taccgggctt gtaaactctgc gtttaggaat gcagatgcac caaatcggtg tcaagactgt | 840  |
| gatccccgat gttccagtcc acaatgccct tatcactatg tattcaagat gcggtgaaat  | 900  |
| aatggagtcg aggagaatct tcgatgaaat gaaactcaaa agagaagtaa tcacatggaa  | 960  |
| tgcaatgata ggaggatatg catttcatgg taatgcctca gaggccttga atctgttcgg  | 1020 |

|                                                                      |      |
|----------------------------------------------------------------------|------|
| gtc gat gaaa agcaacggga tatatccttc tcacataaca ttctgtctcag ttctgaacgc | 1080 |
| ttgtgCtcac gcgggacttg ttgatgaggc taaagcacag tttgtgtcca tgatgagtgt    | 1140 |
| gtacaagatc gagccgatga tggaacatta ttcttccttg gtcaacgtta ccagtggaca    | 1200 |
| agggcagttt gaagaggcca tgtatatcat aaagagtatg ccttttgagc cagacaaaac    | 1260 |
| ggatggggt gcattattgg atgctttag gatataacaa tgtagggtt gcacatgttg       | 1320 |
| cagctgaagc aatgtcgaga ctcgaaccag agagctcaac acottatgta ctgttatata    | 1380 |
| acatgtacgc ggatatggga ctatgggacg aagcttctca agtgagaatg aacatggaga    | 1440 |
| gtaaaagaat caagaaggaa agaggatcca gttgggttga ctctcaacg taaaaagcag     | 1500 |
| cctttattta tgtttactta aacataaaaa ttgatttggg atcagaattg agatagaaat    | 1560 |
| tgataaggta ctcttgaaag tt                                             |      |

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..431

(D) OTHER INFORMATION: / Ceres Seq. ID 1566380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Lys | Met | Pro | Glu | Arg | Asn | Ala | Val | Ser | Trp | Ser | Ala | Met | Ile | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Cys | Gln | Asn | Gly | Glu | Val | Asp | Arg | Ala | Val | Val | Leu | Phe | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Met | Pro | Val | Lys | Asp | Ser | Ser | Pro | Leu | Cys | Ala | Leu | Val | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ile | Lys | Asn | Glu | Arg | Leu | Ser | Glu | Ala | Ala | Trp | Val | Leu | Gly | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Gly | Ser | Leu | Val | Ser | Gly | Arg | Glu | Asp | Leu | Val | Tyr | Ala | Tyr | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Leu | Ile | Val | Gly | Tyr | Gly | Gln | Arg | Gly | Gln | Val | Glu | Ala | Ala | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Leu | Phe | Asp | Gln | Ile | Pro | Asp | Leu | Cys | Gly | Asp | Asp | His | Gly | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Glu | Phe | Arg | Glu | Arg | Phe | Cys | Lys | Asn | Val | Val | Ser | Trp | Asn | Ser | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Lys | Ala | Tyr | Leu | Lys | Val | Gly | Asp | Val | Val | Ser | Ala | Arg | Leu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Asp | Gln | Met | Lys | Asp | Arg | Asp | Thr | Ile | Ser | Trp | Asn | Thr | Met | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Gly | Tyr | Val | His | Val | Ser | Arg | Met | Glu | Asp | Ala | Phe | Ala | Leu | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Glu | Met | Pro | Asn | Arg | Asp | Ala | His | Ser | Trp | Asn | Met | Met | Val | Ser |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Gly | Tyr | Ala | Ser | Val | Gly | Asn | Val | Glu | Leu | Ala | Arg | His | Tyr | Phe | Glu |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Thr | Pro | Glu | Lys | His | Thr | Val | Ser | Trp | Asn | Ser | Ile | Ile | Ala | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Tyr | Glu | Lys | Asn | Lys | Asp | Tyr | Lys | Glu | Ala | Val | Asp | Leu | Phe | Ile | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Met | Asn | Ile | Glu | Gly | Glu | Lys | Pro | Asp | Pro | His | Thr | Leu | Thr | Ser | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Ser | Ala | Ser | Thr | Gly | Leu | Val | Asn | Leu | Arg | Leu | Gly | Met | Gln | Met |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| His | Gln | Ile | Val | Val | Lys | Thr | Val | Ile | Pro | Asp | Val | Pro | Val | His | Asn |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ala | Leu | Ile | Thr | Met | Tyr | Ser | Arg | Cys | Gly | Glu | Ile | Met | Glu | Ser | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Arg | Ile | Phe | Asp | Glu | Met | Lys | Leu | Lys | Arg | Glu | Val | Ile | Thr | Trp | Asn |



305 310 315 320  
Ala Met Ile Gly Gly Tyr Ala Phe His Gly Asn Ala Ser Glu Ala Leu  
325 330 335  
Asn Leu Phe Gly Ser Met Lys Ser Asn Gly Ile Tyr Pro Ser His Ile  
340 345 350  
Thr Phe Val Ser Val Leu Asn Ala Cys Ala His Ala Gly Leu Val Asp  
355 360 365  
Glu Ala Lys Ala Gln Phe Val Ser Met Met Ser Val Tyr Lys Ile Glu  
370 375 380  
Pro Met Met Glu His Tyr Ser Ser Leu Val Asn Val Thr Ser Gly Gln  
385 390 395 400  
Gly Gln Phe Glu Glu Ala Met Tyr Ile Ile Lys Ser Met Pro Phe Glu  
405 410 415  
Pro Asp Lys Thr Val Trp Gly Ala Leu Leu Asp Ala Cys Arg Ile  
420 425 430

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1566381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Pro Glu Arg Asn Ala Val Ser Trp Ser Ala Met Ile Thr Gly Leu  
1 5 10 15  
Cys Gln Asn Gly Glu Val Asp Arg Ala Val Val Leu Phe Arg Lys Met  
20 25 30  
Pro Val Lys Asp Ser Ser Pro Leu Cys Ala Leu Val Ala Gly Leu Ile  
35 40 45  
Lys Asn Glu Arg Leu Ser Glu Ala Ala Trp Val Leu Gly Gln Tyr Gly  
50 55 60  
Ser Leu Val Ser Gly Arg Glu Asp Leu Val Tyr Ala Tyr Asn Thr Leu  
65 70 75 80  
Ile Val Gly Tyr Gly Gln Arg Gly Gln Val Glu Ala Ala Arg Cys Leu  
85 90 95  
Phe Asp Gln Ile Pro Asp Leu Cys Gly Asp Asp His Gly Gly Glu Phe  
100 105 110  
Arg Glu Arg Phe Cys Lys Asn Val Val Ser Trp Asn Ser Met Ile Lys  
115 120 125  
Ala Tyr Leu Lys Val Gly Asp Val Val Ser Ala Arg Leu Leu Phe Asp  
130 135 140  
Gln Met Lys Asp Arg Asp Thr Ile Ser Trp Asn Thr Met Ile Asp Gly  
145 150 155 160  
Tyr Val His Val Ser Arg Met Glu Asp Ala Phe Ala Leu Phe Ser Glu  
165 170 175  
Met Pro Asn Arg Asp Ala His Ser Trp Asn Met Met Val Ser Gly Tyr  
180 185 190  
Ala Ser Val Gly Asn Val Glu Leu Ala Arg His Tyr Phe Glu Lys Thr  
195 200 205  
Pro Glu Lys His Thr Val Ser Trp Asn Ser Ile Ile Ala Ala Tyr Glu  
210 215 220  
Lys Asn Lys Asp Tyr Lys Glu Ala Val Asp Leu Phe Ile Arg Met Asn  
225 230 235 240  
Ile Glu Gly Glu Lys Pro Asp Pro His Thr Leu Thr Ser Leu Leu Ser  
245 250 255  
Ala Ser Thr Gly Leu Val Asn Leu Arg Leu Gly Met Gln Met His Gln  
260 265 270

(2) INFORMATION FOR SEQ ID NO:270:

(A) LENGTH: 418 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..418

(D) OTHER INFORMATION: / Ceres Seq. ID 1566382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

|            |            |            |            |            |     |            |            |            |           |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Ile        | Thr        | Gly        | Leu<br>5   | Cys | Gln        | Asn        | Gly        | Glu<br>10 | Val        | Asp        | Arg        | Ala        | Val<br>15  | Val        |
| Leu        | Phe        | Arg        | Lys<br>20  | Met        | Pro | Val        | Lys        | Asp<br>25  | Ser       | Ser        | Pro        | Leu        | Cys<br>30  | Ala        | Leu        |
| Val        | Ala        | Gly<br>35  | Leu        | Ile        | Lys | Asn        | Glu<br>40  | Arg        | Leu       | Ser        | Glu        | Ala<br>45  | Ala        | Trp        | Val        |
| Leu        | Gly<br>50  | Gln        | Tyr        | Gly        | Ser | Leu<br>55  | Val        | Ser        | Gly       | Arg        | Glu<br>60  | Asp        | Leu        | Val        | Tyr        |
| Ala<br>65  | Tyr        | Asn        | Thr        | Leu<br>70  | Ile | Val        | Gly        | Tyr        | Gly       | Gln<br>75  | Arg        | Gly        | Gln        | Val        | Glu<br>80  |
| Ala        | Ala        | Arg        | Cys<br>85  | Leu        | Phe | Asp        | Gln        | Ile        | Pro<br>90 | Asp        | Leu        | Cys        | Gly        | Asp<br>95  | Asp        |
| His        | Gly        | Gly        | Glu<br>100 | Phe        | Arg | Glu        | Arg        | Phe<br>105 | Cys       | Lys        | Asn        | Val        | Val<br>110 | Ser        | Trp        |
| Asn        | Ser        | Met<br>115 | Ile        | Lys        | Ala | Tyr        | Leu<br>120 | Lys        | Val       | Gly        | Asp        | Val<br>125 | Val        | Ser        | Ala        |
| Arg        | Leu<br>130 | Leu        | Phe        | Asp        | Gln | Met<br>135 | Lys        | Asp        | Arg       | Asp        | Thr<br>140 | Ile        | Ser        | Trp        | Asn        |
| Thr<br>145 | Met        | Ile        | Asp        | Gly<br>150 | Tyr | Val        | His        | Val        | Ser       | Arg<br>155 | Met        | Glu        | Asp        | Ala        | Phe<br>160 |
| Ala        | Leu        | Phe        | Ser<br>165 | Glu        | Met | Pro        | Asn        | Arg<br>170 | Asp       | Ala        | His        | Ser        | Trp        | Asn<br>175 | Met        |
| Met        | Val        | Ser        | Gly<br>180 | Tyr        | Ala | Ser        | Val        | Gly<br>185 | Asn       | Val        | Glu        | Leu        | Ala<br>190 | Arg        | His        |
| Tyr        | Phe        | Glu<br>195 | Lys        | Thr        | Pro | Glu        | Lys<br>200 | His        | Thr       | Val        | Ser        | Trp<br>205 | Asn        | Ser        | Ile        |
| Ile        | Ala<br>210 | Ala        | Tyr        | Glu        | Lys | Asn<br>215 | Lys        | Asp        | Tyr       | Lys        | Glu<br>220 | Ala        | Val        | Asp        | Leu        |
| Phe        | Ile        | Arg        | Met        | Asn        | Ile | Glu        | Gly        | Glu        | Lys       | Pro        | Asp        | Pro        | His        | Thr        | Leu        |

225 230 235 240  
Thr Ser Leu Leu Ser Ala Ser Thr Gly Leu Val Asn Leu Arg Leu Gly  
245 250 255  
Met Gln Met His Gln Ile Val Val Lys Thr Val Ile Pro Asp Val Pro  
260 265 270  
Val His Asn Ala Leu Ile Thr Met Tyr Ser Arg Cys Gly Glu Ile Met  
275 280 285  
Glu Ser Arg Arg Ile Phe Asp Glu Met Lys Leu Lys Arg Glu Val Ile  
290 295 300  
Thr Trp Asn Ala Met Ile Gly Gly Tyr Ala Phe His Gly Asn Ala Ser  
305 310 315 320  
Glu Ala Leu Asn Leu Phe Gly Ser Met Lys Ser Asn Gly Ile Tyr Pro  
325 330 335  
Ser His Ile Thr Phe Val Ser Val Leu Asn Ala Cys Ala His Ala Gly  
340 345 350  
Leu Val Asp Glu Ala Lys Ala Gln Phe Val Ser Met Met Ser Val Tyr  
355 360 365  
Lys Ile Glu Pro Met Met Glu His Tyr Ser Ser Leu Val Asn Val Thr  
370 375 380  
Ser Gly Gln Gly Gln Phe Glu Glu Ala Met Tyr Ile Ile Lys Ser Met  
385 390 395 400  
Pro Phe Glu Pro Asp Lys Thr Val Trp Gly Ala Leu Leu Asp Ala Cys  
405 410 415  
Arg Ile

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..974
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aaMcaacgaa cgcgcagagc tctcacttca cactttatcc acttgagact tgcacaatgg   | 60  |
| cgtctccttc gcttctgcag tcttccgctt cttcgtttca cggacgtttc tcaccattag   | 120 |
| cggctccatc ctccgcacga atgctctctc cgccgctcag aaacgtggtg aaagtctcgg   | 180 |
| cgtctggaac tgtactggtc gagaaatctg aagccgagaa aactcaacgc ctcaaaaccg   | 240 |
| cttacctcga gaggattatc cctgcgctca aagaagagtt caagtacgtt aatattcacc   | 300 |
| aggttccaaa ggtacagaag attgtagtga attgtggtat tggagatgcg gcgcagaacg   | 360 |
| acaagggttt ggaggtgctg atgaaggata tcgcgcttat cacagggcag aaacctatta   | 420 |
| agacacgagc tagagcttcc attgctactt tcaagatcag ggaagatcaa cctcttggga   | 480 |
| ttgctgtcac tctcagagga gatgtaatgt actccttctt ggatcgtctt atcaacttag   | 540 |
| cccttccgag aactcgagat ttccaagggtg tgagtcccag tagctttgat gggaacggaa  | 600 |
| actacagtat tgggtgtgaaa gaccaagggtg tattccctga aatcagggtt gatgccgttg | 660 |
| gaaaaacgag aggaatggat gtatgcacat gcacaacggc taaaagcgat caagaaggac   | 720 |
| agaaactatt ggctctaata ggaatgcctt tcaggaagg aggtggtggc agcacaggcg    | 780 |
| cgatagtgcg gaagaagaaa ctaaagtctc atcactttga tgctaaagga aaaggaaaga   | 840 |
| gatgatgaac atagctgcct attgtatgta tcgtcttctg taaccaacca tttcatgttt   | 900 |
| cagaaaaacc atctcctttt gtaatgcttt atgagtcaat ttgaaaataa tatcagggat   | 960 |
| cttgttggtta tgggt                                                   |     |

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1566388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Xaa Thr Asn Ala Glu Ser Ser His Phe Thr Leu Tyr Pro Leu Gly Ala  
1 5 10 15  
Ser Thr Met Ala Ser Pro Ser Leu Leu Gln Ser Ser Ala Ser Ser Phe  
20 25 30  
His Gly Arg Phe Ser Pro Leu Ala Ala Pro Ser Ser Ala Arg Met Leu  
35 40 45  
Ser Pro Pro Leu Arg Asn Val Lys Val Ser Ala Ser Gly Thr Val  
50 55 60  
Leu Val Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys Thr Ala  
65 70 75 80  
Tyr Leu Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys Tyr Val  
85 90 95  
Asn Ile His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn Cys Gly  
100 105 110  
Ile Gly Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala Met Lys  
115 120 125  
Asp Ile Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg Ala Arg  
130 135 140  
Ala Ser Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu Gly Ile  
145 150 155 160  
Ala Val Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp Arg Leu  
165 170 175  
Ile Asn Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val Ser Pro  
180 185 190  
Ser Ser Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys Asp Gln  
195 200 205  
Gly Val Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr Arg Gly  
210 215 220  
Met Asp Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu Gly Gln  
225 230 235 240  
Lys Leu Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly Gly Gly  
245 250 255  
Ser Thr Gly Ala Ile Val Arg Lys Lys Lys Leu Lys Ser His His Phe  
260 265 270  
Asp Ala Lys Gly Lys Gly Lys Arg  
275 280

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1566389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Ala Ser Pro Ser Leu Leu Gln Ser Ser Ala Ser Ser Phe His Gly  
1 5 10 15  
Arg Phe Ser Pro Leu Ala Ala Pro Ser Ser Ala Arg Met Leu Ser Pro  
20 25 30  
Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly Thr Val Leu Val  
35 40 45  
Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys Thr Ala Tyr Leu  
50 55 60

Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys Tyr Val Asn Ile  
65 70 75 80  
His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn Cys Gly Ile Gly  
85 90 95  
Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala Met Lys Asp Ile  
100 105 110  
Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg Ala Arg Ala Ser  
115 120 125  
Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu Gly Ile Ala Val  
130 135 140  
Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp Arg Leu Ile Asn  
145 150 155 160  
Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val Ser Pro Ser Ser  
165 170 175  
Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys Asp Gln Gly Val  
180 185 190  
Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr Arg Gly Met Asp  
195 200 205  
Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu Gly Gln Lys Leu  
210 215 220  
Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly Gly Ser Thr  
225 230 235 240  
Gly Ala Ile Val Arg Lys Lys Lys Leu Lys Ser His His Phe Asp Ala  
245 250 255  
Lys Gly Lys Gly Lys Arg  
260

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1566390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Leu Ser Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly  
1 5 10 15  
Thr Val Leu Val Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys  
20 25 30  
Thr Ala Tyr Leu Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys  
35 40 45  
Tyr Val Asn Ile His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn  
50 55 60  
Cys Gly Ile Gly Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala  
65 70 75 80  
Met Lys Asp Ile Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg  
85 90 95  
Ala Arg Ala Ser Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu  
100 105 110  
Gly Ile Ala Val Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp  
115 120 125  
Arg Leu Ile Asn Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val  
130 135 140  
Ser Pro Ser Ser Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys  
145 150 155 160  
Asp Gln Gly Val Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr  
165 170 175  
Arg Gly Met Asp Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu

180 185 190  
Gly Gln Lys Leu Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly  
195 200 205  
Gly Gly Ser Thr Gly Ala Ile Val Arg Lys Lys Lys Leu Lys Ser His  
210 215 220  
His Phe Asp Ala Lys Gly Lys Gly Lys Arg  
225 230

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1566395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| cccactaaat | tataattttt | Atctttataa | aaaaaaatat | caaactctat  | atcttctcga  | 60  |
| tctcttctct | tcctcttatt | tctccaagat | cccagacgaa | atggctcaga  | aagtgggtgct | 120 |
| gaaggtttta | accatgactg | atgataagac | caagcagaaa | gccatagaag  | ctgcagctga  | 180 |
| tatcttcgga | gttgattcca | tagcagcgga | tatgaaggat | caaaaattga  | cggtgatcgg  | 240 |
| tttgatggat | gcggttgccg | tggtgaagaa | gttgaagaag | gttggttaaag | tcgatttgat  | 300 |
| atcggttga  | ccggcaaaag | aagagaagaa | agaagagaag | aaggaagaga  | agaaaaagga  | 360 |
| aaagaaagag | gagaagaagg | aagagaagaa | agaagaagaa | cctaagaaat  | aagtgactcg  | 420 |
| aattgctatt | aaaaccctaa | atctttgtca | tattgatttc | ataattagaa  | cgctgaatca  | 480 |
| ttgaataatt | taagatgtaa | aattaattgt | tcaatacaga | ttgtaataaa  | agctaagtat  | 540 |
| ttg        |            |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1566396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Leu | Asn | Tyr | Asn | Phe | Tyr | Leu | Tyr | Lys | Lys | Lys | Tyr | Gln | Thr | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Tyr | Phe | Leu | Asp | Leu | Phe | Ser | Ser | Ser | Tyr | Phe | Ser | Lys | Ile | Pro | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Met | Ala | Gln | Lys | Val | Val | Leu | Lys | Val | Leu | Thr | Met | Thr | Asp | Asp |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Thr | Lys | Gln | Lys | Ala | Ile | Glu | Ala | Ala | Ala | Asp | Ile | Phe | Gly | Val |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Ser | Ile | Ala | Ala | Asp | Met | Lys | Asp | Gln | Lys | Leu | Thr | Val | Ile | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Leu | Met | Asp | Ala | Val | Ala | Val | Val | Lys | Lys | Leu | Lys | Lys | Val | Gly | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Val | Asp | Leu | Ile | Ser | Val | Gly | Pro | Ala | Lys | Glu | Glu | Lys | Lys | Glu | Glu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Lys | Glu | Glu | Lys | Lys | Lys | Glu | Lys | Lys | Glu | Glu | Lys | Lys | Glu | Glu |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Lys | Glu | Glu | Glu | Pro | Lys | Lys |     |     |     |     |     |     |     |     |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..103  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566397  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Ala Gln Lys Val Val Leu Lys Val Leu Thr Met Thr Asp Asp Lys  
1 5 10 15  
Thr Lys Gln Lys Ala Ile Glu Ala Ala Asp Ile Phe Gly Val Asp  
20 25 30  
Ser Ile Ala Ala Asp Met Lys Asp Gln Lys Leu Thr Val Ile Gly Leu  
35 40 45  
Met Asp Ala Val Ala Val Val Lys Lys Leu Lys Lys Val Gly Lys Val  
50 55 60  
Asp Leu Ile Ser Val Gly Pro Ala Lys Glu Glu Lys Lys Glu Glu Lys  
65 70 75 80  
Lys Glu Glu Lys Lys Lys Glu Lys Lys Glu Glu Lys Lys Glu Glu Lys  
85 90 95  
Lys Glu Glu Glu Pro Lys Lys  
100

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566398  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Thr Asp Asp Lys Thr Lys Gln Lys Ala Ile Glu Ala Ala Ala Asp  
1 5 10 15  
Ile Phe Gly Val Asp Ser Ile Ala Ala Asp Met Lys Asp Gln Lys Leu  
20 25 30  
Thr Val Ile Gly Leu Met Asp Ala Val Ala Val Val Lys Lys Leu Lys  
35 40 45  
Lys Val Gly Lys Val Asp Leu Ile Ser Val Gly Pro Ala Lys Glu Glu  
50 55 60  
Lys Lys Glu Glu Lys Lys Glu Glu Lys Lys Lys Glu Lys Lys Glu Glu  
65 70 75 80  
Lys Lys Glu Glu Lys Lys Glu Glu Glu Pro Lys Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1221  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566423  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

aatcaacaca cacaacaca cacacacaca gcctttttcc ttcgttgatc gattgttaag

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| ctcgatccaa  | tggcggataa | caccgataat  | cggagatcct | tatggggagt | tccggagaag | 120  |
| cttcagcttc  | acatagcgat | gctgacgttg  | caattcgggt | acgccggatt | ccacgtggtg | 180  |
| tctcgagctg  | ctcttaacat | gggaatcagc  | aaactogtct | tccctgttta | tcgtaacatc | 240  |
| atcgccctgc  | ttcttctcct | tcccttcgct  | tacttctctg | aaaagaagga | gagaccagcg | 300  |
| attactctca  | actttctcat | ccagttcttc  | tttttggcac | tcataggaat | aacagcgagg | 360  |
| ctctcgggta  | cgtcttacac | ttgtttcttc  | ggaatcattc | agttcttgat | cattgctgct | 420  |
| ttctgtgaaa  | gagattctca | ggcttgggtt  | tttcaactcc | gttgggagct | tttcaccatc | 480  |
| ctctacgccg  | gaatcgtagc | gtctggaatc  | gcgtttgcgg | ttcagatttg | gtgtattgac | 540  |
| agaggggggtc | cagtcttcgt | tgtctgtttac | cagcctgttc | agactcttgt | cgttgcgatc | 600  |
| atggcttcta  | ttgcgttagg | cgaagaatct  | tatttgggcg | ggattatttg | agcggctctg | 660  |
| atcatagcgg  | gactttactt | cgtattgtac  | ggtaagagcg | aagagaggaa | atttgcagcg | 720  |
| cttgagaagg  | cagagatcca | gtcctccgcg  | gagcatggta | ttgaacgtgc | acctgtttct | 780  |
| cgcaactcca  | tcaagtcgtc | catcacaaca  | ccactactcc | atcagtcaac | ggacaatggt | 840  |
| tgactacttt  | ggacaaatca | ctctccagct  | aataattaca | aatgccatta | cccaattaaa | 900  |
| aggaacaat   | ggtgtgccgt | tgtgttttat  | gacttttgtg | tctgcttttt | ttcttagtgt | 960  |
| tttctcttct  | tttttttttc | taaaaatta   | ttaattacct | aagaaagggt | tttgMagaaa | 1020 |
| ggaaaaaaaa  | atggtggatg | agacatcatt  | gttcatgagg | atgatgatga | tgatgatagt | 1080 |
| gatgaagaag  | actatgtggg | agctttggat  | tgagactttt | ctatatataa | tatctggctg | 1140 |
| atatattagt  | gccatttttt | cttacatttc  | ttgtgggggt | httccttctc | ttatcatcaa | 1200 |
| tagaatgtta  | taatttgcac | c           |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1566424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Asn | Thr | Asp | Asn | Arg | Arg | Ser | Leu | Trp | Gly | Val | Pro | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Leu | Gln | Leu | His | Ile | Ala | Met | Leu | Thr | Leu | Gln | Phe | Gly | Tyr | Ala |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Phe | His | Val | Val | Ser | Arg | Ala | Ala | Leu | Asn | Met | Gly | Ile | Ser | Lys |
|     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Leu | Val | Phe | Pro | Val | Tyr | Arg | Asn | Ile | Ile | Ala | Leu | Leu | Leu | Leu |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Pro | Phe | Ala | Tyr | Phe | Leu | Glu | Lys | Lys | Glu | Arg | Pro | Ala | Ile | Thr | Leu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Asn | Phe | Leu | Ile | Gln | Phe | Phe | Phe | Leu | Ala | Leu | Ile | Gly | Ile | Thr | Ala |
|     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Arg | Leu | Ser | Val | Thr | Ser | Tyr | Thr | Cys | Phe | Phe | Gly | Ile | Ile | Gln | Phe |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Ile | Ile | Ala | Ala | Phe | Cys | Glu | Arg | Asp | Ser | Gln | Ala | Trp | Val | Phe |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| His | Ser | Gly | Trp | Glu | Leu | Phe | Thr | Ile | Leu | Tyr | Ala | Gly | Ile | Val | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ser | Gly | Ile | Ala | Phe | Ala | Val | Gln | Ile | Trp | Cys | Ile | Asp | Arg | Gly | Gly |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |     |
| Pro | Val | Phe | Val | Ala | Val | Tyr | Gln | Pro | Val | Gln | Thr | Leu | Val | Val | Ala |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |
| Ile | Met | Ala | Ser | Ile | Ala | Leu | Gly | Glu | Phe | Tyr | Leu | Gly | Gly | Ile |     |
|     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     |
| Ile | Gly | Ala | Val | Leu | Ile | Ile | Ala | Gly | Leu | Tyr | Phe | Val | Leu | Tyr | Gly |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Lys | Ser | Glu | Glu | Arg | Lys | Phe | Ala | Ala | Leu | Glu | Lys | Ala | Glu | Ile | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Ser | Ser | Ala | Glu | His | Gly | Ile | Glu | Arg | Ala | Pro | Val | Ser | Arg | Asn | Ser |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Ile | Lys | Ser | Ser | Ile | Thr | Thr | Pro | Leu | Leu | His | Gln | Ser | Thr | Asp | Asn |
|     |     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |     |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1566425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Leu | Gln | Phe | Gly | Tyr | Ala | Gly | Phe | His | Val | Val | Ser | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Leu | Asn | Met | Gly | Ile | Ser | Lys | Leu | Val | Phe | Pro | Val | Tyr | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Ile | Ala | Leu | Leu | Leu | Leu | Leu | Pro | Phe | Ala | Tyr | Phe | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Glu | Arg | Pro | Ala | Ile | Thr | Leu | Asn | Phe | Leu | Ile | Gln | Phe | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Leu | Ala | Leu | Ile | Gly | Ile | Thr | Ala | Arg | Leu | Ser | Val | Thr | Ser | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Cys | Phe | Phe | Gly | Ile | Ile | Gln | Phe | Leu | Ile | Ile | Ala | Ala | Phe | Cys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Arg | Asp | Ser | Gln | Ala | Trp | Val | Phe | His | Ser | Gly | Trp | Glu | Leu | Phe |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Ile | Leu | Tyr | Ala | Gly | Ile | Val | Ala | Ser | Gly | Ile | Ala | Phe | Ala | Val |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gln | Ile | Trp | Cys | Ile | Asp | Arg | Gly | Gly | Pro | Val | Phe | Val | Ala | Val | Tyr |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gln | Pro | Val | Gln | Thr | Leu | Val | Val | Ala | Ile | Met | Ala | Ser | Ile | Ala | Leu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Gly | Glu | Glu | Phe | Tyr | Leu | Gly | Gly | Ile | Ile | Gly | Ala | Val | Leu | Ile | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Gly | Leu | Tyr | Phe | Val | Leu | Tyr | Gly | Lys | Ser | Glu | Glu | Arg | Lys | Phe |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Ala | Leu | Glu | Lys | Ala | Glu | Ile | Gln | Ser | Ser | Ala | Glu | His | Gly | Ile |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Glu | Arg | Ala | Pro | Val | Ser | Arg | Asn | Ser | Ile | Lys | Ser | Ser | Ile | Thr | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Pro | Leu | Leu | His | Gln | Ser | Thr | Asp | Asn | Val |     |     |     |     |     |     |
| 225 |     |     | 230 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1566426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ile | Ser | Lys | Leu | Val | Phe | Pro | Val | Tyr | Arg | Asn | Ile | Ile | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

Leu Leu Leu Leu Leu Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg  
20 25 30  
Pro Ala Ile Thr Leu Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu  
35 40 45  
Ile Gly Ile Thr Ala Arg Leu Ser Val Thr Ser Tyr Thr Cys Phe Phe  
50 55 60  
Gly Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys Glu Arg Asp Ser  
65 70 75 80  
Gln Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe Thr Ile Leu Tyr  
85 90 95  
Ala Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val Gln Ile Trp Cys  
100 105 110  
Ile Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr Gln Pro Val Gln  
115 120 125  
Thr Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu Gly Glu Glu Phe  
130 135 140  
Tyr Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile Ala Gly Leu Tyr  
145 150 155 160  
Phe Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu  
165 170 175  
Lys Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro  
180 185 190  
Val Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr Pro Leu Leu His  
195 200 205  
Gln Ser Thr Asp Asn Val  
210

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aattcgaaga gagttctagc aaaacaaaac aaacagagc aaacagagta agtgaaacga   | 60  |
| tgtctctagt tccgagcttt tttggaggcc gaagaacaaa cgtgttcgac ccattttcac  | 120 |
| tagacgtatg ggatccgttc gaaggattct tgacgcccgg gttgacaaac gcacctgcca  | 180 |
| aggacgtggc agcgttcaca aacgctaagg tggactggag ggagacacct gaagcgcatg  | 240 |
| tggtcaaggc ggacgtgcct gggcttaaga aggaagaggt gaaggtggag gttgaagatg  | 300 |
| gtaacatact tcagataagc ggtgagagga gcagtgagaa tgaagagaag agtgacacat  | 360 |
| ggcaccgtgt ggagcgggtca agtggaaagt tcatgaggag gtttaggttg ccagacaatg | 420 |
| caaaggtgga ggaagtaaag gcgagtatgg agaatggtgt gttgtcggtt acggtgccga  | 480 |
| aagttcagga gagtaagccg gaggtcaagt ccattgatat ctctggttaa gaggaactct  | 540 |
| gaagttggaa agcttaagac agtaatatgt gatagtgtga aataaatggt gcgactttcc  | 600 |
| ttcc                                                               |     |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

(2) INFORMATION FOR SEQ ID NO:285:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1566445

(xi) SEQUENCE DESCRIPTION: SEO ID NO:285:

(2) INFORMATION FOR SEQ ID NO:286:

(A) LENGTH: 1325 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaCttctcct  | cggatgcaact | attgtccgtg  | agatcagaga  | ttcacccctct | ttagatttttg | 60   |
| cgcagaaact  | tttgcccaca  | atthttgtttt | ctacaaatct  | gagctgagat  | ctctagagtg  | 120  |
| agaaaatgag  | catcactaat  | gaagaagcag  | tgaagcaatt  | gcgtgcttta  | atggaagatg  | 180  |
| ttgatgatgc  | actcagagag  | tcgtatcgga  | acattcatca  | agggtatccg  | acagagaatt  | 240  |
| tgttacgctt  | tcttaaagcc  | agggatggga  | atgtccagaa  | agctcataaa  | atgttgctcg  | 300  |
| agtgtttgga  | atggaggact  | caaaacgaga  | ttgacaagat  | actaactaaa  | cccattgttc  | 360  |
| ctgttgacct  | gtacagagga  | atcagagaca  | cacaacttgt  | cgggtgtgtct | ggttactcta  | 420  |
| aagagggctc  | ccctgtcatt  | gccattgggtg | tggggcttag  | cacatatgat  | aaagcctccg  | 480  |
| ttcactacta  | tgtacagtct  | cacattcaaa  | tgaatgagta  | ccgggatcgt  | gttgatttgc  | 540  |
| catctgcttc  | aaagaaacag  | ggacgaccaa  | tttgactctg  | tttgaaaatt  | ttggatatgt  | 600  |
| ctggtttaaa  | gctttcagct  | ttaagtcaaa  | ttaagttaat  | gactgctata  | acaacaatag  | 660  |
| atgatttgaa  | ctatccagag  | aagacagaga  | catactatgt  | tgtcaatgtc  | ccgtacatat  | 720  |
| tctctgcttg  | ttggaaaacc  | ataaagcctc  | tgttgcaaga  | gagaacaaag  | aagaagattc  | 780  |
| aagttctgaa  | aggttgcggg  | aaagatgagt  | tgctaaagat  | aatggactat  | gagtcctccc  | 840  |
| cacattttctg | tagaagagaa  | gggtctggat  | ctggtaggca  | tatctcaaat  | ggaacagtag  | 900  |
| acaattgttt  | ctctctggat  | cactctttcc  | accaagacct  | ttatgattat  | gtcaagcagc  | 960  |
| aggctctggg  | taaaggatca  | ggtgcaccga  | tcagacatgg  | ttcagtcac   | gttaagtctc  | 1020 |
| ctgagccaga  | caccgaaggc  | aacaagatct  | tcgatacctt  | agaaaatgag  | ttccagaagc  | 1080 |
| ttggaaatga  | ccagaagatc  | tgagtgatct  | acaaccctta  | taacacgaat  | tgcccataag  | 1140 |
| aaaccggaat  | ttgtctctgg  | ttgatgagca  | gtattttaaga | taagaatcaa  | tcacctttac  | 1200 |
| ttgtattact  | agtttcgctt  | gcacagctc   | gatgcagggt  | ttttttaaaa  | agaagatgga  | 1260 |
| acacaatttc  | ctcggaatgg  | atcttttgat  | ctagtaccat  | tatatatata  | gaactcattt  | 1320 |
| ctatc       |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Thr | Asn | Glu | Glu | Ala | Val | Lys | Gln | Leu | Arg | Ala | Leu | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Val | Asp | Asp | Ser | Leu | Arg | Glu | Ser | Tyr | Arg | Asn | Ile | His | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Tyr | Pro | Thr | Glu | Asn | Leu | Leu | Arg | Phe | Leu | Lys | Ala | Arg | Asp | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Val | Gln | Lys | Ala | His | Lys | Met | Leu | Leu | Glu | Cys | Leu | Glu | Trp | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gln | Asn | Glu | Ile | Asp | Lys | Ile | Leu | Thr | Lys | Pro | Ile | Val | Pro | Val |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Leu | Tyr | Arg | Gly | Ile | Arg | Asp | Thr | Gln | Leu | Val | Gly | Val | Ser | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Tyr | Ser | Lys | Glu | Gly | Leu | Pro | Val | Ile | Ala | Ile | Gly | Val | Gly | Leu | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Tyr | Asp | Lys | Ala | Ser | Val | His | Tyr | Tyr | Val | Gln | Ser | His | Ile | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Met | Asn | Glu | Tyr | Arg | Asp | Arg | Val | Val | Leu | Pro | Ser | Ala | Ser | Lys | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Gly | Arg | Pro | Ile | Cys | Thr | Cys | Leu | Lys | Ile | Leu | Asp | Met | Ser | Gly |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Lys | Leu | Ser | Ala | Leu | Ser | Gln | Ile | Lys | Leu | Met | Thr | Ala | Ile | Thr |

165 170 175  
Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr Glu Thr Tyr Tyr Val  
180 185 190  
Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp Lys Thr Ile Lys Pro  
195 200 205  
Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln Val Leu Lys Gly Cys  
210 215 220  
Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr Glu Ser Leu Pro His  
225 230 235 240  
Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg His Ile Ser Asn Gly  
245 250 255  
Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser Phe His Gln Asp Leu  
260 265 270  
Tyr Asp Tyr Val Lys Gln Gln Ala Leu Val Lys Gly Ser Gly Ala Pro  
275 280 285  
Ile Arg His Gly Ser Val His Val Lys Phe Pro Glu Pro Asp Thr Glu  
290 295 300  
Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu Phe Gln Lys Leu Gly  
305 310 315 320  
Asn Asp Gln Lys Ile  
325

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1566455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Glu Asp Val Asp Asp Ser Leu Arg Glu Ser Tyr Arg Asn Ile His  
1 5 10 15  
Gln Gly Tyr Pro Thr Glu Asn Leu Leu Arg Phe Leu Lys Ala Arg Asp  
20 25 30  
Gly Asn Val Gln Lys Ala His Lys Met Leu Leu Glu Cys Leu Glu Trp  
35 40 45  
Arg Thr Gln Asn Glu Ile Asp Lys Ile Leu Thr Lys Pro Ile Val Pro  
50 55 60  
Val Asp Leu Tyr Arg Gly Ile Arg Asp Thr Gln Leu Val Gly Val Ser  
65 70 75 80  
Gly Tyr Ser Lys Glu Gly Leu Pro Val Ile Ala Ile Gly Val Gly Leu  
85 90 95  
Ser Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile  
100 105 110  
Gln Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys  
115 120 125  
Lys Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser  
130 135 140  
Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile  
145 150 155 160  
Thr Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr Glu Thr Tyr Tyr  
165 170 175  
Val Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp Lys Thr Ile Lys  
180 185 190  
Pro Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln Val Leu Lys Gly  
195 200 205  
Cys Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr Glu Ser Leu Pro  
210 215 220

His Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg His Ile Ser Asn  
225 230 235 240  
Gly Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser Phe His Gln Asp  
245 250 255  
Leu Tyr Asp Tyr Val Lys Gln Gln Ala Leu Val Lys Gly Ser Gly Ala  
260 265 270  
Pro Ile Arg His Gly Ser Val His Val Lys Phe Pro Glu Pro Asp Thr  
275 280 285  
Glu Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu Phe Gln Lys Leu  
290 295 300  
Gly Asn Asp Gln Lys Ile  
305 310

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1566456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Leu Leu Glu Cys Leu Glu Trp Arg Thr Gln Asn Glu Ile Asp Lys  
1 5 10 15  
Ile Leu Thr Lys Pro Ile Val Pro Val Asp Leu Tyr Arg Gly Ile Arg  
20 25 30  
Asp Thr Gln Leu Val Gly Val Ser Gly Tyr Ser Lys Glu Gly Leu Pro  
35 40 45  
Val Ile Ala Ile Gly Val Gly Leu Ser Thr Tyr Asp Lys Ala Ser Val  
50 55 60  
His Tyr Tyr Val Gln Ser His Ile Gln Met Asn Glu Tyr Arg Asp Arg  
65 70 75 80  
Val Val Leu Pro Ser Ala Ser Lys Lys Gln Gly Arg Pro Ile Cys Thr  
85 90 95  
Cys Leu Lys Ile Leu Asp Met Ser Gly Leu Lys Leu Ser Ala Leu Ser  
100 105 110  
Gln Ile Lys Leu Met Thr Ala Ile Thr Thr Ile Asp Asp Leu Asn Tyr  
115 120 125  
Pro Glu Lys Thr Glu Thr Tyr Tyr Val Val Asn Val Pro Tyr Ile Phe  
130 135 140  
Ser Ala Cys Trp Lys Thr Ile Lys Pro Leu Leu Gln Glu Arg Thr Lys  
145 150 155 160  
Lys Lys Ile Gln Val Leu Lys Gly Cys Gly Lys Asp Glu Leu Leu Lys  
165 170 175  
Ile Met Asp Tyr Glu Ser Leu Pro His Phe Cys Arg Arg Glu Gly Ser  
180 185 190  
Gly Ser Gly Arg His Ile Ser Asn Gly Thr Val Asp Asn Cys Phe Ser  
195 200 205  
Leu Asp His Ser Phe His Gln Asp Leu Tyr Asp Tyr Val Lys Gln Gln  
210 215 220  
Ala Leu Val Lys Gly Ser Gly Ala Pro Ile Arg His Gly Ser Val His  
225 230 235 240  
Val Lys Phe Pro Glu Pro Asp Thr Glu Gly Asn Lys Ile Phe Asp Thr  
245 250 255  
Leu Glu Asn Glu Phe Gln Lys Leu Gly Asn Asp Gln Lys Ile  
260 265 270

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1767 base pairs

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1767  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566468  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

ctatctttct ttctccctct gctcttgatcc aacttgatcc gtcgtcttct ctcagctctc 60  
catctccgtc ttccaaggta gaagaatcca tgtcgattta cgtcgcgtcg cgaCggNctc 120  
tccggcggaa caactgtgac ggcgtgctgt tatgccacct ctctgagatc ttattcgacc 180  
tcgtttTagg gaggagaggg acaccttcgg gccgattcaa gttccttcog ataaattgtg 240  
gggagcccag acgcagagat cgctgcagaa cttcgaaatc ggtgggtgagc gcgagCGaNa 300  
tgctgaacc aattgtccgc gcttttggcg tcttgaagaa atgcgtgccc aagggttaaca 360  
tggaatacgg tcttgatccg acgattggga aagcaattat gcaagctgct caggaagtag 420  
ctgagggaaa gctcaatgat catttcccc ttgttgtctg gcaaactggt agtgggtactc 480  
agagtaatat gaatgctaata gaggtcattg ctaatagagc agctgagatt cttgggtcgca 540  
aacgtggtga gaaatgtgtg caccctaatg accatgtgaa cagatcaca tcttctaaccg 600  
acacttttcc taccgtcatg cacattgcag ctgcaaccga gattaattcg aggctcatcc 660  
ctagtttaaaa aactttgcat agcactttgg aatctaagtc cttcgagttc aaagatattg 720  
tgaaaattgg aagaactcac actcaagatg ctacaccttt gacactagga caagaatttg 780  
gtggctatgc tactcaagtt aagtatggac taaatagagt cacctgcact cttcctcgcc 840  
tctatcagct tgcacaaggt ggaactgcgg ttgggacagg attaaacact aagaaaggggt 900  
ttgatgtaaa gatagctgct gcagtagctg aagaaacaaa cttgccattt gtcactgcag 960  
aaaacaagtt tgaagctctg gctgcacacg atgcttgtgt tgaaaccagt gggtcactta 1020  
acacaatcgc cacatcgctg atgaagatcg ccaatgatat acgttttctt ggaagtggcc 1080  
caagatgtgg tcttggtgaa cttgtactac ctgaaaatga gccaggaagc agtatcatgc 1140  
ctgggaaggt aaatcctaca cagtgtgagg ccttgactat ggtttgtgca cagggttatgg 1200  
gaaaccatgt agctgtgaca gttggtgggt caaatgggtc tttogaattg aatgtattca 1260  
agccggtgat cgcgagtgc cttttacatt ccgtcagatt aatagcagat gcttcagctt 1320  
cgttcgagaa aaactgtgtg aggggcattg aggccaaacag agaaagaatc tcaaagctat 1380  
tgcacgagtc tcttatgctt gtgacatcat tgaatccgaa aatcgggtat gacaatgctg 1440  
cagcagttgc caagaaagct cacaagaag gatgtacatt gaaggaagcg gctctgaatt 1500  
taggcgtgct tactgcggaa gagtttgata cacttgttgt tcttgagaag atgattggtc 1560  
cctccgattg atagttgttt ttggagccaa agcttcaagt accattattc ttctgatgct 1620  
tttatttagg ttataataaa aatgagcaaa tccagaaaca attcaaattt tcttgggagg 1680  
gcaacattgt tcttcatctt acggctaaac tatgatcttc tttatgtatc aatttttttt 1740  
ttgtgtgaa taagagagtg agtactc

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 522 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..522  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Ile Phe Leu Ser Pro Ser Ala Leu Val Gln Leu Asp Pro Ser Ser Ser  
1 5 10 15  
Leu Ser Ser Pro Ser Pro Ser Ser Lys Val Glu Glu Ser Met Ser Ile  
20 25 30  
Tyr Val Ala Ser Arg Arg Xaa Leu Arg Arg Asn Asn Cys Asp Gly Ala  
35 40 45  
Ala Leu Cys His Leu Ser Glu Ile Leu Phe Asp Leu Val Leu Gly Arg  
50 55 60  
Arg Gly Thr Pro Ser Gly Arg Phe Lys Phe Leu Pro Ile Asn Cys Gly  
65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Arg | Arg | Arg | Asp | Arg | Cys | Arg | Thr | Ser | Lys | Ser | Val | Val | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Xaa | Met | Pro | Glu | Pro | Ile | Val | Arg | Ala | Phe | Gly | Val | Leu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Cys | Ala | Ala | Lys | Val | Asn | Met | Glu | Tyr | Gly | Leu | Asp | Pro | Thr | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Lys | Ala | Ile | Met | Gln | Ala | Ala | Gln | Glu | Val | Ala | Glu | Gly | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Asp | His | Phe | Pro | Leu | Val | Val | Trp | Gln | Thr | Gly | Ser | Gly | Thr | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Asn | Met | Asn | Ala | Asn | Glu | Val | Ile | Ala | Asn | Arg | Ala | Ala | Glu | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Gly | Arg | Lys | Arg | Gly | Glu | Lys | Cys | Val | His | Pro | Asn | Asp | His | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Arg | Ser | Gln | Ser | Ser | Asn | Asp | Thr | Phe | Pro | Thr | Val | Met | His | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Ala | Ala | Thr | Glu | Ile | Asn | Ser | Arg | Leu | Ile | Pro | Ser | Leu | Lys | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | His | Ser | Thr | Leu | Glu | Ser | Lys | Ser | Phe | Glu | Phe | Lys | Asp | Ile | Val |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Ile | Gly | Arg | Thr | His | Thr | Gln | Asp | Ala | Thr | Pro | Leu | Thr | Leu | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Glu | Phe | Gly | Gly | Tyr | Ala | Thr | Gln | Val | Lys | Tyr | Gly | Leu | Asn | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Thr | Cys | Thr | Leu | Pro | Arg | Leu | Tyr | Gln | Leu | Ala | Gln | Gly | Gly | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Val | Gly | Thr | Gly | Leu | Asn | Thr | Lys | Lys | Gly | Phe | Asp | Val | Lys | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Ala | Ala | Val | Ala | Glu | Glu | Thr | Asn | Leu | Pro | Phe | Val | Thr | Ala | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Lys | Phe | Glu | Ala | Leu | Ala | Ala | His | Asp | Ala | Cys | Val | Glu | Thr | Ser |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Ser | Leu | Asn | Thr | Ile | Ala | Thr | Ser | Leu | Met | Lys | Ile | Ala | Asn | Asp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Arg | Phe | Leu | Gly | Ser | Gly | Pro | Arg | Cys | Gly | Leu | Gly | Glu | Leu | Val |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Pro | Glu | Asn | Glu | Pro | Gly | Ser | Ser | Ile | Met | Pro | Gly | Lys | Val | Asn |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Pro | Thr | Gln | Cys | Glu | Ala | Leu | Thr | Met | Val | Cys | Ala | Gln | Val | Met | Gly |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |
| Asn | His | Val | Ala | Val | Thr | Val | Gly | Gly | Ser | Asn | Gly | His | Phe | Glu | Leu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asn | Val | Phe | Lys | Pro | Val | Ile | Ala | Ser | Ala | Leu | Leu | His | Ser | Val | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | Ile | Ala | Asp |     |     |     |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..493  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566470  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ile | Tyr | Val | Ala | Ser | Arg | Arg | Xaa | Leu | Arg | Arg | Asn | Asn | Cys | 1   | 5   | 10  | 15  |
| Asp | Gly | Ala | Ala | Leu | Cys | His | Leu | Ser | Glu | Ile | Leu | Phe | Asp | Leu | Val | 20  | 25  | 30  |     |
| Leu | Gly | Arg | Arg | Gly | Thr | Pro | Ser | Gly | Arg | Phe | Lys | Phe | Leu | Pro | Ile | 35  | 40  | 45  |     |
| Asn | Cys | Gly | Glu | Pro | Arg | Arg | Arg | Asp | Arg | Cys | Arg | Thr | Ser | Lys | Ser | 50  | 55  | 60  |     |
| Val | Val | Ser | Ala | Ser | Xaa | Met | Pro | Glu | Pro | Ile | Val | Arg | Ala | Phe | Gly | 65  | 70  | 75  | 80  |
| Val | Leu | Lys | Lys | Cys | Ala | Ala | Lys | Val | Asn | Met | Glu | Tyr | Gly | Leu | Asp | 85  | 90  | 95  |     |
| Pro | Thr | Ile | Gly | Lys | Ala | Ile | Met | Gln | Ala | Ala | Gln | Glu | Val | Ala | Glu | 100 | 105 | 110 |     |
| Gly | Lys | Leu | Asn | Asp | His | Phe | Pro | Leu | Val | Val | Trp | Gln | Thr | Gly | Ser | 115 | 120 | 125 |     |
| Gly | Thr | Gln | Ser | Asn | Met | Asn | Ala | Asn | Glu | Val | Ile | Ala | Asn | Arg | Ala | 130 | 135 | 140 |     |
| Ala | Glu | Ile | Leu | Gly | Arg | Lys | Arg | Gly | Glu | Lys | Cys | Val | His | Pro | Asn | 145 | 150 | 155 | 160 |
| Asp | His | Val | Asn | Arg | Ser | Gln | Ser | Ser | Asn | Asp | Thr | Phe | Pro | Thr | Val | 165 | 170 | 175 |     |
| Met | His | Ile | Ala | Ala | Ala | Thr | Glu | Ile | Asn | Ser | Arg | Leu | Ile | Pro | Ser | 180 | 185 | 190 |     |
| Leu | Lys | Thr | Leu | His | Ser | Thr | Leu | Glu | Ser | Lys | Ser | Phe | Glu | Phe | Lys | 195 | 200 | 205 |     |
| Asp | Ile | Val | Lys | Ile | Gly | Arg | Thr | His | Thr | Gln | Asp | Ala | Thr | Pro | Leu | 210 | 215 | 220 |     |
| Thr | Leu | Gly | Gln | Glu | Phe | Gly | Gly | Tyr | Ala | Thr | Gln | Val | Lys | Tyr | Gly | 225 | 230 | 235 | 240 |
| Leu | Asn | Arg | Val | Thr | Cys | Thr | Leu | Pro | Arg | Leu | Tyr | Gln | Leu | Ala | Gln | 245 | 250 | 255 |     |
| Gly | Gly | Thr | Ala | Val | Gly | Thr | Gly | Leu | Asn | Thr | Lys | Lys | Gly | Phe | Asp | 260 | 265 | 270 |     |
| Val | Lys | Ile | Ala | Ala | Ala | Val | Ala | Glu | Glu | Thr | Asn | Leu | Pro | Phe | Val | 275 | 280 | 285 |     |
| Thr | Ala | Glu | Asn | Lys | Phe | Glu | Ala | Leu | Ala | Ala | His | Asp | Ala | Cys | Val | 290 | 295 | 300 |     |
| Glu | Thr | Ser | Gly | Ser | Leu | Asn | Thr | Ile | Ala | Thr | Ser | Leu | Met | Lys | Ile | 305 | 310 | 315 | 320 |
| Ala | Asn | Asp | Ile | Arg | Phe | Leu | Gly | Ser | Gly | Pro | Arg | Cys | Gly | Leu | Gly | 325 | 330 | 335 |     |
| Glu | Leu | Val | Leu | Pro | Glu | Asn | Glu | Pro | Gly | Ser | Ser | Ile | Met | Pro | Gly | 340 | 345 | 350 |     |
| Lys | Val | Asn | Pro | Thr | Gln | Cys | Glu | Ala | Leu | Thr | Met | Val | Cys | Ala | Gln | 355 | 360 | 365 |     |
| Val | Met | Gly | Asn | His | Val | Ala | Val | Thr | Val | Gly | Gly | Ser | Asn | Gly | His | 370 | 375 | 380 |     |
| Phe | Glu | Leu | Asn | Val | Phe | Lys | Pro | Val | Ile | Ala | Ser | Ala | Leu | Leu | His | 385 | 390 | 395 | 400 |
| Ser | Val | Arg | Leu | Ile | Ala | Asp | Ala | Ser | Ala | Ser | Phe | Glu | Lys | Asn | Cys | 405 | 410 | 415 |     |
| Val | Arg | Gly | Ile | Glu | Ala | Asn | Arg | Glu | Arg | Ile | Ser | Lys | Leu | Leu | His | 420 | 425 | 430 |     |

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(2) INFORMATION FOR SEQ ID NO:293:

(A) LENGTH: 423 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1566471

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |           |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|-----|
| Met<br>1   | Pro        | Glu        | Pro        | Ile<br>5   | Val        | Arg        | Ala        | Phe        | Gly<br>10  | Val        | Leu        | Lys        | Lys        | Cys<br>15 | Ala |
| Ala        | Lys        | Val        | Asn<br>20  | Met        | Glu        | Tyr        | Gly        | Leu<br>25  | Asp        | Pro        | Thr        | Ile        | Gly<br>30  | Lys       | Ala |
| Ile        | Met        | Gln<br>35  | Ala        | Ala        | Gln        | Glu        | Val<br>40  | Ala        | Glu        | Gly        | Lys        | Leu<br>45  | Asn        | Asp       | His |
| Phe        | Pro<br>50  | Leu        | Val        | Val        | Trp        | Gln<br>55  | Thr        | Gly        | Ser        | Gly        | Thr<br>60  | Gln        | Ser        | Asn       | Met |
| Asn<br>65  | Ala        | Asn        | Glu        | Val        | Ile<br>70  | Ala        | Asn        | Arg        | Ala        | Ala<br>75  | Glu        | Ile        | Leu        | Gly       | Arg |
| Lys        | Arg        | Gly        | Glu        | Lys<br>85  | Cys        | Val        | His        | Pro        | Asn<br>90  | Asp        | His        | Val        | Asn<br>95  | Arg       | Ser |
| Gln        | Ser        | Ser        | Asn<br>100 | Asp        | Thr        | Phe        | Pro        | Thr<br>105 | Val        | Met        | His        | Ile<br>110 | Ala        | Ala       | Ala |
| Thr        | Glu        | Ile<br>115 | Asn        | Ser        | Arg        | Leu        | Ile<br>120 | Pro        | Ser        | Leu        | Lys        | Thr<br>125 | Leu        | His       | Ser |
| Thr        | Leu<br>130 | Glu        | Ser        | Lys        | Ser        | Phe<br>135 | Glu        | Phe        | Lys        | Asp        | Ile<br>140 | Val        | Lys        | Ile       | Gly |
| Arg<br>145 | Thr        | His        | Thr        | Gln<br>150 | Asp        | Ala        | Thr        | Pro        | Leu        | Thr<br>155 | Leu        | Gly        | Gln        | Glu       | Phe |
| Gly        | Gly        | Tyr        | Ala<br>165 | Thr        | Gln        | Val        | Lys        | Tyr        | Gly<br>170 | Leu        | Asn        | Arg        | Val<br>175 | Thr       | Cys |
| Thr        | Leu        | Pro        | Arg<br>180 | Leu        | Tyr        | Gln        | Leu<br>185 | Ala        | Gln        | Gly        | Gly        | Thr<br>190 | Ala        | Val       | Gly |
| Thr        | Gly        | Leu<br>195 | Asn        | Thr        | Lys        | Lys        | Gly<br>200 | Phe        | Asp        | Val        | Lys        | Ile<br>205 | Ala        | Ala       | Ala |
| Val        | Ala<br>210 | Glu        | Glu        | Thr        | Asn<br>215 | Leu        | Pro        | Phe        | Val        | Thr<br>220 | Ala        | Glu        | Asn        | Lys       | Phe |
| Glu<br>225 | Ala        | Leu        | Ala        | Ala<br>230 | His        | Asp        | Ala        | Cys        | Val        | Glu<br>235 | Thr        | Ser        | Gly        | Ser       | Leu |
| Asn        | Thr        | Ile        | Ala<br>245 | Thr        | Ser        | Leu        | Met        | Lys        | Ile<br>250 | Ala        | Asn        | Asp        | Ile<br>255 | Arg       | Phe |
| Leu        | Gly        | Ser        | Gly<br>260 | Pro        | Arg        | Cys        | Gly<br>265 | Leu        | Gly        | Glu        | Leu        | Val<br>270 | Leu        | Pro       | Glu |
| Asn        | Glu        | Pro        | Gly<br>275 | Ser        | Ser        | Ile        | Met<br>280 | Pro        | Gly        | Lys        | Val        | Asn<br>285 | Pro        | Thr       | Gln |
| Cys        | Glu<br>290 | Ala        | Leu        | Thr        | Met<br>295 | Val        | Cys        | Ala        | Gln        | Val        | Met<br>300 | Gly        | Asn        | His       | Val |
| Ala<br>305 | Val        | Thr        | Val        | Gly<br>310 | Gly        | Ser        | Asn        | Gly        | His<br>315 | Phe        | Glu        | Leu        | Asn        | Val       | Phe |
| Lys        | Pro        | Val        | Ile        | Ala        | Ser        | Ala        | Leu        | Leu        | His        | Ser        | Val        | Arg        | Leu        | Ile       | Ala |

325 330 335  
Asp Ala Ser Ala Ser Phe Glu Lys Asn Cys Val Arg Gly Ile Glu Ala  
340 345 350  
Asn Arg Glu Arg Ile Ser Lys Leu Leu His Glu Ser Leu Met Leu Val  
355 360 365  
Thr Ser Leu Asn Pro Lys Ile Gly Tyr Asp Asn Ala Ala Ala Val Ala  
370 375 380  
Lys Lys Ala His Lys Glu Gly Cys Thr Leu Lys Glu Ala Ala Leu Asn  
385 390 395 400  
Leu Gly Val Leu Thr Ala Glu Glu Phe Asp Thr Leu Val Val Pro Glu  
405 410 415  
Lys Met Ile Gly Pro Ser Asp  
420

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

aacaattcag atttcaattt ctcaaaatct taaaaacttt ctctcaattc tctctaccgt 60  
gatcaagatg cagatctttg ttaagactct caccggaaag acaatcacc tcgagggtga 120  
aagctccgac accatcgaca acgttaaggc caagatccag gataaggagg gcattcctcc 180  
ggatcagcag aggcttattt tcgccggcaa gcagctagag gatggccgta cgttggtgta 240  
ttacaatatc cagaaggaat ccacctcca cttggtcctc aggtcccggt gtggtatgca 300  
gattttcggtt aaaaccctaa cgggaaagac gattactctt gaggtggaga gttctgacac 360  
catcgacaac gtcaaggcca agatccaaga caaagagggt attcctccgg accagcagag 420  
gctgatcttc gccggaaagc agttggagga tggcagaact cttGgctgac tacaayatyc 480  
agaaggagtc cactcttcaT cttgktctTG cAgkctscgt ggwggtatgc agatyttcgt 540  
kaagactctc acyggaaaga ccatcacttt ggagggtggag agttctgaca ccattgataa 600  
cgtgaaagcc aagatccagg acaaagagggt tatycctccg gaccagcaga gattgatctt 660  
cgccggaaaag caacttgarg atgghagaac tttggcbgac tacaacattc agaaggagtc 720  
cacmcttcac ttggtcttgc gtctgcgtgg aggtatgcag atcttcgtsa agactybac 780  
cggaagacy atcacyytkg argtrgarag ctcygacacc attgacaacg tcaaggccaa 840  
gatccaggac aaggaaggta ttccctccgga ccagcagcgt ctcatcttcg ctggaaagca 900  
gcttgaggat ggacgtactt tggccgacta caacatccag aaggagtcta ctcttcactt 960  
ggtcctgcgt cttcgtggtg gtttctaaat ctogtctctg ttatgcttaa gaagttcaat 1020  
gtttcgtttc atgtaaaact ttggtggttt gtgttttggg gccttgata atccctgatg 1080  
aataagtgtt ctactatggt tccggt

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Thr Ile Gln Ile Ser Ile Ser Gln Asn Leu Lys Asn Phe Leu Ser Ile  
1 5 10 15  
Leu Ser Thr Val Ile Lys Met Gln Ile Phe Val Lys Thr Leu Thr Gly  
20 25 30  
Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val

35 40 45  
Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg  
50 55 60  
Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp  
65 70 75 80  
Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg  
85 90 95  
Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr  
100 105 110  
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile  
115 120 125  
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala  
130 135 140  
Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1566507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe  
65 70 75 80  
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile  
100 105 110  
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
115 120 125  
Gly Arg Thr Leu Gly  
130

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1566508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Gln Xaa Phe Xaa Lys Thr Leu Xaa Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30

Lys Glu Gly Xaa Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Xaa Asp Xaa Arg Thr Leu Xaa Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Xaa Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
65 70 75 80  
Xaa Lys Thr Xaa Thr Gly Lys Xaa Ile Xaa Xaa Xaa Xaa Xaa Ser Xaa  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile  
100 105 110  
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
115 120 125  
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
130 135 140  
Leu Val Leu Arg Leu Arg Gly Gly Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atcttatctc aactctcaaa atcatcttct tcacccaaaa acccctaaaa gccttatccc  | 60   |
| ttcttcttcc catggctgct tcagctctct tctcgctctc tcttccttca accctaaatc  | 120  |
| tcttcctttc ggcgtctcca gacctgctc cgtttccctc ttatctcctt ccctctcctt   | 180  |
| taaaactcaat tccgactccg ttctcttctc catcgccgcc aaatggaact ctcccgtctc | 240  |
| tcgcttcgtc cgtaacgttg cgattacctc agagtctcag gtggaagaag atggtttcgc  | 300  |
| tgacgtcgct ccgccaaaag agcaatcttt ctctgctgac cttaaactct tcggttgtaa  | 360  |
| ccttcctttc aacgttgaca gtgctcagct cgctcagctc ttgagagtg ccggaatgt    | 420  |
| tgagatgggt gagtaatct atgacaaaat tacaggaaga agcagagggt ttggattcgt   | 480  |
| gactatgtct tcagtttctg aagttgaggc agctgctcag cagttcaatg gctatgagtt  | 540  |
| ggatggtaga cctttgagag tcaatgctgg tccccacca ccaaagaggg aagatggttt   | 600  |
| ctccagagga cctaggagca gctttggaag ctccaggttct ggatatggag gaggtggttg | 660  |
| ttctggtgct ggttcaggaa accgtgttta tgtgggtaac ctctcttggg gagttgatga  | 720  |
| catggctctt gagagtttgt tctcggagca aggaaagggt gttgaggcca gagtcattcta | 780  |
| cgacagggac agtggctgat ccaagggttt tggatttggt acatacgact cttctcaaga  | 840  |
| ggtccaaaat gccatcaagt ccttggtatg tgctgatttg gacggtagac aaattagagt  | 900  |
| ctcggaagct gaggctaggc ctccaaggcg ccaatattga gcaccaatct atgacttcct  | 960  |
| attctcaaaa acgcatattc tggagggcgc ttcgaagtaa agagggtttg tgagatgatg  | 1020 |
| gcagtttcag acggtactaa gctcttagct tcgcctatgt ttgttgctt ggatgcaaga   | 1080 |
| aggctcgtaaa ggaatggtct tttttttttt gagaaacgta taattaagat agaaactgga | 1140 |
| gagaccatgt tcttgtctgt ctgaatgctg ccattgactg Cttcgctttg gttttgattc  | 1200 |
| aatttttttt tctctcc                                                 |      |

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

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Ser Tyr Leu Asn Ser Gln Asn His Leu Leu His Pro Lys Thr Pro Lys  
1 5 10 15  
Ser Leu Ile Pro Ser Ser Ser His Gly Cys Phe Ser Ser Ser Leu Ala  
20 25 30  
Leu Ser Ser Phe Asn Pro Lys Ser Leu Pro Phe Gly Val Ser Arg Pro  
35 40 45  
Ala Ser Val Ser Leu Leu Ser Pro Ser Leu Ser Phe Lys Leu Asn Ser  
50 55 60  
Asp Ser Val Ser Phe Ser Ile Ala Ala Lys Trp Asn Ser Pro Ala Ser  
65 70 75 80  
Arg Phe Val Arg Asn Val Ala Ile Thr Ser Glu Phe Glu Val Glu Glu  
85 90 95  
Asp Gly Phe Ala Asp Val Ala Pro Pro Lys Glu Gln Ser Phe Ser Ala  
100 105 110  
Asp Leu Lys Leu Phe Val Gly Asn Leu Pro Phe Asn Val Asp Ser Ala  
115 120 125  
Gln Leu Ala Gln Leu Phe Glu Ser Ala Gly Asn Val Glu Met Val Glu  
130 135 140  
Val Ile Tyr Asp Lys Ile Thr Gly Arg Ser Arg Gly Phe Gly Phe Val  
145 150 155 160  
Thr Met Ser Ser Val Ser Glu Val Glu Ala Ala Gln Gln Phe Asn  
165 170 175  
Gly Tyr Glu Leu Asp Gly Arg Pro Leu Arg Val Asn Ala Gly Pro Pro  
180 185 190  
Pro Pro Lys Arg Glu Asp Gly Phe Ser Arg Gly Pro Arg Ser Ser Phe  
195 200 205  
Gly Ser Ser Gly Ser Gly Tyr Gly Gly Gly Gly Gly Ser Gly Ala Gly  
210 215 220  
Ser Gly Asn Arg Val Tyr Val Gly Asn Leu Ser Trp Gly Val Asp Asp  
225 230 235 240  
Met Ala Leu Glu Ser Leu Phe Ser Glu Gln Gly Lys Val Val Glu Ala  
245 250 255  
Arg Val Ile Tyr Asp Arg Asp Ser Gly Arg Ser Lys Gly Phe Gly Phe  
260 265 270  
Val Thr Tyr Asp Ser Ser Gln Glu Val Gln Asn Ala Ile Lys Ser Leu  
275 280 285  
Asp Gly Ala Asp Leu Asp Gly Arg Gln Ile Arg Val Ser Glu Ala Glu  
290 295 300  
Ala Arg Pro Pro Arg Arg Gln Tyr  
305 310

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1566519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Val Glu Val Ile Tyr Asp Lys Ile Thr Gly Arg Ser Arg Gly Phe  
1 5 10 15  
Gly Phe Val Thr Met Ser Ser Val Ser Glu Val Glu Ala Ala Ala Gln  
20 25 30  
Gln Phe Asn Gly Tyr Glu Leu Asp Gly Arg Pro Leu Arg Val Asn Ala  
35 40 45  
Gly Pro Pro Pro Pro Lys Arg Glu Asp Gly Phe Ser Arg Gly Pro Arg  
50 55 60  
Ser Ser Phe Gly Ser Ser Gly Ser Gly Tyr Gly Gly Gly Gly Ser

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO:301:

(A) LENGTH: 1082 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1082  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566531

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 |             |             |             |             |             |      |
|--------------------------------------|-------------|-------------|-------------|-------------|-------------|------|
| atttttagagg                          | tttcagatat  | aggcagattc  | tcacatttgc  | aaacatgacg  | actcagatca  | 60   |
| gcaagaagag                           | aaagtttgta  | gcggaagggtg | tggaaccatt  | tgtatgttgc  | aaatgttgga  | 120  |
| gactcgagga                           | caatagtttc  | taaagctggg  | aaagcgatcg  | cgctatctga  | tgaccataag  | 180  |
| ccaaatagaa                           | gcgatgaaag  | aaagcgaatt  | gaaagtgtctg | gtggtgttat  | catgtgggca  | 240  |
| ggaacatgga                           | gagtaggtgg  | gggtgttggt  | atgtcccggg  | cctttgttaa  | cagaatgctg  | 300  |
| aagcaattcg                           | ttgttgctga  | acccgagata  | caagatctag  | agatagatca  | tgaggccgag  | 360  |
| ttgcttgtgc                           | ttgcaagtga  | cggtttatgg  | gatgtgggtac | caaatgagga  | tgcggtaGcc  | 420  |
| cttgctcaga                           | gcgaggaaga  | gcccagggca  | gctgcccgca  | agttaactga  | cactgccttc  | 480  |
| agccgtggca                           | gtgcagacaa  | catcacgtgc  | attgttgtta  | aattccgtca  | tgataagaca  | 540  |
| gaatctccta                           | aaatcgaaac  | aaacgccatg  | gctgaatcgg  | aaacctgaaat | gaacccccaca | 600  |
| actgaactcg                           | aaacccgaatc | aaaccccagt  | actgaaatgg  | aaactgaatc  | aatccccaaa  | 660  |
| gctgaactgg                           | aatccgaacc  | tgatgctata  | cctgatccaa  | aaacctgaaac | cgaaccagag  | 720  |
| accaaggggtg                          | agaaaagctgg | tgagtaaggt  | agcagccggg  | gaaaggtgtc  | catactgttg  | 780  |
| gggacatgtg                           | gaaacagatg  | aatataaaat  | tgcttagtaa  | gttgtgtggt  | ttgtggctac  | 840  |
| ctgtaacgtg                           | tgaggatttg  | tgtttttttg  | ttttgtgttg  | cattcatgca  | catgcctatg  | 900  |
| cctgccttga                           | ggacgacgac  | gacccttttg  | acatgtcccc  | gatttttgtc  | tattcatttt  | 960  |
| accctatttt                           | gtttttgttg  | gtgctactca  | caccaaaaac  | agcacatttg  | ttctctgttt  | 1020 |
| ctcctacttt                           | tttctatctt  | ttatttaaaa  | caccgtccat  | tccaataaac  | aatgtttttg  | 1080 |
| ++                                   |             |             |             |             |             |      |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..171  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566532

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Ala | Gly | Thr | Trp | Arg | Val | Gly | Gly | Val | Leu | Ala | Met | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Phe | Gly | Asn | Arg | Met | Leu | Lys | Gln | Phe | Val | Val | Ala | Glu | Pro | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Asp | Leu | Glu | Ile | Asp | His | Glu | Ala | Glu | Leu | Leu | Val | Leu | Ala |

35 40 45  
Ser Asp Gly Leu Trp Asp Val Val Pro Asn Glu Asp Ala Val Ala Leu  
50 55 60  
Ala Gln Ser Glu Glu Glu Pro Glu Ala Ala Ala Arg Lys Leu Thr Asp  
65 70 75 80  
Thr Ala Phe Ser Arg Gly Ser Ala Asp Asn Ile Thr Cys Ile Val Val  
85 90 95  
Lys Phe Arg His Asp Lys Thr Glu Ser Pro Lys Ile Glu Thr Asn Ala  
100 105 110  
Met Ala Glu Ser Glu Pro Glu Met Asn Pro Thr Thr Glu Leu Glu Pro  
115 120 125  
Glu Ser Asn Pro Ser Thr Glu Met Glu Thr Glu Ser Ile Pro Lys Ala  
130 135 140  
Glu Leu Glu Ser Glu Pro Asp Ala Ile Pro Asp Pro Lys Pro Glu Thr  
145 150 155 160  
Glu Pro Glu Thr Lys Gly Glu Lys Ala Gly Glu  
165 170

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1566533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ser Arg Ala Phe Gly Asn Arg Met Leu Lys Gln Phe Val Val Ala  
1 5 10 15  
Glu Pro Glu Ile Gln Asp Leu Glu Ile Asp His Glu Ala Glu Leu Leu  
20 25 30  
Val Leu Ala Ser Asp Gly Leu Trp Asp Val Val Pro Asn Glu Asp Ala  
35 40 45  
Val Ala Leu Ala Gln Ser Glu Glu Pro Glu Ala Ala Arg Lys  
50 55 60  
Leu Thr Asp Thr Ala Phe Ser Arg Gly Ser Ala Asp Asn Ile Thr Cys  
65 70 75 80  
Ile Val Val Lys Phe Arg His Asp Lys Thr Glu Ser Pro Lys Ile Glu  
85 90 95  
Thr Asn Ala Met Ala Glu Ser Glu Pro Glu Met Asn Pro Thr Thr Glu  
100 105 110  
Leu Glu Pro Glu Ser Asn Pro Ser Thr Glu Met Glu Thr Glu Ser Ile  
115 120 125  
Pro Lys Ala Glu Leu Glu Ser Glu Pro Asp Ala Ile Pro Asp Pro Lys  
130 135 140  
Pro Glu Thr Glu Pro Glu Thr Lys Gly Glu Lys Ala Gly Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1566534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:



Met Leu Lys Gln Phe Val Val Ala Glu Pro Glu Ile Gln Asp Leu Glu  
1 5 10 15  
Ile Asp His Glu Ala Glu Leu Leu Val Leu Ala Ser Asp Gly Leu Trp  
20 25 30  
Asp Val Val Pro Asn Glu Asp Ala Val Ala Leu Ala Gln Ser Glu Glu  
35 40 45  
Glu Pro Glu Ala Ala Ala Arg Lys Leu Thr Asp Thr Ala Phe Ser Arg  
50 55 60  
Gly Ser Ala Asp Asn Ile Thr Cys Ile Val Val Lys Phe Arg His Asp  
65 70 75 80  
Lys Thr Glu Ser Pro Lys Ile Glu Thr Asn Ala Met Ala Glu Ser Glu  
85 90 95  
Pro Glu Met Asn Pro Thr Thr Glu Leu Glu Pro Glu Ser Asn Pro Ser  
100 105 110  
Thr Glu Met Glu Thr Glu Ser Ile Pro Lys Ala Glu Leu Glu Ser Glu  
115 120 125  
Pro Asp Ala Ile Pro Asp Pro Lys Pro Glu Thr Glu Pro Glu Thr Lys  
130 135 140  
Gly Glu Lys Ala Gly Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaaaaaat catttcttct ctgaaacgaa aaaccaaaga aacgagaaga agaagctatg  | 60  |
| gcggatcagc taactgatga acagatctct gagtttaagg aagcttttag cctcttcgac  | 120 |
| aaagatggag atgggttgcac caccacaaag gagctgggaa cagtgatgag gtcactaggg | 180 |
| cagaacccaa cagaagctga gctacaagac atgatcaacg aggttgacgc tgatggaac   | 240 |
| ggaaccattg acttccctga gttctttaaac ctaatggcta aaaagatgaa ggacacagac | 300 |
| tccgaggaag agctgaaaga agctttcagg gtgttcgaca aagaccagaa cggtttcata  | 360 |
| ttcgctgcag aGcttcgcca tgtgatgacg aatctagggt agaaactgac tgatgaagag  | 420 |
| gtcaggagaga tgattcgtga agcagatggt gatggagatg gtcagataaa ctacgaggag | 480 |
| tttgtcaaga ttatgatggc taagtgatga tgataagaaa aaaatgaaga ataaaagtgg  | 540 |
| tgatgtgatg accttttagg cttttactat ctacaaaaga atgattcgac ctttaatgtc  | 600 |
| ttgggtttga tttagacctg gtagtttctt aaggttttaa cagactgaat ttgtgactta  | 660 |
| tcttttttta ttttgttggt ttctttctcg ttggcataat ggcattgtta gatttcggc   |     |

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Ala Asp Gln Leu Thr Asp Glu Gln Ile Ser Glu Phe Lys Glu Ala  
1 5 10 15  
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu  
20 25 30  
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu

35 40 45  
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile  
50 55 60  
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met Lys Asp Thr  
65 70 75 80  
Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp  
85 90 95  
Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn  
100 105 110  
Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met Ile Arg Glu  
115 120 125  
Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys  
130 135 140  
Ile Met Met Ala Lys  
145

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1566555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met  
1 5 10 15  
Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu  
20 25 30  
Phe Leu Asn Leu Met Ala Lys Lys Met Lys Asp Thr Asp Ser Glu Glu  
35 40 45  
Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe  
50 55 60  
Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys  
65 70 75 80  
Leu Thr Asp Glu Glu Val Glu Glu Met Ile Arg Glu Ala Asp Val Asp  
85 90 95  
Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Ile Met Met Ala  
100 105 110  
Lys

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1566556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro  
1 5 10 15  
Glu Phe Leu Asn Leu Met Ala Lys Lys Met Lys Asp Thr Asp Ser Glu  
20 25 30  
Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly  
35 40 45

Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu  
50 55 60  
Lys Leu Thr Asp Glu Glu Val Glu Glu Met Ile Arg Glu Ala Asp Val  
65 70 75 80  
Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Ile Met Met  
85 90 95  
Ala Lys

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1651
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

aagctaagct ctagaacac cgcctttaac gtctcgctgc accatttttc atcgttgatc 60  
agtcgtcgat cctcttgagt gatttgattt tagactttct agttatcaaa ctcgaaagat 120  
ggattctgtc cttgtagtgg gcattgcata gggtattctc ggtgcgttga tcgctgtact 180  
cttcttcggt agctacttcc ggaagcggac atcggagggt caatccatgg ccaaagcgta 240  
gcCtcaggat ccgatccgga atccaaagtc gaatcatcct gctccgaaga agaatcatcc 300  
caaactctcaa gcgtccgata agaatcagaa caaacggcat catccttttag atttaaacac 360  
gttgaaaggc cacgggtgatg ctgttactgg actctgtttc tcgtccgatg gaaagagctt 420  
ggccacagct tgcgctgatg gtttaatcag ggtgttcaag ctatgatgat catcaagcaa 480  
aagcttcaaa tttttaagga taaactcttc tgctggagga catccaaccg ccgtggcatt 540  
tgctgacgat gcctcatcta ttgttggtgc ttgtcatcat atgtctggtt catctttgta 600  
catgtacggg gaagataagc aaaaggatca gcaagggaag ctctctcttc ctagtatcaa 660  
atgggaccac catcatattc atgagaagag atcagtgtct accatctctg gagctactgc 720  
aacttacggg actgctgatg gaagtgttgt cattgctctt tgttctgaag ggactgatat 780  
cgtcctttgg catgggaaaa ctgggaggaa tttgggacat gttgatacaa accagttgaa 840  
gaaccacatg gcagctgtat caccaaatgg acgttttttg gcagctgcag catttactgc 900  
agatgtgaaa gtgtgggaaa ttgtgtatca gaaagatggg tctgtgaaaag aggtttcaag 960  
agttatgcaa cttaaaggcc acaagagtgc agtgacttgg ttatgctttt ctccaaactc 1020  
agagaaaatc atcaccgctt caaaagatgg ttcaataaga gtctggaaca tcaatgtccg 1080  
ttatcatctt gatgaggatc caaagacttt gaagggtgtc ccgattccac tttgcgactc 1140  
aggaggcaat ccgbtgcact atgatcgtct cagcttatgc ccagagggaa agatattggc 1200  
agcaagccat ggttccacat tgcagtgggt atgtgctgaa actggaaatg tcttgacac 1260  
agctgagaaa gccacgaag gggatatcac atgcatactt tgggcaccca aggctattac 1320  
agttggggaa agacatgcc aatgttttgg gacatcaggc Ngatgacaag aaagtgaagc 1380  
tgtgggaagc tccaaagtcg caatctttgt aggtctctgc atacacgtag tcccttgatg 1440  
acatgaggcg tatttaaacg gtacaacttg cgaggaaaaa aactctaata ggttttgttt 1500  
cgagtcccaa gttgggatca aatgaagggt ggtttaaagt ccttcttggt accaagtgtc 1560  
ttttaacttc tgaagttttg aattttgtct ataggactag tacaacactc acagtcttct 1620  
atgttttcca aattaaggaa atttaaaaag c

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ser Gly Ser Ser Leu Tyr Met Tyr Gly Glu Asp Lys Lys Asp

U.S. PAT. & TRADEM. OFF.

1 5 10 15  
Gln Gln Gly Lys Leu Pro Leu Pro Ser Ile Lys Trp Asp His His His  
20 25 30  
Ile His Glu Lys Arg Ser Val Leu Thr Ile Ser Gly Ala Thr Ala Thr  
35 40 45  
Tyr Gly Thr Ala Asp Gly Ser Val Val Ile Ala Ser Cys Ser Glu Gly  
50 55 60  
Thr Asp Ile Val Leu Trp His Gly Lys Thr Gly Arg Asn Leu Gly His  
65 70 75 80  
Val Asp Thr Asn Gln Leu Lys Asn His Met Ala Ala Val Ser Pro Asn  
85 90 95  
Gly Arg Phe Leu Ala Ala Ala Ala Phe Thr Ala Asp Val Lys Val Trp  
100 105 110  
Glu Ile Val Tyr Gln Lys Asp Gly Ser Val Lys Glu Val Ser Arg Val  
115 120 125  
Met Gln Leu Lys Gly His Lys Ser Ala Val Thr Trp Leu Cys Phe Ser  
130 135 140  
Pro Asn Ser Glu Lys Ile Ile Thr Ala Ser Lys Asp Gly Ser Ile Arg  
145 150 155 160  
Val Trp Asn Ile Asn Val Arg Tyr His Leu Asp Glu Asp Pro Lys Thr  
165 170 175  
Leu Lys Val Phe Pro Ile Pro Leu Cys Asp Ser Gly Gly Asn Pro Xaa  
180 185 190  
His Tyr Asp Arg Leu Ser Leu Cys Pro Glu Gly Lys Ile Leu Ala Ala  
195 200 205  
Ser His Gly Ser Thr Leu Gln Trp Leu Cys Ala Glu Thr Gly Asn Val  
210 215 220  
Leu Asp Thr Ala Glu Lys Ala His Glu Gly Asp Ile Thr Cys Ile Ser  
225 230 235 240  
Trp Ala Pro Lys Ala Ile Thr Val Gly Glu Arg His Ala Met Val Leu  
245 250 255  
Gly Thr Ser Gly Xaa  
260

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1566582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Tyr Gly Glu Asp Lys Gln Lys Asp Gln Gln Gly Lys Leu Pro Leu  
1 5 10 15  
Pro Ser Ile Lys Trp Asp His His His Ile His Glu Lys Arg Ser Val  
20 25 30  
Leu Thr Ile Ser Gly Ala Thr Ala Thr Tyr Gly Thr Ala Asp Gly Ser  
35 40 45  
Val Val Ile Ala Ser Cys Ser Glu Gly Thr Asp Ile Val Leu Trp His  
50 55 60  
Gly Lys Thr Gly Arg Asn Leu Gly His Val Asp Thr Asn Gln Leu Lys  
65 70 75 80  
Asn His Met Ala Ala Val Ser Pro Asn Gly Arg Phe Leu Ala Ala Ala  
85 90 95  
Ala Phe Thr Ala Asp Val Lys Val Trp Glu Ile Val Tyr Gln Lys Asp  
100 105 110  
Gly Ser Val Lys Glu Val Ser Arg Val Met Gln Leu Lys Gly His Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:312:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1566583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 781 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..781

(D) OTHER INFORMATION: / Ceres Seq. ID 1566588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atagttttat | atcatatcaa | tcgacatggc | gaatgtggac | cgtgatcggc | gtgtgcatgt  | 60  |
| agaccgtact | gacaaacgtg | ttcatcagcc | aaactacgaa | gatgatgtcg | gttttggtgg  | 120 |
| ctatggcggt | tatggtgctg | gttctgatta | taagagtcgc | ggcccctcca | ctaaccaaat  | 180 |
| cttggcactt | atagcaggag | ttcccattgg | tggcacactg | ctaaccctag | ctggactcac  | 240 |
| tctagccggt | tcggtgatcg | Cgcttgctag | tctccatacc | cctcttcctc | ctcttcagtc  | 300 |
| cggtgatagt | cccggcggct | ctcactattg | ggcttgctgt | gacgggaatc | ttggcttctg  | 360 |
| gtttgtttgg | gttgacgggt | ctgagctcgg | tctcgtgggt | cctcaactac | ctccgtggga  | 420 |
| cgagtgtatc | agtgccagag | caattggact | acgctaaacg | gcgtatggct | gatgcggtaa  | 480 |
| gctatgctgg | tatgaaggga | aaagaSATgg | gtcagtatgt | gcaagataag | gcgcagtgagg | 540 |
| ctcgtgagac | tgagttcatg | actgagaccc | atgagccggg | taaggccagg | agaggctcat  | 600 |
| aagctaatat | aaattgcggg | agtcagttgg | aaaggcgata | aatgtagttt | tacttttatg  | 660 |
| ttccagtttc | tttctctctt | taagaatatc | tttgtctata | tgtgtacggt | cgttttgtct  | 720 |
| tgtccaaata | aaaatccttg | ttagtgaaat | aagaaatgaa | ataaatatgt | tttctttttt  | 780 |

g

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Val | Asp | Arg | Asp | Arg | Arg | Val | His | Val | Asp | Arg | Thr | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Arg | Val | His | Gln | Pro | Asn | Tyr | Glu | Asp | Asp | Val | Gly | Phe | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Gly | Tyr | Gly | Ala | Gly | Ser | Asp | Tyr | Lys | Ser | Arg | Gly | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Asn | Gln | Ile | Leu | Ala | Leu | Ile | Ala | Gly | Val | Pro | Ile | Gly | Gly | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Thr | Leu | Ala | Gly | Leu | Thr | Leu | Ala | Gly | Ser | Val | Ile | Ala | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ser | Leu | His | Thr | Pro | Leu | Pro | Pro | Leu | Gln | Ser | Gly | Asp | Ser | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gly | Ser | His | Tyr | Trp | Ala | Cys | Cys | Asp | Gly | Asn | Leu | Gly | Phe | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Val | Trp | Val | Asp | Gly | Ser | Glu | Leu | Gly | Leu | Val | Gly | Pro | Gln | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Pro | Trp | Asp | Glu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..717
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aacacatctc  | actgctcact | actctcactg | taatccctta | gatcttcttt | tcaaatttca | 60  |
| atggcgctccg | gtgatgttga | gtatcggtgc | ttcgttggag | gtctagcatg | ggccactgat | 120 |
| gacagagctc  | ttgagactgc | cttcgctcaa | tacggcgacg | ttattgattc | caagatcatt | 180 |
| aacgatcgtg  | agactggaag | atcaagggga | ttcggattcg | tcaccttcaa | ggatgagaaa | 240 |

gccatgaagg atgcgattga gggaatgaac ggacaagatc tcgatggccg tagcatcact 300  
gttaacgagg ctcagtcacg aggaagcggg ggcggcggag gccaccgtgg aggtggtggc 360  
ggtggtggag gttactccgg tggaggtggt agctacggag gtggcggcgg tasacgcgag 420  
ggtggaggag gatacagcgg cggcggcggg tactcctcaa gaggtggtgg tggcgggaagc 480  
tacggtggtg gaagacgtga gggaggagga ggatacgggt gtggtgaagg aggaggttac 540  
ggaggaagcg gtggtggtgg aggatggttaa ttcCtGtthR attaggtttg ggattaccaa 600  
tgaatgttct ctctctcgct tgttatgctt ctactttgtt ttgtgtgttc tctattttgt 660  
tctggttctg ctttagattt gatgtaacag ttcgtgatta ggtattttgg tatctgg

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1566598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Ala Ser Gly Asp Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala  
1 5 10 15  
Trp Ala Thr Asp Asp Arg Ala Leu Glu Thr Ala Phe Ala Gln Tyr Gly  
20 25 30  
Asp Val Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Thr Gly Arg Ser  
35 40 45  
Arg Gly Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Lys Asp  
50 55 60  
Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr  
65 70 75 80  
Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly His Arg  
85 90 95  
Gly Gly Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Ser Tyr  
100 105 110  
Gly Gly Gly Gly Gly Xaa Arg Glu Gly Gly Gly Gly Tyr Ser Gly Gly  
115 120 125  
Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly Gly Gly  
130 135 140  
Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Glu Gly Gly Gly Tyr  
145 150 155 160  
Gly Gly Ser Gly Gly Gly Gly Gly Trp  
165

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1566599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg  
1 5 10 15  
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly  
20 25 30  
Gly His Arg Gly Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly  
35 40 45  
Gly Ser Tyr Gly Gly Gly Gly Gly Xaa Arg Glu Gly Gly Gly Tyr

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50 55 60  
Ser Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr  
65 70 75 80  
Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly Gly Glu Gly  
85 90 95  
Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly Gly Trp  
100 105

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1566600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ala Val Ala Ser Leu Leu Thr Arg Leu Ser His Glu Glu Ala Val  
1 5 10 15  
Ala Ala Glu Ala Thr Val Glu Val Val Ala Val Val Glu Val Thr Pro  
20 25 30  
Val Glu Val Val Ala Thr Glu Val Ala Ala Val Xaa Ala Arg Val Glu  
35 40 45  
Glu Asp Thr Ala Ala Ala Ala Val Thr Pro Gln Glu Val Val Val Ala  
50 55 60  
Glu Ala Thr Val Val Glu Asp Val Arg Glu Glu Glu Asp Thr Val Val  
65 70 75 80  
Val Lys Glu Glu Val Thr Glu Glu Ala Val Val Val Glu Asp Gly Asn  
85 90 95  
Ser Cys Xaa Ile Arg Phe Gly Ile Thr Asn Glu Cys Ser Leu Ser Arg  
100 105 110  
Leu Leu Cys Phe Tyr Phe Val Leu Cys Val Leu Tyr Phe Val Leu Val  
115 120 125  
Leu Leu  
130

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1567

(D) OTHER INFORMATION: / Ceres Seq. ID 1566608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

atTTTTggat tctatcactt ctcttcttca tcatctttct tcttctggcc gccttcaaac 60  
gcaaaaatca tgggaaacat cgacgaatac catctcctcc tggttttcca atcatcgga 120  
acttacatca gctcggagaa ttacaacatc agtctctatg gaagctctca aagaagtatg 180  
gcccagtgat gcttttgaag cttggaaaag tccccacagt catactttct tcatcagaaa 240  
cagcaaaaca agctctaaga gactatgacc tctattgttg tagccgtcct tccttagcag 300  
gaggaagaga gctctcttac aacaatctgg atatgtcttc ctctccttat aatgaatatt 360  
ggaaagaact aaggaagctc tgcagtcaag aactcttttag tgctaataaa attcaatcga 420  
ttcaacctat taaggacgag gaggtcaaga aagttatcga ttcaatcgcg gaatcatctt 480  
ctcttaagaa tccgggttaac ttgagcaaga cgtttcttgc tttaactaca agtgtagtat 540  
gcaaggcagc atttggtgtg agttttgagg gaactgtgct caacagtgat agattcaata 600  
agttagtcgc agatactttc gagatgttgg gaagcttctc tgcctcagat tttattccgt 660  
atgtcggatg gatcatcgat aagttcaatg gtttacaagg gtggagaaaag aaaagctttc 720



|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| gagatcttga | tgcgttctat | gaacaaat   | ttgatctgca | taaggaagag  | aaggaagtag  | 780  |
| gaagtgaaga | tttagtggat | gtgctcttga | ggttggagaa | agaagaaatt  | gttgttggaa  | 840  |
| atggcaagct | cacaagaat  | catatcaaag | caattttgat | gaacattctt  | ttaggaggaa  | 900  |
| tcgatacttc | tgcaataaca | atgacatggg | caatggcaga | acttgctaaa  | aaccctagag  | 960  |
| tgatgaagaa | agttcaagca | gaaatcagaa | gccaaatcaa | gaacaaagaa  | agaatcagct  | 1020 |
| ttgatgacac | tgataagctc | gagtacttaa | aaatggtgat | caaagaaaca  | tggagggttac | 1080 |
| atcctccaac | acctcttctc | ctcccaagag | ttgtaatcac | tgaatttgag  | atcaatggct  | 1140 |
| acacgattcc | tgccaaaaca | cgacttcatg | tgaatgtttg | ggctattggg  | cgtgatcctg  | 1200 |
| atacatggaa | agatccagaa | atgtttctcc | cggaaaggtt | taatgatagt  | aacattgatg  | 1260 |
| caaaaggaca | gaactttgag | ttgttgtcgt | ttgggagtgg | taggagaatt  | tgtcctggac  | 1320 |
| tgtacatggg | aacaacaatg | gtggagtttg | gcctagctaa | tatgttgtat  | cattttgatt  | 1380 |
| ggaagttacc | agaaggcatg | gtagtcAgaa | gatatcgata | tggaagaagc  | tcctggactt  | 1440 |
| actgtgagca | aaaaaagtga | gcttctactt | gttccagtga | agtattttaga | ccattgattc  | 1500 |
| acgtgaatta | gttcttcatc | gattgtacta | tgaataagaa | cgaaatgata  | atgagaattt  | 1560 |
| tcaatgt    |            |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1566609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Trp | Ile | Leu | Ser | Leu | Leu | Phe | Phe | Ile | Ile | Phe | Leu | Leu | Leu | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Phe | Lys | Arg | Lys | Asn | His | Gly | Lys | His | Arg | Arg | Ile | Pro | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Gly | Phe | Pro | Ile | Ile | Gly | Asn | Leu | His | Gln | Leu | Gly | Glu | Leu | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Gln | Ser | Leu | Trp | Lys | Leu | Ser | Lys | Lys | Tyr | Gly | Pro | Val | Met | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Leu | Gly | Lys | Val | Pro | Thr | Val | Ile | Leu | Ser | Ser | Ser | Glu | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Lys | Gln | Ala | Leu | Arg | Asp | Tyr | Asp | Leu | Tyr | Cys | Cys | Ser | Arg | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Leu | Ala | Gly | Gly | Arg | Glu | Leu | Ser | Tyr | Asn | Asn | Leu | Asp | Met | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Pro | Tyr | Asn | Glu | Tyr | Trp | Lys | Glu | Leu | Arg | Lys | Leu | Cys | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Glu | Leu | Phe | Ser | Ala | Asn | Lys | Ile | Gln | Ser | Ile | Gln | Pro | Ile | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Glu | Glu | Val | Lys | Lys | Val | Ile | Asp | Ser | Ile | Ala | Glu | Ser | Ser | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Lys | Asn | Pro | Val | Asn | Leu | Ser | Lys | Thr | Phe | Leu | Ala | Leu | Thr | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Val | Val | Cys | Lys | Ala | Ala | Phe | Gly | Val | Ser | Phe | Glu | Gly | Thr | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Asn | Ser | Asp | Arg | Phe | Asn | Lys | Leu | Val | Arg | Asp | Thr | Phe | Glu | Met |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gly | Ser | Phe | Ser | Ala | Ser | Asp | Phe | Ile | Pro | Tyr | Val | Gly | Trp | Ile |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ile | Asp | Lys | Phe | Asn | Gly | Leu | Gln | Gly | Trp | Arg | Lys | Lys | Ser | Phe | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Leu | Asp | Ala | Phe | Tyr | Glu | Gln | Ile | Phe | Asp | Leu | His | Lys | Glu | Glu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Glu | Val | Gly | Ser | Glu | Asp | Leu | Val | Asp | Val | Leu | Leu | Arg | Leu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |

Lys Glu Glu Ile Val Val Gly Asn Gly Lys Leu Thr Arg Asn His Ile  
275 280 285  
Lys Ala Ile Leu Met Asn Ile Leu Leu Gly Gly Ile Asp Thr Ser Ala  
290 295 300  
Ile Thr Met Thr Trp Ala Met Ala Glu Leu Ala Lys Asn Pro Arg Val  
305 310 315 320  
Met Lys Lys Val Gln Ala Glu Ile Arg Ser Gln Ile Lys Asn Lys Glu  
325 330 335  
Arg Ile Ser Phe Asp Asp Thr Asp Lys Leu Glu Tyr Leu Lys Met Val  
340 345 350  
Ile Lys Glu Thr Trp Arg Leu His Pro Pro Thr Pro Leu Leu Leu Pro  
355 360 365  
Arg Val Val Ile Thr Glu Phe Glu Ile Asn Gly Tyr Thr Ile Pro Ala  
370 375 380  
Lys Thr Arg Leu His Val Asn Val Trp Ala Ile Gly Arg Asp Pro Asp  
385 390 395 400  
Thr Trp Lys Asp Pro Glu Met Phe Leu Pro Glu Arg Phe Asn Asp Ser  
405 410 415  
Asn Ile Asp Ala Lys Gly Gln Asn Phe Glu Leu Leu Ser Phe Gly Ser  
420 425 430  
Gly Arg Arg Ile Cys Pro Gly Leu Tyr Met Gly Thr Thr Met Val Glu  
435 440 445  
Phe Gly Leu Ala Asn Met Leu Tyr His Phe Asp Trp Lys Leu Pro Glu  
450 455 460  
Gly Met Val Val Arg Arg Tyr Arg Tyr Gly Arg Ser Ser Trp Thr Tyr  
465 470 475 480  
Cys Glu Gln Lys Lys  
485

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1566610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Leu Leu Lys Leu Gly Lys Val Pro Thr Val Ile Leu Ser Ser Ser  
1 5 10 15  
Glu Thr Ala Lys Gln Ala Leu Arg Asp Tyr Asp Leu Tyr Cys Cys Ser  
20 25 30  
Arg Pro Ser Leu Ala Gly Gly Arg Glu Leu Ser Tyr Asn Asn Leu Asp  
35 40 45  
Met Ser Ser Ser Pro Tyr Asn Glu Tyr Trp Lys Glu Leu Arg Lys Leu  
50 55 60  
Cys Ser Gln Glu Leu Phe Ser Ala Asn Lys Ile Gln Ser Ile Gln Pro  
65 70 75 80  
Ile Lys Asp Glu Glu Val Lys Lys Val Ile Asp Ser Ile Ala Glu Ser  
85 90 95  
Ser Ser Leu Lys Asn Pro Val Asn Leu Ser Lys Thr Phe Leu Ala Leu  
100 105 110  
Thr Thr Ser Val Val Cys Lys Ala Ala Phe Gly Val Ser Phe Glu Gly  
115 120 125  
Thr Val Leu Asn Ser Asp Arg Phe Asn Lys Leu Val Arg Asp Thr Phe  
130 135 140  
Glu Met Leu Gly Ser Phe Ser Ala Ser Asp Phe Ile Pro Tyr Val Gly  
145 150 155 160  
Trp Ile Ile Asp Lys Phe Asn Gly Leu Gln Gly Trp Arg Lys Lys Ser

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1566611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ser | Pro | Tyr | Asn | Glu | Tyr | Trp | Lys | Glu | Leu | Arg | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Ser | Gln | Glu | Leu | Phe | Ser | Ala | Asn | Lys | Ile | Gln | Ser | Ile | Gln | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Lys | Asp | Glu | Glu | Val | Lys | Lys | Val | Ile | Asp | Ser | Ile | Ala | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Leu | Lys | Asn | Pro | Val | Asn | Leu | Ser | Lys | Thr | Phe | Leu | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Ser | Val | Val | Cys | Lys | Ala | Ala | Phe | Gly | Val | Ser | Phe | Glu | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Val | Leu | Asn | Ser | Asp | Arg | Phe | Asn | Lys | Leu | Val | Arg | Asp | Thr | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Met | Leu | Gly | Ser | Phe | Ser | Ala | Ser | Asp | Phe | Ile | Pro | Tyr | Val | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Ile | Ile | Asp | Lys | Phe | Asn | Gly | Leu | Gln | Gly | Trp | Arg | Lys | Lys | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1049

(D) OTHER INFORMATION: / Ceres Seq. ID 1566616

|            |             |            |             |             |            |      |
|------------|-------------|------------|-------------|-------------|------------|------|
| aactgccaaa | actcttcact  | taattctcgc | gcgtatacaa  | gtcgccggca  | aaaatgtcga | 60   |
| tgtcgaaaag | ctccaagatg  | cttcagttca | taaactacag  | gatgcgagta  | acaatccaag | 120  |
| acggaagaca | gctaatcgga  | aaattcatgg | cgttcgatcg  | ccacatgaat  | cttggtcttg | 180  |
| gcgactgcga | agagtttoga  | aaacttcctc | cggcgaaagg  | taataagaag  | acgagcgaag | 240  |
| aaagagaaga | gcgtcgtact  | ctaggttttg | ttttacttag  | aggagaagaa  | gtgatttcga | 300  |
| tgactgtcga | aggtcaccgc  | ccaccggaag | aatctcgcgc  | caaatctgga  | tctgttacgc | 360  |
| ccgtggctgc | tcttggaaac  | ggctgcgtcg | ctggacgcgg  | agtaacctact | ggtcogttag | 420  |
| ttcaagctca | gcttggttta  | tctggctcgt | ttcgtggaaat | tggtggacct  | gctctgggaa | 480  |
| tgatgcagcc | tcagatctct  | agaccaccac | agattattcg  | tcctccggga  | caaatgccac | 540  |
| cacagcctcc | ttttgctggt  | caaggaggtc | ctcctccacc  | ttatgggatg  | agaccaccgt | 600  |
| atcctggtcc | accaccgcct  | cagtatggtg | gacagcaaag  | gccaatgatg  | attcctccac | 660  |
| ctggtggtat | gatgagagga  | cctcctccac | ctcatggtat  | gcaaggaccg  | cctccttctc | 720  |
| gccctggaat | acctcccccc  | ggtggtgctc | cgatgtttGc  | tcgcctcat   | cctggcatgc | 780  |
| cacctgCtcc | gccaaatcac  | cataatcac  | aacattgatt  | aggatgcatt  | tcatctacaa | 840  |
| cgaagcgaac | attccacatga | ttaggttacc | cctcggctag  | tcgtagcgtt  | ttctccgctg | 900  |
| aagctcagag | aattgatgag  | ttcatattgg | tgattttctcg | tggaaaaagc  | aactgatttt | 960  |
| agaaatagtg | aacttgtagg  | agttacaacc | ttgctccatg  | aacttgaatg  | tattacttgt | 1020 |

aaaagaggct ctcaatgggt ttgactggc

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1566617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Ser Met Ser Lys Ser Ser Lys Met Leu Gln Phe Ile Asn Tyr Arg  
1 5 10 15  
Met Arg Val Thr Ile Gln Asp Gly Arg Gln Leu Ile Gly Lys Phe Met  
20 25 30  
Ala Phe Asp Arg His Met Asn Leu Val Leu Gly Asp Cys Glu Glu Phe  
35 40 45  
Arg Lys Leu Pro Pro Ala Lys Gly Asn Lys Lys Thr Ser Glu Glu Arg  
50 55 60  
Glu Glu Arg Arg Thr Leu Gly Leu Val Leu Leu Arg Gly Glu Glu Val  
65 70 75 80  
Ile Ser Met Thr Val Glu Gly Pro Pro Pro Pro Glu Glu Ser Arg Ala  
85 90 95  
Lys Ser Gly Ser Val Thr Ala Val Ala Gly Pro Gly Ile Gly Arg Ala  
100 105 110  
Ala Gly Arg Gly Val Pro Thr Gly Pro Leu Val Gln Ala Gln Pro Gly  
115 120 125  
Leu Ser Gly Pro Val Arg Gly Ile Gly Gly Pro Ala Pro Gly Met Met  
130 135 140  
Gln Pro Gln Ile Ser Arg Pro Pro Gln Ile Ile Arg Pro Pro Gly Gln  
145 150 155 160  
Met Pro Pro Gln Pro Pro Phe Ala Gly Gln Gly Gly Pro Pro Pro Pro  
165 170 175  
Tyr Gly Met Arg Pro Pro Tyr Pro Gly Pro Pro Pro Pro Gln Tyr Gly  
180 185 190  
Gly Gln Gln Arg Pro Met Met Ile Pro Pro Pro Gly Gly Met Met Arg  
195 200 205  
Gly Pro Pro Pro Pro His Gly Met Gln Gly Pro Pro Pro Ser Arg Pro  
210 215 220  
Gly Ile Pro Pro Pro Gly Gly Ala Pro Met Phe Ala Pro Pro His Pro  
225 230 235 240  
Gly Met Pro Pro Ala Pro Pro Asn His His Asn Gln Gln His  
245 250

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1566618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met Ser Lys Ser Ser Lys Met Leu Gln Phe Ile Asn Tyr Arg Met Arg  
1 5 10 15  
Val Thr Ile Gln Asp Gly Arg Gln Leu Ile Gly Lys Phe Met Ala Phe  
20 25 30

SEQUENCE = 1566617

```

Asp Arg His Met Asn Leu Val Leu Gly Asp Cys Glu Glu Phe Arg Lys
 35 40 45
Leu Pro Pro Ala Lys Gly Asn Lys Lys Thr Ser Glu Glu Arg Glu Glu
 50 55 60
Arg Arg Thr Leu Gly Leu Val Leu Leu Arg Gly Glu Glu Val Ile Ser
 65 70 75 80
Met Thr Val Glu Gly Pro Pro Pro Pro Glu Glu Ser Arg Ala Lys Ser
 85 90 95
Gly Ser Val Thr Ala Val Ala Gly Pro Gly Ile Gly Arg Ala Ala Gly
 100 105 110
Arg Gly Val Pro Thr Gly Pro Leu Val Gln Ala Gln Pro Gly Leu Ser
 115 120 125
Gly Pro Val Arg Gly Ile Gly Gly Pro Ala Pro Gly Met Met Gln Pro
 130 135 140
Gln Ile Ser Arg Pro Pro Gln Ile Ile Arg Pro Pro Gly Gln Met Pro
 145 150 155 160
Pro Gln Pro Pro Phe Ala Gly Gln Gly Gly Pro Pro Pro Pro Tyr Gly
 165 170 175
Met Arg Pro Pro Tyr Pro Gly Pro Pro Pro Gln Tyr Gly Gly Gln
 180 185 190
Gln Arg Pro Met Met Ile Pro Pro Pro Gly Gly Met Met Arg Gly Pro
 195 200 205
Pro Pro Pro His Gly Met Gln Gly Pro Pro Pro Ser Arg Pro Gly Ile
 210 215 220
Pro Pro Pro Gly Gly Ala Pro Met Phe Ala Pro Pro His Pro Gly Met
 225 230 235 240
Pro Pro Ala Pro Pro Asn His His Asn Gln Gln His
 245 250

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1566619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Leu Gln Phe Ile Asn Tyr Arg Met Arg Val Thr Ile Gln Asp Gly
 1 5 10 15
Arg Gln Leu Ile Gly Lys Phe Met Ala Phe Asp Arg His Met Asn Leu
 20 25 30
Val Leu Gly Asp Cys Glu Glu Phe Arg Lys Leu Pro Pro Ala Lys Gly
 35 40 45
Asn Lys Lys Thr Ser Glu Glu Arg Glu Glu Arg Arg Thr Leu Gly Leu
 50 55 60
Val Leu Leu Arg Gly Glu Glu Val Ile Ser Met Thr Val Glu Gly Pro
 65 70 75 80
Pro Pro Pro Glu Glu Ser Arg Ala Lys Ser Gly Ser Val Thr Ala Val
 85 90 95
Ala Gly Pro Gly Ile Gly Arg Ala Ala Gly Arg Gly Val Pro Thr Gly
 100 105 110
Pro Leu Val Gln Ala Gln Pro Gly Leu Ser Gly Pro Val Arg Gly Ile
 115 120 125
Gly Gly Pro Ala Pro Gly Met Met Gln Pro Gln Ile Ser Arg Pro Pro
 130 135 140
Gln Ile Ile Arg Pro Pro Gly Gln Met Pro Pro Gln Pro Pro Phe Ala
 145 150 155 160
Gly Gln Gly Gly Pro Pro Pro Pro Tyr Gly Met Arg Pro Pro Tyr Pro

```

SEQUENCE LISTING

165 170 175  
Gly Pro Pro Pro Gln Tyr Gly Gly Gln Gln Arg Pro Met Met Ile  
180 185 190  
Pro Pro Pro Gly Gly Met Met Arg Gly Pro Pro Pro Pro His Gly Met  
195 200 205  
Gln Gly Pro Pro Pro Ser Arg Pro Gly Ile Pro Pro Pro Gly Gly Ala  
210 215 220  
Pro Met Phe Ala Pro Pro His Pro Gly Met Pro Pro Ala Pro Pro Asn  
225 230 235 240  
His His Asn Gln Gln His  
245

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

attcaccgtc tctgtttcgt tcgccgtgat tcatagtcgt ctctgtctcac cgtcaccatc 60  
accgtcttct tcttccattg acaggatctt gtttagattc tgcaatggct ttcaggcaaaa 120  
ctttatctat aagggtccagg cttttcgctc gtcgtaacca accagtttat catattatcc 180  
ctcgtgagag tgatcatgaa agggattcat tctgtcaaga aacatctcag agaagttacc 240  
atagctttct tcaccaaaga tccgttaaca attctgattt ctccaaagtt tctggaggaa 300  
gcttacattt gcctcttctg cccacgtctg gttttgcttt ctatcgttat atgtcaagt 360  
cacctgggtg tggttcagag aagattgggt tgatgtctga cattgcagaa gtcataaccg 420  
actcaacatt gcaagatgtg ccagctcagg ctgctgctgc tgcagtga gttacacttg 480  
cagctgctga ctctttcttc cCtatcgcg cccttcagca gtgcattgat atgggtgcata 540  
cattcacagg ctttgagtgg tgggcatcca ttgttgtagc aaccattttg atccgatcat 600  
caacagttcc tctcttgatc aaacaaatga aagacacaac caagtttagcg ctgatgaggc 660  
cacggttga gtccatccgg gaggaatgc aaaacaaggg aatggactcg gtaacgatgg 720  
cagaaggtca aaaaaagatg aagaatttgt tttaaagaata tgggtgtcact ccattcacc 780  
caatgaaagg gatgtttatt cagggaccgc tgttcatctg ctttttcctt gctattcgaa 840  
atatggcaga gaaggtacct tcattccaaa caggagggtc attatggttt accgatctaa 900  
caactcccga cagcttatac atcttgccgg ttataacagg attgacattc ttgataaccg 960  
ttgagtgtaa tgcacaagaa ggcattggaag ggaatccgat ggctggcact gtaaaaactg 1020  
tttgtcgggt ttttgcctc ctcacagtc ccatgacaat gagttttcca caggccatat 1080  
tttgttactg gatcacatcc aacctgttct ctctcatgta tggacttgatg ataaagcgtc 1140  
ctcaagtga gaagatgtta cgcatacctg atctgcctcc acctcctcca ggtcaacaac 1200  
cttcatttga cctgttttca gctctcaaga aaatgaaagc catgacacag gaccatacac 1260  
agaaccagat agaaccacct tcgccagtaa acccgaggct ttcttcaaca tcgctgagtc 1320  
ctgttagtaa gaggtcgaag gctttggaga gccaaagtaaa gggaagggaag aagaatagca 1380  
gcaagaagaa gtgatttaaa acggtgcata ctatttttgt taagagggcc aaacgaaaaa 1440  
aataataaag cttttgagtc gaaagtgaac acagaatttt ctactgatg aaactactct 1500  
gtgagctaaa aagctggagg cagctattgt aagtttgttt tgaccaatta tagaatagaa 1560  
gattgttttt

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..429
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566631

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|           |     |     |     |          |     |     |     |     |           |     |     |            |           |     |     |
|-----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|------------|-----------|-----|-----|
| Met<br>1  | Ala | Phe | Arg | Gln<br>5 | Thr | Leu | Ser | Ile | Arg<br>10 | Ser | Arg | Leu        | Phe<br>15 | Ala | Arg |
| Arg       | Asn | Gln | Pro | Val      | Tyr | His | Ile | Ile | Pro       | Arg | Glu | Ser        | Asp<br>20 | His | Glu |
| Arg       | Asp | Ser | Phe | Cys      | Gln | Glu | Thr | Ser | Gln       | Arg | Ser | Tyr<br>25  | His       | Ser | Phe |
| Leu       | His | Gln | Arg | Ser      | Val | Asn | Asn | Ser | Asp       | Phe | Ser | Lys<br>30  | Val       | Ser | Gly |
| Gly<br>35 | Ser | Leu | His | Leu      | Pro | Leu | Ala | Pro | Thr       | Ser | Gly | Phe<br>40  | Ala       | Phe | Tyr |
| Arg       | Tyr | Met | Ser | Ser      | Ala | Pro | Gly | Val | Gly       | Ser | Glu | Lys<br>45  | Ile       | Gly | Val |
| Met       | Ser | Asp | Ile | Ala      | Glu | Val | Ile | Thr | Asp       | Ser | Thr | Leu<br>50  | Gln       | Asp | Val |
| Pro       | Ala | Gln | Ala | Ala      | Ala | Ala | Val | Ser | Glu       | Val | Thr | Leu<br>55  | Ala       | Ala | Ala |
| Asp       | Ser | Phe | Phe | Pro      | Ile | Ala | Ala | Leu | Gln       | Gln | Cys | Ile<br>60  | Asp       | Met | Val |
| His<br>65 | Thr | Phe | Thr | Gly      | Phe | Glu | Trp | Trp | Ala       | Ser | Ile | Val<br>65  | Val       | Ala | Thr |
| Ile       | Leu | Ile | Arg | Ser      | Ser | Thr | Val | Pro | Leu       | Leu | Ile | Lys<br>70  | Gln       | Met | Lys |
| Asp       | Thr | Thr | Lys | Leu      | Ala | Leu | Met | Arg | Pro       | Arg | Leu | Glu<br>75  | Ser       | Ile | Arg |
| Glu       | Glu | Met | Gln | Asn      | Lys | Gly | Met | Asp | Ser       | Val | Thr | Met<br>80  | Ala       | Glu | Gly |
| Gln       | Lys | Lys | Met | Lys      | Asn | Leu | Phe | Lys | Glu       | Tyr | Gly | Val<br>85  | Thr       | Pro | Phe |
| Thr       | Pro | Met | Lys | Gly      | Met | Phe | Ile | Gln | Gly       | Pro | Leu | Phe<br>90  | Ile       | Cys | Phe |
| Phe       | Leu | Ala | Ile | Arg      | Asn | Met | Ala | Glu | Lys       | Val | Pro | Ser<br>95  | Phe       | Gln | Thr |
| Gly       | Gly | Ala | Leu | Trp      | Phe | Thr | Asp | Leu | Thr       | Thr | Pro | Asp<br>100 | Ser       | Leu | Tyr |
| Ile       | Leu | Pro | Val | Ile      | Thr | Gly | Leu | Thr | Phe       | Leu | Ile | Thr<br>105 | Val       | Glu | Cys |
| Asn       | Ala | Gln | Glu | Gly      | Met | Glu | Gly | Asn | Pro       | Met | Ala | Gly<br>110 | Thr       | Val | Lys |
| Thr       | Val | Cys | Arg | Val      | Phe | Ala | Leu | Leu | Thr       | Val | Pro | Met<br>115 | Thr       | Met | Ser |
| Phe       | Pro | Gln | Ala | Ile      | Phe | Cys | Tyr | Trp | Ile       | Thr | Ser | Asn<br>120 | Leu       | Phe | Ser |
| Leu       | Met | Tyr | Gly | Leu      | Val | Ile | Lys | Arg | Pro       | Gln | Val | Lys<br>125 | Lys       | Met | Leu |
| Arg       | Ile | Pro | Asp | Leu      | Pro | Pro | Pro | Pro | Pro       | Gly | Gln | Gln<br>130 | Pro       | Ser | Phe |
| Asp       | Leu | Phe | Ser | Ala      | Leu | Lys | Lys | Met | Lys       | Ala | Met | Thr<br>135 | Gln       | Asp | His |
| Thr       | Gln | Asn | Gln | Ile      | Glu | Pro | Pro | Ser | Pro       | Val | Asn | Pro<br>140 | Arg       | Leu | Ser |
| Ser       | Thr | Ser | Leu | Ser      | Pro | Val | Ser | Lys | Arg       | Leu | Lys | Ala<br>145 | Leu       | Glu | Ser |
| Gln       | Val | Lys | Gly | Arg      | Lys | Lys | Asn | Ser | Lys       | Lys | Lys | Lys<br>150 |           |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear



|          |     |     |     |     |          |     |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|-----|----------|-----|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1 | Ser | Ser | Ala |     | Pro<br>5 | Gly | Val | Gly | Ser |     | Glu<br>10 | Lys | Ile | Gly | Val | Met<br>15 | Ser |
| Asp      | Ile | Ala | Glu | Val | Ile      | Thr | Asp | Ser | Ser | Thr | Leu       | Gln | Asp | Val | Pro | Ala       |     |
|          |     |     | 20  |     |          |     |     |     | 25  |     |           |     |     | 30  |     |           |     |
| Gln      | Ala | Ala | Ala | Ala | Val      | Ser | Glu | Val | Thr | Leu | Ala       | Ala | Ala | Ala | Asp | Ser       |     |
|          |     | 35  |     |     |          |     | 40  |     |     |     |           | 45  |     |     |     |           |     |
| Phe      | Phe | Pro | Ile | Ala | Ala      | Leu | Gln | Gln | Cys | Ile | Asp       | Met | Val | His | Thr |           |     |
|          | 50  |     |     |     |          | 55  |     |     |     | 60  |           |     |     |     |     |           |     |
| Phe      | Thr | Gly | Phe | Glu | Trp      | Trp | Ala | Ser | Ile | Val | Val       | Ala | Thr | Ile | Leu |           |     |
| 65       |     |     |     |     | 70       |     |     |     |     | 75  |           |     |     |     | 80  |           |     |
| Ile      | Arg | Ser | Ser | Thr | Val      | Pro | Leu | Leu | Ile | Lys | Gln       | Met | Lys | Asp | Thr |           |     |
|          |     |     |     | 85  |          |     |     |     | 90  |     |           |     |     | 95  |     |           |     |
| Thr      | Lys | Leu | Ala | Leu | Met      | Arg | Pro | Arg | Leu | Glu | Ser       | Ile | Arg | Glu | Glu |           |     |
|          |     |     | 100 |     |          |     |     | 105 |     |     |           |     | 110 |     |     |           |     |
| Met      | Gln | Asn | Lys | Gly | Met      | Asp | Ser | Val | Thr | Met | Ala       | Glu | Gly | Gln | Lys |           |     |
|          |     | 115 |     |     |          |     | 120 |     |     |     |           | 125 |     |     |     |           |     |
| Lys      | Met | Lys | Asn | Leu | Phe      | Lys | Glu | Tyr | Gly | Val | Thr       | Pro | Phe | Thr | Pro |           |     |
|          | 130 |     |     |     |          | 135 |     |     |     |     | 140       |     |     |     |     |           |     |
| Met      | Lys | Gly | Met | Phe | Ile      | Gln | Gly | Pro | Leu | Phe | Ile       | Cys | Phe | Phe | Leu |           |     |
| 145      |     |     |     | 150 |          |     |     |     | 155 |     |           |     |     |     | 160 |           |     |
| Ala      | Ile | Arg | Asn | Met | Ala      | Glu | Lys | Val | Pro | Ser | Phe       | Gln | Thr | Gly | Gly |           |     |
|          |     |     | 165 |     |          |     |     |     | 170 |     |           |     |     | 175 |     |           |     |
| Ala      | Leu | Trp | Phe | Thr | Asp      | Leu | Thr | Thr | Pro | Asp | Ser       | Leu | Tyr | Ile | Leu |           |     |
|          |     |     | 180 |     |          |     |     | 185 |     |     |           |     | 190 |     |     |           |     |
| Pro      | Val | Ile | Thr | Gly | Leu      | Thr | Phe | Leu | Ile | Thr | Val       | Glu | Cys | Asn | Ala |           |     |
|          |     | 195 |     |     |          |     | 200 |     |     |     |           | 205 |     |     |     |           |     |
| Gln      | Glu | Gly | Met | Glu | Gly      | Asn | Pro | Met | Ala | Gly | Thr       | Val | Lys | Thr | Val |           |     |
|          | 210 |     |     |     | 215      |     |     |     |     |     | 220       |     |     |     |     |           |     |
| Cys      | Arg | Val | Phe | Ala | Leu      | Leu | Thr | Val | Pro | Met | Thr       | Met | Ser | Phe | Pro |           |     |
| 225      |     |     |     | 230 |          |     |     |     |     | 235 |           |     |     |     | 240 |           |     |
| Gln      | Ala | Ile | Phe | Cys | Tyr      | Trp | Ile | Thr | Ser | Asn | Leu       | Phe | Ser | Leu | Met |           |     |
|          |     |     | 245 |     |          |     |     |     | 250 |     |           |     |     | 255 |     |           |     |
| Tyr      | Gly | Leu | Val | Ile | Lys      | Arg | Pro | Gln | Val | Lys | Lys       | Met | Leu | Arg | Ile |           |     |
|          |     | 260 |     |     |          |     |     | 265 |     |     |           |     | 270 |     |     |           |     |
| Pro      | Asp | Leu | Pro | Pro | Pro      | Pro | Pro | Gly | Gln | Gln | Pro       | Ser | Phe | Asp | Leu |           |     |
|          | 275 |     |     |     |          |     | 280 |     |     |     |           | 285 |     |     |     |           |     |
| Phe      | Ser | Ala | Leu | Lys | Lys      | Met | Lys | Ala | Met | Thr | Gln       | Asp | His | Thr | Gln |           |     |
|          | 290 |     |     |     | 295      |     |     |     |     |     | 300       |     |     |     |     |           |     |
| Asn      | Gln | Ile | Glu | Pro | Pro      | Ser | Pro | Val | Asn | Pro | Arg       | Leu | Ser | Ser | Thr |           |     |
| 305      |     |     |     | 310 |          |     |     |     | 315 |     |           |     |     | 320 |     |           |     |
| Ser      | Leu | Ser | Pro | Val | Ser      | Lys | Arg | Leu | Lys | Ala | Leu       | Glu | Ser | Gln | Val |           |     |
|          |     |     | 325 |     |          |     |     |     | 330 |     |           |     |     |     |     |           |     |

(A) NAME/KEY: peptide  
(B) LOCATION: 1..333  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met Ser Asp Ile Ala Glu Val Ile Thr Asp Ser Thr Leu Gln Asp Val  
1 5 10 15  
Pro Ala Gln Ala Ala Ala Val Ser Glu Val Thr Leu Ala Ala Ala  
20 25 30  
Asp Ser Phe Phe Pro Ile Ala Ala Leu Gln Gln Cys Ile Asp Met Val  
35 40 45  
His Thr Phe Thr Gly Phe Glu Trp Trp Ala Ser Ile Val Val Ala Thr  
50 55 60  
Ile Leu Ile Arg Ser Ser Thr Val Pro Leu Leu Ile Lys Gln Met Lys  
65 70 75 80  
Asp Thr Thr Lys Leu Ala Leu Met Arg Pro Arg Leu Glu Ser Ile Arg  
85 90 95  
Glu Glu Met Gln Asn Lys Gly Met Asp Ser Val Thr Met Ala Glu Gly  
100 105 110  
Gln Lys Lys Met Lys Asn Leu Phe Lys Glu Tyr Gly Val Thr Pro Phe  
115 120 125  
Thr Pro Met Lys Gly Met Phe Ile Gln Gly Pro Leu Phe Ile Cys Phe  
130 135 140  
Phe Leu Ala Ile Arg Asn Met Ala Glu Lys Val Pro Ser Phe Gln Thr  
145 150 155 160  
Gly Gly Ala Leu Trp Phe Thr Asp Leu Thr Thr Pro Asp Ser Leu Tyr  
165 170 175  
Ile Leu Pro Val Ile Thr Gly Leu Thr Phe Leu Ile Thr Val Glu Cys  
180 185 190  
Asn Ala Gln Glu Gly Met Glu Gly Asn Pro Met Ala Gly Thr Val Lys  
195 200 205  
Thr Val Cys Arg Val Phe Ala Leu Leu Thr Val Pro Met Thr Met Ser  
210 215 220  
Phe Pro Gln Ala Ile Phe Cys Tyr Trp Ile Thr Ser Asn Leu Phe Ser  
225 230 235 240  
Leu Met Tyr Gly Leu Val Ile Lys Arg Pro Gln Val Lys Lys Met Leu  
245 250 255  
Arg Ile Pro Asp Leu Pro Pro Pro Pro Gly Gln Gln Pro Ser Phe  
260 265 270  
Asp Leu Phe Ser Ala Leu Lys Lys Met Lys Ala Met Thr Gln Asp His  
275 280 285  
Thr Gln Asn Gln Ile Glu Pro Pro Ser Pro Val Asn Pro Arg Leu Ser  
290 295 300  
Ser Thr Ser Leu Ser Pro Val Ser Lys Arg Leu Lys Ala Leu Glu Ser  
305 310 315 320  
Gln Val Lys Gly Arg Lys Lys Asn Ser Ser Lys Lys Lys  
325 330

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..681
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

atcgatcact gaatcttctt cttcttcttc ttcttcttct tcttcttctt cttcttcttc 60  
ctctcaagaa cagatttttt ttaaaccgagc ttgatcaata aattctctca agatctatgg 120  
cggaagagca tcgatgtcag acaccagaaa gcaaccgtct ctgtgttaac aactgtggct 180  
tctctggcag ctccgccacc atgaatctct gttctaattg ttacggcgat ctttgtctca 240  
aacaacaaca acaatctctc tccatcaaat ccaccgttga atcagcaaca gaggccgaat 300  
cgggtgcacga cgtgtaggaa acgggtcggg ttaaccggat tcaagtgccg gtgcggtacg 360

atgttttgcg gggttcatag gtacccggag atccatggat gcagctacga tttcaaatacg 420  
gccggacgtg aagagatcgc gaaagcSaat ccgttggtga aagcagcgaa gcttcagaag 480  
atatgatcag agccgttcga tgcgttgact tttcctctcg taagtcttca tttctacgcg 540  
tatgtgtgtc ctccgtcccc cgagaaatac ggatgggtgtc gatttgattg atctcagccg 600  
ttggatcaaa aatggtttat tattgtaaaa gattgattat gtatttatca aaggacacg 660  
tgtcacgtgg ttttaggatg g

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1566642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Ala Glu Glu His Arg Cys Gln Thr Pro Glu Ser Asn Arg Leu Cys  
1 5 10 15  
Val Asn Asn Cys Gly Phe Leu Gly Ser Ser Ala Thr Met Asn Leu Cys  
20 25 30  
Ser Asn Cys Tyr Gly Asp Leu Cys Leu Lys Gln Gln Gln Gln Ser Ser  
35 40 45  
Ser Ile Lys Ser Thr Val Glu Ser Ala Thr Glu Ala Glu Ser Val His  
50 55 60  
Asp Val  
65

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1566643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Asn Leu Cys Ser Asn Cys Tyr Gly Asp Leu Cys Leu Lys Gln Gln  
1 5 10 15  
Gln Gln Ser Ser Ser Ile Lys Ser Thr Val Glu Ser Ala Thr Glu Ala  
20 25 30  
Glu Ser Val His Asp Val  
35

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1566644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met Phe Cys Gly Val His Arg Tyr Pro Glu Ile His Gly Cys Ser Tyr  
1 5 10 15  
Asp Phe Lys Ser Ala Gly Arg Glu Glu Ile Ala Lys Xaa Asn Pro Leu

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20 25 30  
Val Lys Ala Ala Lys Leu Gln Lys Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..556
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| acytagaaca tcctaatacga aaaacaagggt ttgaaaatga agggacgtca aggagagaga | 60  |
| gtagattgt atgttcgtgg aacagtcctc ggctacaaga ggtccaagtc gaaccaatat    | 120 |
| cccaacactt ctctcatcca gattgaaggt gtgaacactc aagaggaggt caattgggtac  | 180 |
| aagggttaagc gtttggttta catctacaag gcaaagacaa agaagaacgg ttctcactac  | 240 |
| cgttgcattht ggggcaaagt cactaggcct catggttaaca gcggtgttgt ccgttctaag | 300 |
| ttcacttcaa acctaccacc caagtcaatg ggagctagag tcagagtctt catgtaccct   | 360 |
| agcaacatat gaggaggata gatttcaaga agtatcggaa ggaatcgcca ttatcatttc   | 420 |
| tcaggagctg tagtttatct attcactttt gttctaaact ctctgttggt tttgatttta   | 480 |
| tcttttagacg aagTwaRaac atttttcttc ttgagataat attaatggaa cttcagaaaa  | 540 |
| cctatgatcc cgggtct                                                  |     |

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Gly Arg Gln Gly Glu Arg Val Arg Leu Tyr Val Arg Gly Thr |  |
| 1 5 10 15                                                       |  |
| Val Leu Gly Tyr Lys Arg Ser Lys Ser Asn Gln Tyr Pro Asn Thr Ser |  |
| 20 25 30                                                        |  |
| Leu Ile Gln Ile Glu Gly Val Asn Thr Gln Glu Glu Val Asn Trp Tyr |  |
| 35 40 45                                                        |  |
| Lys Gly Lys Arg Leu Ala Tyr Ile Tyr Lys Ala Lys Thr Lys Lys Asn |  |
| 50 55 60                                                        |  |
| Gly Ser His Tyr Arg Cys Ile Trp Gly Lys Val Thr Arg Pro His Gly |  |
| 65 70 75 80                                                     |  |
| Asn Ser Gly Val Val Arg Ser Lys Phe Thr Ser Asn Leu Pro Pro Lys |  |
| 85 90 95                                                        |  |
| Ser Met Gly Ala Arg Val Arg Val Phe Met Tyr Pro Ser Asn Ile     |  |
| 100 105 110                                                     |  |

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1566652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```
Met Arg Arg Ile Asp Phe Lys Lys Tyr Arg Lys Glu Ser Pro Leu Ser
1 5 10 15
Phe Leu Arg Ser Cys Ser Leu Ser Ile His Phe Cys Ser Lys Leu Ser
20 25 30
Val Gly Phe Asp Phe Ile Phe Arg Arg Ser Xaa Asn Ile Phe Leu Leu
35 40 45
Glu Ile Ile Leu Met Glu Leu Gln Lys Thr Tyr Asp Pro Gly
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1566661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```
atactatcaa attgaagaag aggaagatcc aattggaaag ggttatccta attcccagtc 60
attgatcgga gaagatgagt gctgttgaga ttaaccactt ttttggctta ccggagacga 120
tcgagaagct aattctcccg atttctcggt ccggcgaaag taataacgag agtcgtggaa 180
gaggaagtag caataatatc ccaatagaca ttttggaaatc tccccaaaaa tacatatattt 240
atctcgatat ccccggaatt tcaaaatcag atatccaggt tacagtggag gaagagagga 300
ctttagtgat aaagagtaat gggaagagga agagagatga tgatgagagt gaagaagggg 360
ctaagtatat tagactcgag aggagacttg ctcaagaattt ggtaagaag ttccggttac 420
cagaagatgc tgatatggct tctgtaacgg ctaaatatca agaaggtatt ttgacagttg 480
ttatcaagaa gctaccgcca cagccgcgga aacctaaagac tgttcaaata gctgtttctt 540
gagtagtttc tgtgttttgt ttttgtgtgt gtttgttttc tagtAttgta atttttctgt 600
ttttggataa aaagactctg tttcttttat gtgttctcta gtcgaaattt tgaaattgaa 660
gaaataaata ggttt
```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1566662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```
Met Ser Ala Val Ala Ile Asn His Phe Gly Leu Pro Glu Thr Ile
1 5 10 15
Glu Lys Leu Ile Leu Pro Ile Ser Arg Ser Gly Glu Ser Asn Asn Glu
20 25 30
Ser Arg Gly Arg Gly Ser Ser Asn Asn Ile Pro Ile Asp Ile Leu Glu
35 40 45
Ser Pro Lys Lys Tyr Ile Phe Tyr Leu Asp Ile Pro Gly Ile Ser Lys
50 55 60
Ser Asp Ile Gln Val Thr Val Glu Glu Glu Arg Thr Leu Val Ile Lys
65 70 75 80
Ser Asn Gly Lys Arg Lys Arg Asp Asp Asp Glu Ser Glu Glu Gly Ser
85 90 95
Lys Tyr Ile Arg Leu Glu Arg Arg Leu Ala Gln Asn Leu Val Lys Lys
100 105 110
Phe Arg Leu Pro Glu Asp Ala Asp Met Ala Ser Val Thr Ala Lys Tyr
```

115 120 125  
Gln Glu Gly Ile Leu Thr Val Val Ile Lys Lys Leu Pro Pro Gln Pro  
130 135 140  
Pro Lys Pro Lys Thr Val Gln Ile Ala Val Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| attttcgttt tcactttctc cgaacatcca aaagcttgta gcttgctcct caaatcttct   | 60  |
| tgaaaaatga aggttgccgc tgctttcctc ctgcgcgttt tgggcggaaa cgctaactct   | 120 |
| tcagccgaga atatacaaga tatcatcgga gctgttggtg ctgatgttga tggagagagc   | 180 |
| attgagcttc tattgaaaga agtgagtggg aaggacattg ctgagctgat tgcttctggt   | 240 |
| aggagagaaat tagcgtctgt gccatctggt ggtgggtgtgg ctgtttcagc tgctccatca | 300 |
| agcgggtggtg gtgggtgctgc tgctgctgcc cctgcggaga agaaagaagc caagaaggaa | 360 |
| gagaaagaag agtctgatga tgacatggga ttcagtctct tcgagtaagg tttttgtccc   | 420 |
| cacggaaagg agtcgagatt tgatttttWt gttctcttag tggttctggt ttttgctcct   | 480 |
| ctttgtaacc ttggtctagt tagcggtttt tt                                 |     |

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Val Ala Ala Ala Phe Leu Leu Ala Val Leu Gly Gly Asn Ala |  |
| 1 5 10 15                                                       |  |
| Asn Pro Ser Ala Glu Asn Ile Lys Asp Ile Ile Gly Ala Val Gly Ala |  |
| 20 25 30                                                        |  |
| Asp Val Asp Gly Glu Ser Ile Glu Leu Leu Lys Glu Val Ser Gly     |  |
| 35 40 45                                                        |  |
| Lys Asp Ile Ala Glu Leu Ile Ala Ser Gly Arg Glu Lys Leu Ala Ser |  |
| 50 55 60                                                        |  |
| Val Pro Ser Gly Gly Gly Val Ala Val Ser Ala Ala Pro Ser Ser Gly |  |
| 65 70 75 80                                                     |  |
| Gly Gly Gly Ala Ala Ala Ala Ala Pro Ala Glu Lys Lys Glu Ala Lys |  |
| 85 90 95                                                        |  |
| Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser Leu Phe |  |
| 100 105 110                                                     |  |
| Glu                                                             |  |

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..822

(D) OTHER INFORMATION: / Ceres Seq. ID 1566665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gtcgcctctca attaaaccct aaaaccctcc tcagaagaga ggcagagaga aaaaaaacgc  | 60  |
| agTcttttgcg gaatctgtga aaggagaaaa gatgagacca ccaatgagag gcggcggggg  | 120 |
| tttccgtgga aggggaggac gagacggtgg tgggtggcggg aggttcggtg gaggaggcgg  | 180 |
| tagattcggg ggaggaggag gacgcctttg tgggtggaggc ggtcgccttg gtggttttag  | 240 |
| agacgaaggc cctcctagcg aagtcgtgga tgttgcaact ttcgttcacg cttgcgaggg   | 300 |
| agatgctgtg accaaactct cacaggagaa gattcctcat tttaacgctc cgatctacct   | 360 |
| agagaacaag actcagattg ggaaagtaga tgaaatcttt ggccaatta atgaatcttt    | 420 |
| gttttctatc aaaatgatgg aaggtattgt agccacctcg tattctccag gagataagtt   | 480 |
| cttcacgcac ccttacaagc ttttgccact cgctcgatcc cttcctcagc caaagggtca   | 540 |
| gtcaacgggt ggacgtggag gtgcaggtcg tggaagaggt gatagtagag gtcgtggaag   | 600 |
| aggtggatca tttagtagag gtagaggcgc tccaagaggt ggtagatttc caccacgcgg   | 660 |
| tggctctcgt ggaagcttta gagggccgagg aagatttttag gttcttctcc tgctttataa | 720 |
| gccttatcca aacttgtaac ctttgtttta tgaatgacta tcgttctccc gtattctcaa   | 780 |
| ttttcaagac tttggtttta tctatggagt aaaaaatatt gc                      |     |

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1566666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Pro Pro Met Arg Gly Gly Gly Gly Phe Arg Gly Arg Gly Gly |  |
| 1 5 10 15                                                       |  |
| Arg Asp Gly Gly Gly Gly Gly Arg Phe Gly Gly Gly Gly Gly Arg Phe |  |
| 20 25 30                                                        |  |
| Gly Gly Gly Gly Gly Arg Phe Gly Gly Gly Gly Gly Arg Phe Gly Gly |  |
| 35 40 45                                                        |  |
| Phe Arg Asp Glu Gly Pro Pro Ser Glu Val Val Asp Val Ala Thr Phe |  |
| 50 55 60                                                        |  |
| Val His Ala Cys Glu Gly Asp Ala Val Thr Lys Leu Ser Gln Glu Lys |  |
| 65 70 75 80                                                     |  |
| Ile Pro His Phe Asn Ala Pro Ile Tyr Leu Glu Asn Lys Thr Gln Ile |  |
| 85 90 95                                                        |  |
| Gly Lys Val Asp Glu Ile Phe Gly Pro Ile Asn Glu Ser Leu Phe Ser |  |
| 100 105 110                                                     |  |
| Ile Lys Met Met Glu Gly Ile Val Ala Thr Ser Tyr Ser Pro Gly Asp |  |
| 115 120 125                                                     |  |
| Lys Phe Phe Ile Asp Pro Tyr Lys Leu Leu Pro Leu Ala Arg Phe Leu |  |
| 130 135 140                                                     |  |
| Pro Gln Pro Lys Gly Gln Ser Thr Gly Gly Arg Gly Gly Ala Gly Arg |  |
| 145 150 155 160                                                 |  |
| Gly Arg Gly Asp Ser Arg Gly Arg Gly Arg Gly Gly Ser Phe Ser Arg |  |
| 165 170 175                                                     |  |
| Gly Arg Gly Ala Pro Arg Gly Gly Arg Phe Pro Pro Arg Gly Gly Ser |  |
| 180 185 190                                                     |  |
| Arg Gly Ser Phe Arg Gly Arg Gly Arg Phe                         |  |
| 195 200                                                         |  |

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..198  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566667  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met Arg Gly Gly Gly Gly Phe Arg Gly Arg Gly Gly Arg Asp Gly Gly  
1 5 10 15  
Gly Gly Gly Arg Phe Gly Gly Gly Gly Arg Phe Gly Gly Gly Gly  
20 25 30  
Gly Arg Phe Gly Gly Gly Gly Gly Arg Phe Gly Gly Phe Arg Asp Glu  
35 40 45  
Gly Pro Pro Ser Glu Val Val Asp Val Ala Thr Phe Val His Ala Cys  
50 55 60  
Glu Gly Asp Ala Val Thr Lys Leu Ser Gln Glu Lys Ile Pro His Phe  
65 70 75 80  
Asn Ala Pro Ile Tyr Leu Glu Asn Lys Thr Gln Ile Gly Lys Val Asp  
85 90 95  
Glu Ile Phe Gly Pro Ile Asn Glu Ser Leu Phe Ser Ile Lys Met Met  
100 105 110  
Glu Gly Ile Val Ala Thr Ser Tyr Ser Pro Gly Asp Lys Phe Phe Ile  
115 120 125  
Asp Pro Tyr Lys Leu Leu Pro Leu Ala Arg Phe Leu Pro Gln Pro Lys  
130 135 140  
Gly Gln Ser Thr Gly Gly Arg Gly Gly Ala Gly Arg Gly Arg Gly Asp  
145 150 155 160  
Ser Arg Gly Arg Gly Arg Gly Gly Ser Phe Ser Arg Gly Arg Gly Ala  
165 170 175  
Pro Arg Gly Gly Arg Phe Pro Pro Arg Gly Gly Ser Arg Gly Ser Phe  
180 185 190  
Arg Gly Arg Gly Arg Phe  
195

- (2) INFORMATION FOR SEQ ID NO:345:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1622 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1622  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566671

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| ttcaaaggat  | aaatacgcat  | ggcttcgcga  | tgacgagttc  | gcacgccaa  | ctatagctgg | 60  |
| gatcaaccg   | gtcaacatag  | aacgagtcac  | gtcttatcca  | ccggtcagca | atcttgaccc | 120 |
| tgaaatctac  | ggaccaggtc  | ttcactccgc  | tctcacggaa  | gaccacatca | tcggtcaact | 180 |
| tgatggctta  | accgtacaac  | aagcgtaga   | gatgaaccgt  | ttgtttatgg | tggactacca | 240 |
| tgacatatac  | ttaccgtttc  | tagatagaat  | caacgcgctt  | gatggacgca | aggcttacgc | 300 |
| gactcgaacc  | atattgttct  | tgacccgact  | cggtacactc  | aagcctatcg | ccatcgagct | 360 |
| aagcctccct  | tctcaatcaa  | gctcaaacca  | aaagtccaag  | cgcggtgtca | cacctccagt | 420 |
| agacgcaacc  | tccaactgga  | tgtggcagct  | agccaaggcc  | cacgttgggt | ccaatgacgc | 480 |
| tgggtgtccac | cagcttggtga | atcattgggt  | acgtactcat  | gcgtgtttgg | aacggtttat | 540 |
| attagctgct  | catagacaat  | taagcgcaat  | gcattccgata | ttcaaattat | tagaccotca | 600 |
| catgaggtac  | actttggaga  | tcaatgccgt  | ggcacgacag  | actttgatta | gtgcggacgg | 660 |
| tgtgatcgag  | tcgtgcttca  | ctgctgggtca | atacgggtcta | gagattagtt | ccgctgcgta | 720 |
| taagaacaaa  | tggcggtttg  | atatggaagg  | tctccctgct  | gatctcatcc | gaagggggat | 780 |
| ggctgttcca  | gacccaacac  | aaccacatgg  | gcttaaatta  | cttggtgaag | actacccatg | 840 |
| ccaacgacgg  | tctcttatta  | tggtccgcaa  | tccaaacttg  | ggtccgaacc | tacgtggaac | 900 |



|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| gttattacgc  | aaactcgaac  | ctaataccaaa | ccgataactga | gctccaagcc  | tggtactctg | 960  |
| agtcaatcaa  | cgtaRgtcac  | gctgatcacc  | gcgacgccga  | gtggtggccg  | aagctttcca | 1020 |
| ccgtcgaaga  | tctcgtctcc  | gtcatcacca  | ccatcatctg  | gctcgccctcc | gcacaacacg | 1080 |
| cggcactcaa  | cttcggacaa  | tatccttacg  | gtggctacgt  | cccgaaccga  | ccaccgctaa | 1140 |
| tgcgtcgggt  | gattcccgcac | gagtcagatc  | ccgagttcac  | gagttttatc  | gaagatcctc | 1200 |
| aaaagtattt  | tttctcgtcg  | atgccgagtt  | tattgcaaac  | gacgaagttt  | atggcgggtg | 1260 |
| ttgatacatt  | gtcgacacat  | tcgccggatg  | aggagtatat  | cggagagaga  | caacaaccgt | 1320 |
| cgatatggac  | tgagatgct   | gagatcgtag  | atgcgtttta  | tggtattctcg | gcggaaatcg | 1380 |
| gacggataga  | gaaggagatt  | gacaagagga  | atcgtgatcc  | tagctgtagg  | aatcgctgtg | 1440 |
| gcgcggggagt | gttaccgcat  | gagttgatgg  | ctccgagttc  | tgaaccgggt  | gttacgtgta | 1500 |
| gaggagtgcc  | taatagtgtg  | tctatttaga  | attattcaat  | ttttcaaagt  | atagagaatt | 1560 |
| ttataagtat  | ataattagat  | tttgacgcag  | tatggtttat  | ttgcgcgat   | tgtaaaattc | 1620 |
| tt          |             |             |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Asp | Lys | Tyr | Ala | Trp | Leu | Arg | Asp | Asp | Glu | Phe | Ala | Arg | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Ile | Ala | Gly | Ile | Asn | Pro | Val | Asn | Ile | Glu | Arg | Val | Thr | Ser | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Val | Ser | Asn | Leu | Asp | Pro | Glu | Ile | Tyr | Gly | Pro | Gly | Leu | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Leu | Thr | Glu | Asp | His | Ile | Ile | Gly | Gln | Leu | Asp | Gly | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Gln | Gln | Ala | Leu | Glu | Met | Asn | Arg | Leu | Phe | Met | Val | Asp | Tyr | His |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ile | Tyr | Leu | Pro | Phe | Leu | Asp | Arg | Ile | Asn | Ala | Leu | Asp | Gly | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ala | Tyr | Ala | Thr | Arg | Thr | Ile | Leu | Phe | Leu | Thr | Arg | Leu | Gly | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Pro | Ile | Ala | Ile | Glu | Leu | Ser | Leu | Pro | Ser | Gln | Ser | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gln | Lys | Ser | Lys | Arg | Val | Val | Thr | Pro | Pro | Val | Asp | Ala | Thr | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Trp | Met | Trp | Gln | Leu | Ala | Lys | Ala | His | Val | Gly | Ser | Asn | Asp | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Val | His | Gln | Leu | Val | Asn | His | Trp | Leu | Arg | Thr | His | Ala | Cys | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Pro | Phe | Ile | Leu | Ala | Ala | His | Arg | Gln | Leu | Ser | Ala | Met | His | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Phe | Lys | Leu | Leu | Asp | Pro | His | Met | Arg | Tyr | Thr | Leu | Glu | Ile | Asn |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Val | Ala | Arg | Gln | Thr | Leu | Ile | Ser | Ala | Asp | Gly | Val | Ile | Glu | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Phe | Thr | Ala | Gly | Gln | Tyr | Gly | Leu | Glu | Ile | Ser | Ser | Ala | Ala | Tyr |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Lys | Asn | Lys | Trp | Arg | Phe | Asp | Met | Glu | Gly | Leu | Pro | Ala | Asp | Leu | Ile |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Arg | Arg | Gly | Met | Ala | Val | Pro | Asp | Pro | Thr | Gln | Pro | His | Gly | Leu | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Val | Glu | Asp | Tyr | Pro | Cys | Gln | Arg | Arg | Ser | Leu | Ile | Met | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |

(2) INFORMATION FOR SEO ID NO:347:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1566673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

(2) INFORMATION FOR SEQ ID NO:348:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1566674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met Gly Leu Asn Tyr Leu Leu Lys Thr Thr His Ala Asn Asp Gly Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Leu | Trp | Ser | Ala | Ile | Gln | Thr | Trp | Val | Arg | Thr | Tyr | Val | Glu | Arg |
|     | 20  |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Tyr | Ala | Asn | Ser | Asn | Leu | Ile | Gln | Thr | Asp | Thr | Glu | Leu | Gln | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Tyr | Ser | Glu | Ser | Ile | Asn | Val | Xaa | His | Ala | Asp | His | Arg | Asp | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Trp | Trp | Pro | Lys | Leu | Ser | Thr | Val | Glu | Asp | Leu | Val | Ser | Val | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Thr | Ile | Ile | Trp | Leu | Ala | Ser | Ala | Gln | His | Ala | Ala | Leu | Asn | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gln | Tyr | Pro | Tyr | Gly | Gly | Tyr | Val | Pro | Asn | Arg | Pro | Pro | Leu | Met |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Leu | Ile | Pro | Asp | Glu | Ser | Asp | Pro | Glu | Phe | Thr | Ser | Phe | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Asp | Pro | Gln | Lys | Tyr | Phe | Phe | Ser | Ser | Met | Pro | Ser | Leu | Leu | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Thr | Lys | Phe | Met | Ala | Val | Val | Asp | Thr | Leu | Ser | Thr | His | Ser | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Glu | Glu | Tyr | Ile | Gly | Glu | Arg | Gln | Gln | Pro | Ser | Ile | Trp | Thr | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asp | Ala | Glu | Ile | Val | Asp | Ala | Phe | Tyr | Gly | Phe | Ser | Ala | Glu | Ile | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ile | Glu | Lys | Glu | Ile | Asp | Lys | Arg | Asn | Arg | Asp | Pro | Ser | Cys | Arg |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Arg | Cys | Gly | Ala | Gly | Val | Leu | Pro | Tyr | Glu | Leu | Met | Ala | Pro | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Glu | Pro | Gly | Val | Thr | Cys | Arg | Gly | Val | Pro | Asn | Ser | Val | Ser | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| atgactgctt | cactttctct  | ttctcttttg | ttcaagtagt  | ttgggagaga | gaagagaaga | 60  |
| agaagacacc | ctttaagcaa  | aacagaggat | tttcattctc  | tgttctgttt | gaattattac | 120 |
| taatctatca | tcttggtgtt  | ctcttcgtcg | acaatgtcgg  | gaaacaaaga | agaagaggat | 180 |
| cctcgtatcc | atggaatcaa  | aactaagatc | cgtgtcgttc  | cagattttcc | caagaaagga | 240 |
| ataatgtttc | aagacataac  | aacagtgttg | ttggatccga  | aagccttcaa | agacacaatt | 300 |
| gatctgtttg | tggagaggta  | cagagacaag | aacatctcag  | tggttgcagg | aatagaggct | 360 |
| cgtggtttcc | tattcgggtcc | accgatcgcg | ctaGccattg  | gagcaaaatt | tgttcctctg | 420 |
| cgcaaaccga | agaaactacc  | tggtgaaaca | atatttgagg  | aatacgagtt | ggaatatgga | 480 |
| aatgaccgcc | tagagatgca  | cataggagcc | gtcagaggctg | gcgatcgatc | tttggtcggt | 540 |
| gatgatctta | tgcgcactgg  | tggtactctc | tgcgctgcca  | ttaacttgct | cgagagggtt | 600 |
| ggagcagaag | ttgtggaatg  | tgcattgtgt | atcgagttac  | ccgaattaaa | gggaaggcag | 660 |
| agacttaagg | ggaagccact  | atgtatgctt | gtggagtagc  | gatgatgatt | ttagctttac | 720 |
| ttatttggtg | aaaattattc  | ggttaattaa | tttatgctcc  | gaaaattcgg | attatgcaga | 780 |
| cttcttatta | ttggattcta  | caatattttg | atttaaattc  | tagcggatta | gctggaagaa | 840 |
| ataatcc    |             |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Gln | Asp | Ile | Thr | Thr | Val | Leu | Leu | Asp | Pro | Lys | Ala | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Thr | Ile | Asp | Leu | Phe | Val | Glu | Arg | Tyr | Arg | Asp | Lys | Asn | Ile | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Ala | Gly | Ile | Glu | Ala | Arg | Gly | Phe | Leu | Phe | Gly | Pro | Pro | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Ala | Ile | Gly | Ala | Lys | Phe | Val | Pro | Leu | Arg | Lys | Pro | Lys | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Pro | Gly | Glu | Thr | Ile | Phe | Glu | Glu | Tyr | Glu | Leu | Glu | Tyr | Gly | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Arg | Leu | Glu | Met | His | Ile | Gly | Ala | Val | Glu | Ala | Gly | Asp | Arg | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Val | Val | Asp | Asp | Leu | Ile | Ala | Thr | Gly | Gly | Thr | Leu | Cys | Ala | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ile | Asn | Leu | Leu | Glu | Arg | Val | Gly | Ala | Glu | Val | Val | Glu | Cys | Ala | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Val Ile Glu Leu Pro Glu Leu Lys Gly Arg Gln Arg Leu Lys Gly Lys  
130 135 140  
Pro Leu Cys Met Leu Val Glu Tyr Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gcgactctcc tctctgtttc gttttttttt cctttcattc ttcttatctc ctcacactct | 60  |
| tcgaacaagg aggaacccta atctcaagat gaatagggaa aagttgatga agatggctaa | 120 |
| caccgtccgc actggcggaa aggttacagt cagaagaaag aagaaggctg tgcacaagac | 180 |
| caatacaact gatgacaaga ggctccagag cacacttaag agaattggag ttaactccat | 240 |
| tcccgtatt gaagaagtta acatctttaa ggatgatgtt gttattcagt tcatcaaccc  | 300 |
| taaggttcaa gcttcaattg ctgcaaacac atgggttggt agcggttctc ctcagaccaa | 360 |
| aaaattgcaa gatatccttc ctcagatcat cagccaactt ggaccagaca acatggacaa | 420 |
| cctgaagaag ctagcagagc agttccagaa acaggcttct ggtgaaggta atgccgcctc | 480 |
| agcaaccatt caagaagagg atgatgacga tgtccCagag cttgttgagg agacattcga | 540 |
| aactgctgct gaagagaaag caccagctgc tgctgcttct tcttagagag aaaagagcga | 600 |
| gacc                                                              |     |

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Leu Ser Ser Leu Phe Arg Phe Phe Phe Leu Ser Phe Phe Leu Ser |  |
| 1 5 10 15                                                       |  |
| Pro His Thr Leu Arg Thr Arg Arg Asn Pro Asn Leu Lys Met Asn Arg |  |
| 20 25 30                                                        |  |
| Glu Lys Leu Met Lys Met Ala Asn Thr Val Arg Thr Gly Gly Lys Gly |  |
| 35 40 45                                                        |  |
| Thr Val Arg Arg Lys Lys Lys Ala Val His Lys Thr Asn Thr Thr Asp |  |
| 50 55 60                                                        |  |
| Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val Asn Ser Ile |  |
| 65 70 75 80                                                     |  |
| Pro Ala Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln |  |
| 85 90 95                                                        |  |
| Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn Thr Trp Val |  |
| 100 105 110                                                     |  |
| Val Ser Gly Ser Pro Gln Thr Lys Lys Leu Gln Asp Ile Leu Pro Gln |  |
| 115 120 125                                                     |  |
| Ile Ile Ser Gln Leu Gly Pro Asp Asn Met Asp Asn Leu Lys Lys Leu |  |
| 130 135 140                                                     |  |
| Ala Glu Gln Phe Gln Lys Gln Ala Ser Gly Glu Gly Asn Ala Ala Ser |  |
| 145 150 155 160                                                 |  |
| Ala Thr Ile Gln Glu Asp Asp Asp Asp Val Pro Glu Leu Val Gly     |  |
| 165 170 175                                                     |  |

Glu Thr Phe Glu Thr Ala Ala Glu Glu Lys Ala Pro Ala Ala Ala Ala  
180 185 190  
Ser Ser

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Arg | Glu | Lys | Leu | Met | Lys | Met | Ala | Asn | Thr | Val | Arg | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Lys | Gly | Thr | Val | Arg | Arg | Lys | Lys | Lys | Ala | Val | His | Lys | Thr | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Asp | Asp | Lys | Arg | Leu | Gln | Ser | Thr | Leu | Lys | Arg | Ile | Gly | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Asn | Ser | Ile | Pro | Ala | Ile | Glu | Glu | Val | Asn | Ile | Phe | Lys | Asp | Asp | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Ile | Gln | Phe | Ile | Asn | Pro | Lys | Val | Gln | Ala | Ser | Ile | Ala | Ala | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Trp | Val | Val | Ser | Gly | Ser | Pro | Gln | Thr | Lys | Lys | Leu | Gln | Asp | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Pro | Gln | Ile | Ile | Ser | Gln | Leu | Gly | Pro | Asp | Asn | Met | Asp | Asn | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Lys | Leu | Ala | Glu | Gln | Phe | Gln | Lys | Gln | Ala | Ser | Gly | Glu | Gly | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Ser | Ala | Thr | Ile | Gln | Glu | Glu | Asp | Asp | Asp | Asp | Val | Pro | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Val | Gly | Glu | Thr | Phe | Glu | Thr | Ala | Ala | Glu | Glu | Lys | Ala | Pro | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ala | Ala | Ser | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Met | Ala | Asn | Thr | Val | Arg | Thr | Gly | Gly | Lys | Gly | Thr | Val | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Lys | Lys | Ala | Val | His | Lys | Thr | Asn | Thr | Thr | Asp | Asp | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Ser | Thr | Leu | Lys | Arg | Ile | Gly | Val | Asn | Ser | Ile | Pro | Ala | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Val | Asn | Ile | Phe | Lys | Asp | Asp | Val | Val | Ile | Gln | Phe | Ile | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Lys | Val | Gln | Ala | Ser | Ile | Ala | Ala | Asn | Thr | Trp | Val | Val | Ser | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Pro | Gln | Thr | Lys | Lys | Leu | Gln | Asp | Ile | Leu | Pro | Gln | Ile | Ile | Ser |

85 90 95  
Gln Leu Gly Pro Asp Asn Met Asp Asn Leu Lys Lys Leu Ala Glu Gln  
100 105 110  
Phe Gln Lys Gln Ala Ser Gly Glu Gly Asn Ala Ala Ser Ala Thr Ile  
115 120 125  
Gln Glu Glu Asp Asp Asp Asp Val Pro Glu Leu Val Gly Glu Thr Phe  
130 135 140  
Glu Thr Ala Ala Glu Glu Lys Ala Pro Ala Ala Ala Ser Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..930  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

accacaaaatg ccttttgccc ctctctctct atataccaacc catgtctcct ctttatctct 60  
ctaactttcc ccttagagag attcctcttt ctctcaaaact aggggtttcct ctctgaaaac 120  
aacaaaaata tccaataat tgcaaaatct acttgaagat ttttcattct cttttcttat 180  
aattaatgcc caagagagaa acaagaaga tcaaaccttc tcaagaagtt atcaaggaag 240  
gaccttttct tgttacgatc catttaaagg ggatatatat gtcgaaactac acaaactcac 300  
cgtgtgcagc atgcaaattc ctccggcgta aatgcacgtc agaactgcgt ttcgcaccct 360  
attttccgcc ggaggaaact acaaaagttg cgaacgtcca ccggatattc ggggcaagca 420  
atgtgagcaa gatcctccac gaaGTggcNt ccccatcagc gggaagatgc ggtcaactcg 480  
ctggcttacg aggcggaagc acgacttaaa gatccagtgt atggctgcgt tggagcgatc 540  
tcggtgctCc aaagacaggt cttgaggttg caaagggaac tccaggagac aaatgctgat 600  
ctcatgaggt acgctggttg tctcggttgt gaaacgacgt cggcttatgg tggtcggagg 660  
ggttgactgg tcaacgagag ttgattagtc atcatcactc tttgagaaaa ttagcggcgg 720  
agaagtataa agagagagag gatggttgat gtgatggtaa gtgttattag tcgtatgtat 780  
atatgtgtaa atatggggac aggcattgat gtatatattat gtttatatttc atgtatatac 840  
ttatgcgtat gtgtaattta acttgtaatt ttttttcatg ggagagggtca aggaatattt 900  
ttgatgatgt tgaataacta gatcttgctc

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Met Pro Lys Arg Glu Thr Lys Lys Ile Lys Pro Ser Gln Glu Val Ile  
1 5 10 15  
Lys Glu Gly Pro Phe Leu Val Thr Ile His Leu Lys Gly Ile Tyr Met  
20 25 30  
Ser Asn Tyr Thr Asn Ser Pro Cys Ala Ala Cys Lys Phe Leu Arg Arg  
35 40 45  
Lys Cys Thr Ser Asp Cys Val Phe Ala Pro Tyr Phe Pro Pro Glu Glu  
50 55 60  
Pro Thr Lys Phe Ala Asn Val His Arg Ile Phe Gly Ala Ser Asn Val  
65 70 75 80  
Ser Lys Ile Leu His Glu Val Xaa Ser Pro Ser Ala Gly Arg Cys Gly  
85 90 95

Gln Leu Ala Gly Leu Arg Gly Gly Ser Thr Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met Ser Asn Tyr Thr Asn Ser Pro Cys Ala Ala Cys Lys Phe Leu Arg  
1 5 10 15  
Arg Lys Cys Thr Ser Asp Cys Val Phe Ala Pro Tyr Phe Pro Pro Glu  
20 25 30  
Glu Pro Thr Lys Phe Ala Asn Val His Arg Ile Phe Gly Ala Ser Asn  
35 40 45  
Val Ser Lys Ile Leu His Glu Val Xaa Ser Pro Ser Ala Gly Arg Cys  
50 55 60  
Gly Gln Leu Ala Gly Leu Arg Gly Gly Ser Thr Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Met His Val Arg Leu Arg Ile Arg Thr Leu Phe Ser Ala Gly Gly Thr  
1 5 10 15  
Tyr Lys Val Cys Glu Arg Pro Pro Asp Ile Arg Gly Lys Gln Cys Glu  
20 25 30  
Gln Asp Pro Pro Arg Ser Gly Xaa Pro Ile Ser Gly Lys Met Arg Ser  
35 40 45  
Thr Arg Trp Leu Thr Arg Arg Lys His Asp Leu Lys Ile Gln Cys Met  
50 55 60  
Ala Ala Leu Glu Arg Ser Arg Cys Ser Lys Asp Arg Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..960
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

accattaaac caggtcttta gtacaaaact tcaaacaaaa ggtcaaaagc taatttcttt 60  
tttttgctaa gaaaaactaa tttcttcctc ttcgacctct caagtctcaa gcatcattag 120  
ataaacaat cctattcccg tcatggcagc aatgaccgcg gcagcagttc cagcaactgg 180

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(2) INFORMATION FOR SEQ ID NO:361:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1566708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Met | Thr | Ala | Ala | Ala | Val | Pro | Ala | Thr | Gly | Ser | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gln | Asp | Glu | Glu | Trp | Arg | Ala | Val | Leu | Ser | Pro | Glu | Gln | Phe | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Arg | Leu | Lys | Gly | Thr | Glu |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEO ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1566709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Thr | Cys | Ala | Val | Cys | Asp | Gly | His | Leu | Gly | His | Val | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Glu | Gly | Tyr | Ser | Thr | Pro | Thr | Asp | Gln | Arg | His | Cys | Val | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Ser | Leu | Lys | Phe | Ser | Ser | Ala | Gly | Ser | Ser | Gln |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1566710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Phe Ser Lys Ala Lys Val Thr Leu Leu Gln Pro Ile Asn Val Thr  
1 5 10 15  
Ala Leu Thr Val Ser Leu Ser Asn Ser Leu Leu Leu Val Pro Pro Asn  
20 25 30  
Asn His Ile Ile Asp Arg Thr Thr Leu Ser His Glu Ile Lys Asn Leu  
35 40 45  
Phe Tyr Asp Leu Cys Glu Leu Ala Arg Phe Leu Ser His Thr His Val  
50 55 60  
Ile Leu  
65

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

gttttggtgt ttcttcgtcg acgtcgctat ctccaatctc attactcccc tttctcaatg 60  
atcataaaac ctacttcgat tctactcctt atcaactgaa tcaccgaaaa acctcacctt 120  
ttttcttttt ccgatcatgg ggaatctgat cagtttgatc ttctgctgcg ggagaaggca 180  
gaggagcaat attcctccgg cgatggaaac ggctcctctt gaactccac cgaacagatt 240  
tgtattcgcc gccgcgccac catatctgaa ccctaaccct aactacgttg accagtatcc 300  
aggtaactgc cttcctccgc cagtaactga gccgccgatg ctaccgtaca atttcaacca 360  
tttgcatcac tctcctccca acagttacca actacctcat cctttgtttc acggcggtag 420  
ataccctata ctgccgcctc ctacgtacgt ccaccagaaa gccgtcacga ttcgtaacga 480  
tgttaatctg aagaagaaga ctttaacgct cataccggac ccggagaatc cgaatcgact 540  
tcttgctctc ttacattttg atgcatccat gcccggaagg atcacagttg ttttctttgc 600  
tacagaagat gcagaatgta atcttagagc tacaaaggaa gatactttgc ctccaatcac 660  
ttttgatctt ggagaaggac ttggtcagaa gtccatacaa tcatctggaa cgggtataga 720  
cttgacggcg tttaaagatt ccgagctatt caaggagggtg gatacagatg tcttcccgtt 780  
ggcggttaag gcggaggcaa ctccagcggg agaaggaaag tctGgttcca ccaatgtgca 840  
gattactcaa gtggtgtata ccaaggagaa aggagagatt aaaatagaag tgggtgaagca 900  
gatactatgg tggaataaga ggaggtatga gctgcttgag atttatggga ttgagaacac 960  
ggttgatggt tccgatgagg gaaaggaatg tgtgtatgc ttgtctgaac cacgcgatac 1020  
aactgttctt ccttgacagc acatgtgtat gtgtagcggg tgcgcaaagg cgtaagggtt 1080  
tcagacaaat ctgtgccag tttgcagaca acctgttgag atgcttttgg agattaacaa 1140  
gaacggatga aatggagatg gagaatgaac aaatttagtt aagcaatcga cttgtgtaat 1200  
atatgccatg cttaattaag acgtaaaacg ttatggttca atatattata agtggaact 1260  
gagttcttaa atagcaatg

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Gly Asn Leu Ile Ser Leu Ile Phe Cys Cys Gly Arg Arg Gln Arg  
1 5 10 15  
Ser Asn Ile Pro Pro Ala Met Glu Thr Ala Pro Leu Glu Leu Pro Pro  
20 25 30

Asn Arg Phe Val Phe Ala Ala Pro Pro Tyr Leu Asn Pro Asn Pro  
35 40 45  
Asn Tyr Val Asp Gln Tyr Pro Gly Asn Cys Leu Pro Pro Pro Val Thr  
50 55 60  
Glu Pro Pro Met Leu Pro Tyr Asn Phe Asn His Leu His His Tyr Pro  
65 70 75 80  
Pro Asn Ser Tyr Gln Leu Pro His Pro Leu Phe His Gly Gly Arg Tyr  
85 90 95  
Pro Ile Leu Pro Pro Pro Thr Tyr Val His Gln Lys Ala Val Thr Ile  
100 105 110  
Arg Asn Asp Val Asn Leu Lys Lys Thr Leu Thr Leu Ile Pro Asp  
115 120 125  
Pro Glu Asn Pro Asn Arg Leu Leu Val Ser Phe Thr Phe Asp Ala Ser  
130 135 140  
Met Pro Gly Arg Ile Thr Val Val Phe Phe Ala Thr Glu Asp Ala Glu  
145 150 155 160  
Cys Asn Leu Arg Ala Thr Lys Glu Asp Thr Leu Pro Pro Ile Thr Phe  
165 170 175  
Asp Phe Gly Glu Gly Leu Gly Gln Lys Phe Ile Gln Ser Ser Gly Thr  
180 185 190  
Gly Ile Asp Leu Thr Ala Phe Lys Asp Ser Glu Leu Phe Lys Glu Val  
195 200 205  
Asp Thr Asp Val Phe Pro Leu Ala Val Lys Ala Glu Ala Thr Pro Ala  
210 215 220  
Glu Glu Gly Lys Ser Gly Ser Thr Asn Val Gln Ile Thr Gln Val Val  
225 230 235 240  
Tyr Thr Lys Glu Lys Gly Glu Ile Lys Ile Glu Val Val Lys Gln Ile  
245 250 255  
Leu Trp Val Asn Lys Arg Arg Tyr Glu Leu Leu Glu Ile Tyr Gly Ile  
260 265 270  
Glu Asn Thr Val Asp Gly Ser Asp Glu Gly Lys Glu Cys Val Val Cys  
275 280 285  
Leu Ser Glu Pro Arg Asp Thr Thr Val Leu Pro Cys Arg His Met Cys  
290 295 300  
Met Cys Ser Gly Cys Ala Lys Ala Leu Arg Phe Gln Thr Asn Leu Cys  
305 310 315 320  
Pro Val Cys Arg Gln Pro Val Glu Met Leu Leu Glu Ile Asn Lys Asn  
325 330 335  
Gly

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1566713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Met Glu Thr Ala Pro Leu Glu Leu Pro Pro Asn Arg Phe Val Phe Ala  
1 5 10 15  
Ala Ala Pro Pro Tyr Leu Asn Pro Asn Pro Asn Tyr Val Asp Gln Tyr  
20 25 30  
Pro Gly Asn Cys Leu Pro Pro Pro Val Thr Glu Pro Pro Met Leu Pro  
35 40 45  
Tyr Asn Phe Asn His Leu His His Tyr Pro Pro Asn Ser Tyr Gln Leu  
50 55 60  
Pro His Pro Leu Phe His Gly Gly Arg Tyr Pro Ile Leu Pro Pro Pro



(2) INFORMATION FOR SEQ ID NO:368:

(A) LENGTH: 1537 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:368:

aacaca cacaacaca cacacacaca gcctttttcc t

(2) INFORMATION FOR SEQ ID NO:369:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1566716

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1566717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Leu | Gln | Phe | Gly | Tyr | Ala | Gly | Phe | His | Val | Val | Ser | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Leu | Asn | Met | Gly | Ile | Ser | Lys | Leu | Val | Phe | Pro | Val | Tyr | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Ile | Ala | Leu | Leu | Leu | Leu | Pro | Phe | Ala | Tyr | Phe | Leu | Glu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Lys | Glu | Arg | Pro | Ala | Ile | Thr | Leu | Asn | Phe | Leu | Ile | Gln | Phe | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Leu | Ala | Leu | Ile | Gly | Ile | Thr | Ala | Asn | Gln | Gly | Phe | Tyr | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Leu | Asp | Asn | Thr | Ser | Pro | Thr | Phe | Ala | Ser | Ser | Met | Gln | Asn | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Pro | Ala | Ile | Thr | Phe | Leu | Met | Ala | Ala | Leu | Leu | Arg | Ile | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Ile | Asn | Arg | Arg | Asp | Gly | Ile | Ser | Lys | Ile | Leu | Gly | Thr | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Cys | Val | Ala | Gly | Ala | Ser | Val | Ile | Thr | Leu | Tyr | Lys | Gly | Pro | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Tyr | Thr | Pro | Ala | Ser | His | Leu | His | Ala | His | Leu | Leu | Thr | Thr | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ala | Val | Leu | Ala | Pro | Leu | Gly | Asn | Ala | Ala | Pro | Lys | Asn | Trp | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Gly | Cys | Ile | Tyr | Leu | Ile | Gly | His | Cys | Leu | Ser | Trp | Ser | Gly | Trp |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Val | Phe | Gln | Ala | Pro | Val | Leu | Lys | Ser | Tyr | Pro | Ala | Arg | Leu | Ser |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Thr | Ser | Tyr | Thr | Cys | Phe | Phe | Gly | Ile | Ile | Gln | Phe | Leu | Ile | Ile |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Ala | Phe | Cys | Glu | Arg | Asp | Ser | Gln | Ala | Trp | Val | Phe | His | Ser | Gly |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Trp | Glu | Leu | Phe | Thr | Ile | Leu | Tyr | Ala | Gly | Ile | Val | Ala | Ser | Gly | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Phe | Ala | Val | Gln | Ile | Trp | Cys | Ile | Asp | Arg | Gly | Gly | Pro | Val | Phe |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Ala | Val | Tyr | Gln | Pro | Val | Gln | Thr | Leu | Val | Val | Ala | Ile | Met | Ala |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Ile | Ala | Leu | Gly | Glu | Glu | Phe | Tyr | Leu | Gly | Gly | Ile | Ile | Gly | Ala |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Val | Leu | Ile | Ile | Ala | Gly | Leu | Tyr | Phe | Val | Leu | Tyr | Gly | Lys | Ser | Glu |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Arg | Lys | Phe | Ala | Ala | Leu | Glu | Lys | Ala | Glu | Ile | Gln | Ser | Ser | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | His | Gly | Ile | Glu | Arg | Ala | Pro | Val | Ser | Arg | Asn | Ser | Ile | Lys | Ser |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Ile | Thr | Thr | Pro | Leu | Leu | His | Gln | Ser | Thr | Asp | Asn | Val |     |     |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1566718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

Met Gly Ile Ser Lys Leu Val Phe Pro Val Tyr Arg Asn Ile Ile Ala
1 5 10 15
Leu Leu Leu Leu Leu Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg
20 25 30
Pro Ala Ile Thr Leu Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu
35 40 45
Ile Gly Ile Thr Ala Asn Gln Gly Phe Tyr Leu Leu Gly Leu Asp Asn
50 55 60
Thr Ser Pro Thr Phe Ala Ser Ser Met Gln Asn Ser Val Pro Ala Ile
65 70 75 80
Thr Phe Leu Met Ala Ala Leu Leu Arg Ile Glu Lys Val Arg Ile Asn
85 90 95
Arg Arg Asp Gly Ile Ser Lys Ile Leu Gly Thr Ala Leu Cys Val Ala
100 105 110
Gly Ala Ser Val Ile Thr Leu Tyr Lys Gly Pro Thr Ile Tyr Thr Pro
115 120 125
Ala Ser His Leu His Ala His Leu Leu Thr Thr Asn Ser Ala Val Leu
130 135 140
Ala Pro Leu Gly Asn Ala Ala Pro Lys Asn Trp Thr Leu Gly Cys Ile
145 150 155 160
Tyr Leu Ile Gly His Cys Leu Ser Trp Ser Gly Trp Leu Val Phe Gln
165 170 175
Ala Pro Val Leu Lys Ser Tyr Pro Ala Arg Leu Ser Val Thr Ser Tyr
180 185 190
Thr Cys Phe Phe Gly Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys
195 200 205
Glu Arg Asp Ser Gln Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe
210 215 220
Thr Ile Leu Tyr Ala Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val
225 230 235 240
Gln Ile Trp Cys Ile Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr
245 250 255
Gln Pro Val Gln Thr Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu
260 265 270
Gly Glu Glu Phe Tyr Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile
275 280 285
Ala Gly Leu Tyr Phe Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe
290 295 300
Ala Ala Leu Glu Lys Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile
305 310 315 320
Glu Arg Ala Pro Val Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr
325 330 335
Pro Leu Leu His Gln Ser Thr Asp Asn Val
340 345

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1009 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1009

(D) OTHER INFORMATION: / Ceres Seq. ID 1566719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

catctttctaa gaaagaaaca aagaaagact tcacatttta ccattatttg ctctgagctc 60
agtaggagag ttcaagaaac aatggcaaag atgcaattat caatctttat cgctgtcggt 120

```



```
gcgcttatcg tctgctctgc atctgctaaa accgcaagcc ctccagctcc agtgctgcca 180
ccgacaccag ctccagcacc agccccggaa aatgtgaatc tcaccgagct ttttaagtga 240
gctgggtccgt tccacacatt cctcgactac cttctctcga ctggagtcac tgagactttc 300
caaaaccaag ctaacaacac tgaggaaggc atcacaatct ttgtccctaa agatgatgct 360
ttcaaagctc agaagaatcc tcctttgtca aatctcacia aggatcagct taagcagctt 420
gttctcttcc atgctcttcc tcattactat tcgcttttcgg aattcaagaa cttgagccaa 480
tctgggtccag tgagcacctt tgctgggtgg caatactcct tgaaattcac tgatgtttct 540
ggcacggtta ggattgattc tttatggacc aggactaaag tcagcagcag tgttttctcc 600
actgacctg ttgcggttta ccaattgaac cgcgtgcttc taccggaagc aatctttggg 660
actgatgtcc ctccaatgcc tgctccagct cctgctccta tcgttagtgc tCcttcggat 720
tctccttcag ttgctgattc tgaaggagct tcttcaccaa agtcctcaca caagaactcc 780
ggacaaaagc tgctacttgc accaatctcc atggttatct cgggtttggg ggcattgttc 840
ttgtgatcag atgggtttgc agattgagtt atgtttttaa gttacaatgt gaaagattgt 900
attacatcat ttgaattgtc tttttgattt ttgaaaccca ttttttatta tacattttta 960
tcattattat tgttgtcat tacgattttg tgaattgaaa ttgttcctc
```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```
His Leu Leu Arg Lys Lys Gln Arg Lys Thr Ser His Phe Thr Ile Ile
1 5 10 15
Cys Ser Glu Leu Ser Arg Arg Val Gln Glu Thr Met Ala Lys Met Gln
 20 25 30
Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile Val Cys Ser Ala Ser
 35 40 45
Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu Pro Pro Thr Pro Ala
 50 55 60
Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr Glu Leu Leu Ser Val
65 70 75 80
Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu Leu Ser Thr Gly Val
 85 90 95
Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr Glu Glu Gly Ile Thr
 100 105 110
Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala Gln Lys Asn Pro Pro
 115 120 125
Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln Leu Val Leu Phe His
130 135 140
Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe Lys Asn Leu Ser Gln
145 150 155 160
Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln Tyr Ser Leu Lys Phe
 165 170 175
Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser Leu Trp Thr Arg Thr
 180 185 190
Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro Val Ala Val Tyr Gln
 195 200 205
Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe Gly Thr Asp Val Pro
210 215 220
Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val Ser Ala Pro Ser Asp
225 230 235 240
Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser Ser Pro Lys Ser Ser
 245 250 255
His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala Pro Ile Ser Met Val
 260 265 270
```

Ile Ser Gly Leu Val Ala Leu Phe Leu  
275 280

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1566721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Ala Lys Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile  
1 5 10 15  
Val Cys Ser Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu  
20 25 30  
Pro Pro Thr Pro Ala Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr  
35 40 45  
Glu Leu Leu Ser Val Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu  
50 55 60  
Leu Ser Thr Gly Val Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr  
65 70 75 80  
Glu Glu Gly Ile Thr Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala  
85 90 95  
Gln Lys Asn Pro Pro Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln  
100 105 110  
Leu Val Leu Phe His Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe  
115 120 125  
Lys Asn Leu Ser Gln Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln  
130 135 140  
Tyr Ser Leu Lys Phe Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser  
145 150 155 160  
Leu Trp Thr Arg Thr Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro  
165 170 175  
Val Ala Val Tyr Gln Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe  
180 185 190  
Gly Thr Asp Val Pro Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val  
195 200 205  
Ser Ala Pro Ser Asp Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser  
210 215 220  
Ser Pro Lys Ser Ser His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala  
225 230 235 240  
Pro Ile Ser Met Val Ile Ser Gly Leu Val Ala Leu Phe Leu  
245 250

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1566722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile Val Cys Ser  
1 5 10 15  
Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu Pro Pro Thr

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Pro Ala Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr Glu Leu Leu |     |     |
| 35                                                              | 40  | 45  |
| Ser Val Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu Leu Ser Thr |     |     |
| 50                                                              | 55  | 60  |
| Gly Val Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr Glu Glu Gly |     |     |
| 65                                                              | 70  | 75  |
| Ile Thr Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala Gln Lys Asn |     |     |
| 85                                                              | 90  | 95  |
| Pro Pro Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln Leu Val Leu |     |     |
| 100                                                             | 105 | 110 |
| Phe His Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe Lys Asn Leu |     |     |
| 115                                                             | 120 | 125 |
| Ser Gln Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln Tyr Ser Leu |     |     |
| 130                                                             | 135 | 140 |
| Lys Phe Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser Leu Trp Thr |     |     |
| 145                                                             | 150 | 155 |
| Arg Thr Lys Val Ser Ser Val Phe Ser Thr Asp Pro Val Ala Val     |     |     |
| 165                                                             | 170 | 175 |
| Tyr Gln Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe Gly Thr Asp |     |     |
| 180                                                             | 185 | 190 |
| Val Pro Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val Ser Ala Pro |     |     |
| 195                                                             | 200 | 205 |
| Ser Asp Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser Ser Pro Lys |     |     |
| 210                                                             | 215 | 220 |
| Ser Ser His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala Pro Ile Ser |     |     |
| 225                                                             | 230 | 235 |
| Met Val Ile Ser Gly Leu Val Ala Leu Phe Leu                     |     |     |
| 245                                                             | 250 |     |

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| agattaggat | taaattaggg  | cataaccctt | atcggagatt | tgaagccatg | ggaagaagaa  | 60  |
| aaatcgagat | caagcgaatc  | gagaacaaaa | gcagtcgaca | agtcactttc | tccaaacgac  | 120 |
| gcaatggtct | catcgacaaa  | gctcgacaac | tttcgattct | ctgtgaatcc | tccgtcgcgtg | 180 |
| ttgtcgtcgt | atctgcctcc  | ggaaaactct | atgactcttc | ctccggtgac | gagatagaag  | 240 |
| cgctgttcaa | gccggagaaa  | cctcaatggt | ttgaactcga | tcttgaagaa | aaaattcaga  | 300 |
| attatcttcc | acacaaggag  | ttactagaaa | cagtccaaag | caagcttgaa | gaaccaaatg  | 360 |
| tcgataatgt | aagtgtagat  | tctctaattt | ctctggagga | acaacttgag | actgctctgt  | 420 |
| ccgtaagtag | agctaggaag  | gcagaactga | tgatggagta | tatcgagtc  | cttaaagaaa  | 480 |
| aggagaaatt | gctgagagaa  | gagaaccagg | ttctggctag | ccagatggga | aagaatacgt  | 540 |
| tgctggcaac | agatgatgag  | agaggaaatg | ttccgggaag | tagctccggc | aacaaaatac  | 600 |
| cggagactct | cccgtgctc   | aattagccac | catcatcaac | ggctgagttt | tcaccttaaa  | 660 |
| ctcaaagcct | gattcataat  | taagagaata | aatttgtata | ttataaaaag | ctgtgtaatc  | 720 |
| tcaaaccctt | tatcttctc   | tagtgtggaa | tttaaggtca | aaaagaaaac | gagaaagtat  | 780 |
| ggatcagtgt | tgtaccTcct  | tcggagacaa | gatcagagtt | tgtgtgtttg | tgtctgaatg  | 840 |
| tacggattgg | attttttaaag | ttgtgctttc | tttctcc    |            |             |     |

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..207  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566728  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Ile Arg Ile Lys Leu Gly His Asn Pro Tyr Arg Arg Phe Glu Ala Met  
1                   5                   10                   15  
Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg  
                 20                   25                   30  
Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala Arg  
                 35                   40                   45  
Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Val Ser  
                 50                   55                   60  
Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu Ala  
65                   70                   75                   80  
Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu Glu  
                 85                   90                   95  
Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val Gln  
                 100                   105                   110  
Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser Leu  
                 115                   120                   125  
Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg Ala  
130                   135                   140  
Arg Lys Ala Glu Leu Met Met Glu Tyr Ile Glu Ser Leu Lys Glu Lys  
145                   150                   155                   160  
Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu Ala Ser Gln Met Gly  
                 165                   170                   175  
Lys Asn Thr Leu Leu Ala Thr Asp Asp Glu Arg Gly Met Phe Pro Gly  
                 180                   185                   190  
Ser Ser Ser Gly Asn Lys Ile Pro Glu Thr Leu Pro Leu Leu Asn  
195                   200                   205

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 192 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..192  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser  
1                   5                   10                   15  
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala  
                 20                   25                   30  
Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Val  
                 35                   40                   45  
Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu  
50                   55                   60  
Ala Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu  
65                   70                   75                   80  
Glu Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val  
                 85                   90                   95  
Gln Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser  
                 100                   105                   110  
Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg  
115                   120                   125

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Lys | Ala | Glu | Leu | Met | Met | Glu | Tyr | Ile | Glu | Ser | Leu | Lys | Glu |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Glu | Lys | Leu | Leu | Arg | Glu | Glu | Asn | Gln | Val | Leu | Ala | Ser | Gln | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Lys | Asn | Thr | Leu | Leu | Ala | Thr | Asp | Asp | Glu | Arg | Gly | Met | Phe | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ser | Ser | Ser | Gly | Asn | Lys | Ile | Pro | Glu | Thr | Leu | Pro | Leu | Leu | Asn |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2022

(D) OTHER INFORMATION: / Ceres Seq. ID 1566737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acagtaacaa  | tctctctctc  | gcaccttctt  | aaaagctgct  | ctattttcttc | gcttccctct  | 60   |
| tctcttcact  | cacaaaacat  | tttgttctaa  | tcccgcgaact | gctaaaaaca  | aacccttttg  | 120  |
| tcaaaaatct  | ctcctttcgg  | tggtagacaga | aatctattgc  | aggaaatggc  | agaagcagca  | 180  |
| tacacagtag  | catcagacag  | tgaaaacact  | ggagaggaga  | aatcatcatc  | atctccttca  | 240  |
| ttacccgaaa  | tcgcccttgg  | tatcgacatt  | ggtacttctc  | aatgcagtat  | agctgtttgg  | 300  |
| aacggttctc  | aagttcacat  | cttgaggaac  | acaagaaacc  | agaagctcat  | caaatcattt  | 360  |
| gtcactttca  | aagatgaagt  | tcctgctggt  | ggtgttagca  | accagctcgc  | acatgagcag  | 420  |
| gaaatgctaa  | ccggagccgc  | tatcttcaac  | atgaagcggc  | tcggttggtcg | tgtagacact  | 480  |
| gacctgtggt  | ttcacgctag  | caagaacctt  | cctttcttgg  | ttcaaaactct | tgatattgga  | 540  |
| gtagacacgt  | ttattgcagc  | tttggtgaac  | aatgcttggg  | gatcaacaac  | accagaggaa  | 600  |
| gttttagcta  | tatttctggt  | ggagttacgt  | ctgatggctg  | aagctcagtt  | gaaacgtcct  | 660  |
| gtgagaaatg  | tagtgcttac  | ggttcogggt  | tcggttctct  | ggttccagct  | cacacggttc  | 720  |
| gaaagagcct  | gcgctatggc  | tggacttcat  | gttcttcggt  | tgatgccgga  | accaactgct  | 780  |
| attgcgttgc  | tttatgcgca  | acagcagcag  | atgactacgc  | atgataacat  | gggaagcggg  | 840  |
| agcgagaggc  | ttgcggttat  | attcaatatg  | ggagctgggt  | actgcgatgt  | tgccggttact | 900  |
| gctactgctg  | gtggtgtttc  | acagataaaa  | gcttttagctg | gtagccccat  | tgggggtgaa  | 960  |
| gacattttgc  | agagcacaat  | tcgccatatc  | gtccacaccta | atgaagaagc  | ttcgggggttg | 1020 |
| cttcgtgtag  | cggcacagga  | cgcgattcac  | aggctaacgg  | atcaagaaaa  | tgtccaaatt  | 1080 |
| gaagtggatt  | tgggaaatgg  | taacaagata  | tccaagggtt  | ttgatagggt  | agagtttgag  | 1140 |
| gaagtgaacc  | agaaggtatt  | tgagggaatg  | gagagacttg  | ttgtgcagtg  | cctgcgagat  | 1200 |
| gcgagagtca  | atggtggtga  | tatcgatgat  | ttgataatgg  | ttggagggtg  | ttcgtacatc  | 1260 |
| ccgaaagtaa  | gaactattat  | caagaacgta  | tgcaagaagg  | atgagatata  | caaaggcgtg  | 1320 |
| aatcctttag  | aagctgcggt  | tagaggagct  | gctttggaag  | gtgcggtgac  | ttcagggatt  | 1380 |
| catgatcctt  | ttgggagcct  | agatctgtta  | accatacaag  | ccacacctct  | tgcatgttga  | 1440 |
| gcaagagcta  | acggaaacaa  | attcataccc  | gtgattcctc  | gtaacacgat  | ggttccagcg  | 1500 |
| cggaaagacc  | tcctttttcac | aacggttcaa  | gacaaccaga  | aggaagctct  | gatcattata  | 1560 |
| tacgaaggag  | aaggagagac  | tgttgaagag  | aatcatcttc  | ttggttattt  | caagctcggt  | 1620 |
| gggattccgc  | cagcaccgaa  | aggtgttcca  | gagatcaatg  | tttgtatgga  | catcgatgcg  | 1680 |
| tcgaatgctt  | tacgggtttt  | cgcagctgtg  | ttgatgccgg  | gatcttcgac  | tccggtgggt  | 1740 |
| cctgtgattg  | aggtgaggat  | gCctacgggt  | gatgatggac  | atgggttggtg | tgctcaagct  | 1800 |
| ttgaatgtga  | aatatggagc  | tactcttgat  | ttgattactt  | ttcagagaaa  | gatgtaagat  | 1860 |
| taaaataaaa  | tggtgttggt  | gatagatttt  | agatttagatg | taagatacga  | ggatgcttcg  | 1920 |
| tatagaaaag  | agtttgtaaa  | gtttgtgtgt  | gttttggggt  | ttgtcggtga  | agtggtaaac  | 1980 |
| aatgttttatg | tgtgtaatga  | agtaataatg  | ctttgcagat  | tg          |             |      |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

|           |     |     |     |          |     |     |           |     |           |     |     |     |     |           |     |
|-----------|-----|-----|-----|----------|-----|-----|-----------|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1  | Ala | Glu | Ala | Ala<br>5 | Tyr | Thr | Val       | Ala | Ser<br>10 | Asp | Ser | Glu | Asn | Thr<br>15 | Gly |
| Glu       | Glu | Lys | Ser | Ser      | Ser | Ser | Pro       | Ser | Leu       | Pro | Glu | Ile | Ala | Leu       | Gly |
|           |     |     | 20  |          |     |     |           | 25  |           |     |     |     | 30  |           |     |
| Ile       | Asp | Ile | Gly | Thr      | Ser | Gln | Cys<br>40 | Ser | Ile       | Ala | Val | Trp | Asn | Gly       | Ser |
|           |     | 35  |     |          |     |     |           |     |           |     |     | 45  |     |           |     |
| Gln       | Val | His | Ile | Leu      | Arg | Asn | Thr       | Arg | Asn       | Gln | Lys | Leu | Ile | Lys       | Ser |
|           |     | 50  |     |          |     | 55  |           |     |           |     | 60  |     |     |           |     |
| Phe<br>65 | Val | Thr | Phe | Lys      | Asp | Glu | Val       | Pro | Ala       | Gly | Gly | Val | Ser | Asn       | Gln |
|           |     |     |     | 70       |     |     |           |     |           | 75  |     |     |     |           | 80  |
| Leu       | Ala | His | Glu | Gln      | Glu | Met | Leu       | Thr | Gly       | Ala | Ala | Ile | Phe | Asn       | Met |
|           |     |     |     | 85       |     |     |           |     | 90        |     |     |     |     | 95        |     |
| Lys       | Arg | Leu | Val | Gly      | Arg | Val | Asp       | Thr | Asp       | Pro | Val | Val | His | Ala       | Ser |
|           |     |     | 100 |          |     |     |           | 105 |           |     |     |     | 110 |           |     |
| Lys       | Asn | Leu | Pro | Phe      | Leu | Val | Gln       | Thr | Leu       | Asp | Ile | Gly | Val | Arg       | Pro |
|           |     |     | 115 |          |     |     | 120       |     |           |     |     | 125 |     |           |     |
| Phe       | Ile | Ala | Ala | Leu      | Val | Asn | Asn       | Ala | Trp       | Arg | Ser | Thr | Thr | Pro       | Glu |
|           |     | 130 |     |          |     | 135 |           |     |           |     | 140 |     |     |           |     |
| Glu       | Val | Leu | Ala | Ile      | Phe | Leu | Val       | Glu | Leu       | Arg | Leu | Met | Ala | Glu       | Ala |
| 145       |     |     |     | 150      |     |     |           |     |           | 155 |     |     |     | 160       |     |
| Gln       | Leu | Lys | Arg | Pro      | Val | Arg | Asn       | Val | Val       | Leu | Thr | Val | Pro | Val       | Ser |
|           |     |     |     | 165      |     |     |           |     | 170       |     |     |     |     | 175       |     |
| Phe       | Ser | Arg | Phe | Gln      | Leu | Thr | Arg       | Phe | Glu       | Arg | Ala | Cys | Ala | Met       | Ala |
|           |     |     | 180 |          |     |     |           | 185 |           |     |     |     | 190 |           |     |
| Gly       | Leu | His | Val | Leu      | Arg | Leu | Met       | Pro | Glu       | Pro | Thr | Ala | Ile | Ala       | Leu |
|           |     | 195 |     |          |     | 200 |           |     |           |     | 205 |     |     |           |     |
| Leu       | Tyr | Ala | Gln | Gln      | Gln | Gln | Met       | Thr | Thr       | His | Asp | Asn | Met | Gly       | Ser |
|           |     | 210 |     |          |     | 215 |           |     |           |     | 220 |     |     |           |     |
| Gly       | Ser | Glu | Arg | Leu      | Ala | Val | Ile       | Phe | Asn       | Met | Gly | Ala | Gly | Tyr       | Cys |
| 225       |     |     |     | 230      |     |     |           |     | 235       |     |     |     |     | 240       |     |
| Asp       | Val | Ala | Val | Thr      | Ala | Thr | Ala       | Gly | Gly       | Val | Ser | Gln | Ile | Lys       | Ala |
|           |     |     |     | 245      |     |     |           |     | 250       |     |     |     |     | 255       |     |
| Leu       | Ala | Gly | Ser | Pro      | Ile | Gly | Gly       | Glu | Asp       | Ile | Leu | Gln | Ser | Thr       | Ile |
|           |     |     | 260 |          |     |     |           | 265 |           |     |     |     | 270 |           |     |
| Arg       | His | Ile | Ala | Pro      | Pro | Asn | Glu       | Glu | Ala       | Ser | Gly | Leu | Leu | Arg       | Val |
|           |     | 275 |     |          |     | 280 |           |     |           |     |     | 285 |     |           |     |
| Ala       | Ala | Gln | Asp | Ala      | Ile | His | Arg       | Leu | Thr       | Asp | Gln | Glu | Asn | Val       | Gln |
|           |     | 290 |     |          |     | 295 |           |     |           |     | 300 |     |     |           |     |
| Ile       | Glu | Val | Asp | Leu      | Gly | Asn | Gly       | Asn | Lys       | Ile | Ser | Lys | Val | Leu       | Asp |
| 305       |     |     |     | 310      |     |     |           |     | 315       |     |     |     |     | 320       |     |
| Arg       | Leu | Glu | Phe | Glu      | Glu | Val | Asn       | Gln | Lys       | Val | Phe | Glu | Glu | Cys       | Glu |
|           |     |     |     | 325      |     |     |           |     | 330       |     |     |     |     | 335       |     |
| Arg       | Leu | Val | Val | Gln      | Cys | Leu | Arg       | Asp | Ala       | Arg | Val | Asn | Gly | Gly       | Asp |
|           |     |     | 340 |          |     |     |           | 345 |           |     |     | 350 |     |           |     |
| Ile       | Asp | Asp | Leu | Ile      | Met | Val | Gly       | Gly | Cys       | Ser | Tyr | Ile | Pro | Lys</     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ile | Pro | Val | Ile | Pro | Arg | Asn | Thr | Met | Val | Pro | Ala | Arg | Lys | Asp |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Leu | Phe | Phe | Thr | Thr | Val | Gln | Asp | Asn | Gln | Lys | Glu | Ala | Leu | Ile | Ile |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ile | Tyr | Glu | Gly | Glu | Gly | Glu | Thr | Val | Glu | Glu | Asn | His | Leu | Leu | Gly |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Tyr | Phe | Lys | Leu | Val | Gly | Ile | Pro | Pro | Ala | Pro | Lys | Gly | Val | Pro | Glu |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ile | Asn | Val | Cys | Met | Asp | Ile | Asp | Ala | Ser | Asn | Ala | Leu | Arg | Val | Phe |
|     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |
| Ala | Ala | Val | Leu | Met | Pro | Gly | Ser | Thr | Pro | Val | Val | Pro | Val | Ile |     |
|     |     | 515 |     |     |     | 520 |     |     |     | 525 |     |     |     |     |     |
| Glu | Val | Arg | Met | Pro | Thr | Val | Asp | Asp | Gly | His | Gly | Trp | Cys | Ala | Gln |
|     | 530 |     |     |     |     | 535 |     |     |     | 540 |     |     |     |     |     |
| Ala | Leu | Asn | Val | Lys | Tyr | Gly | Ala | Thr | Leu | Asp | Leu | Ile | Thr | Phe | Gln |
| 545 |     |     |     |     | 550 |     |     |     | 555 |     |     |     |     |     | 560 |
| Arg | Lys | Met |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Gly | Ala | Ala | Ile | Phe | Asn | Met | Lys | Arg | Leu | Val | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Asp | Thr | Asp | Pro | Val | Val | His | Ala | Ser | Lys | Asn | Leu | Pro | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Gln | Thr | Leu | Asp | Ile | Gly | Val | Arg | Pro | Phe | Ile | Ala | Ala | Leu | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Asn | Ala | Trp | Arg | Ser | Thr | Thr | Pro | Glu | Glu | Val | Leu | Ala | Ile | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Glu | Leu | Arg | Leu | Met | Ala | Glu | Ala | Gln | Leu | Lys | Arg | Pro | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Asn | Val | Val | Leu | Thr | Val | Pro | Val | Ser | Phe | Ser | Arg | Phe | Gln | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Arg | Phe | Glu | Arg | Ala | Cys | Ala | Met | Ala | Gly | Leu | His | Val | Leu | Arg |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Met | Pro | Glu | Pro | Thr | Ala | Ile | Ala | Leu | Leu | Tyr | Ala | Gln | Gln | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Met | Thr | Thr | His | Asp | Asn | Met | Gly | Ser | Gly | Ser | Glu | Arg | Leu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ile | Phe | Asn | Met | Gly | Ala | Gly | Tyr | Cys | Asp | Val | Ala | Val | Thr | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Ala | Gly | Gly | Val | Ser | Gln | Ile | Lys | Ala | Leu | Ala | Gly | Ser | Pro | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Gly | Glu | Asp | Ile | Leu | Gln | Ser | Thr | Ile | Arg | His | Ile | Ala | Pro | Pro |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Asn | Glu | Glu | Ala | Ser | Gly | Leu | Leu | Arg | Val | Ala | Ala | Gln | Asp | Ala | Ile |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| His | Arg | Leu | Thr | Asp | Gln | Glu | Asn | Val | Gln | Ile | Glu | Val | Asp | Leu | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Gly | Asn | Lys | Ile | Ser | Lys | Val | Leu | Asp | Arg | Leu | Glu | Phe | Glu | Glu |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Asn | Gln | Lys | Val | Phe | Glu | Glu | Cys | Glu | Arg | Leu | Val | Val | Gln | Cys |

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|                     | Mean | SD   | Median | Mode | Range | Skewness | Kurtosis | Shapiro-Wilk | Normality |
|---------------------|------|------|--------|------|-------|----------|----------|--------------|-----------|
| Age                 | 35.5 | 10.5 | 35     | 35   | 20-55 | 0.15     | 2.5      | 0.95         | Normal    |
| Gender              | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Marital Status      | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Education           | 12.5 | 1.5  | 12     | 12   | 10-15 | 0.15     | 2.5      | 0.95         | Normal    |
| Occupation          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Income              | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Health Status       | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Stress Level        | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Resilience          | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Optimism            | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Emotional Stability | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Self-Esteem         | 1.5  | 0.5  | 1      | 1    | 1-2   | 0.5      | 0.5      | 0.95         | Normal    |
| Life Satisfaction   | 1.5  | 0.5  | 1      | 1    |       |          |          |              |           |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1566740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Leu | Val | Gly | Arg | Val | Asp | Thr | Asp | Pro | Val | Val | His | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Lys | Asn | Leu | Pro | Phe | Leu | Val | Gln | Thr | Leu | Asp | Ile | Gly | Val | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Phe | Ile | Ala | Ala | Leu | Val | Asn | Asn | Ala | Trp | Arg | Ser | Thr | Thr | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Val | Leu | Ala | Ile | Phe | Leu | Val | Glu | Leu | Arg | Leu | Met | Ala | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Gln | Leu | Lys | Arg | Pro | Val | Arg | Asn | Val | Val | Leu | Thr | Val | Pro | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Phe | Ser | Arg | Phe | Gln | Leu | Thr | Arg | Phe | Glu | Arg | Ala | Cys | Ala | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Gly | Leu | His | Val | Leu | Arg | Leu | Met | Pro | Glu | Pro | Thr | Ala | Ile | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Tyr | Ala | Gln | Gln | Gln | Gln | Met | Thr | Thr | His | Asp | Asn | Met | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Ser | Glu | Arg | Leu | Ala | Val | Ile | Phe | Asn | Met | Gly | Ala | Gly | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Asp | Val | Ala | Val | Thr | Ala | Thr | Ala | Gly | Gly | Val | Ser | Gln | Ile | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |



Ala Leu Ala Gly Ser Pro Ile Gly Gly Glu Asp Ile Leu Gln Ser Thr  
165 170 175  
Ile Arg His Ile Ala Pro Pro Asn Glu Glu Ala Ser Gly Leu Leu Arg  
180 185 190  
Val Ala Ala Gln Asp Ala Ile His Arg Leu Thr Asp Gln Glu Asn Val  
195 200 205  
Gln Ile Glu Val Asp Leu Gly Asn Gly Asn Lys Ile Ser Lys Val Leu  
210 215 220  
Asp Arg Leu Glu Phe Glu Glu Val Asn Gln Lys Val Phe Glu Glu Cys  
225 230 235 240  
Glu Arg Leu Val Val Gln Cys Leu Arg Asp Ala Arg Val Asn Gly Gly  
245 250 255  
Asp Ile Asp Asp Leu Ile Met Val Gly Gly Cys Ser Tyr Ile Pro Lys  
260 265 270  
Val Arg Thr Ile Ile Lys Asn Val Cys Lys Lys Asp Glu Ile Tyr Lys  
275 280 285  
Gly Val Asn Pro Leu Glu Ala Ala Val Arg Gly Ala Ala Leu Glu Gly  
290 295 300  
Ala Val Thr Ser Gly Ile His Asp Pro Phe Gly Ser Leu Asp Leu Leu  
305 310 315 320  
Thr Ile Gln Ala Thr Pro Leu Ala Val Gly Ala Arg Ala Asn Gly Asn  
325 330 335  
Lys Phe Ile Pro Val Ile Pro Arg Asn Thr Met Val Pro Ala Arg Lys  
340 345 350  
Asp Leu Phe Phe Thr Thr Val Gln Asp Asn Gln Lys Glu Ala Leu Ile  
355 360 365  
Ile Ile Tyr Glu Gly Glu Gly Glu Thr Val Glu Glu Asn His Leu Leu  
370 375 380  
Gly Tyr Phe Lys Leu Val Gly Ile Pro Pro Ala Pro Lys Gly Val Pro  
385 390 395 400  
Glu Ile Asn Val Cys Met Asp Ile Asp Ala Ser Asn Ala Leu Arg Val  
405 410 415  
Phe Ala Ala Val Leu Met Pro Gly Ser Ser Thr Pro Val Val Pro Val  
420 425 430  
Ile Glu Val Arg Met Pro Thr Val Asp Asp Gly His Gly Trp Cys Ala  
435 440 445  
Gln Ala Leu Asn Val Lys Tyr Gly Ala Thr Leu Asp Leu Ile Thr Phe  
450 455 460  
Gln Arg Lys Met  
465

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1957 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1957

(D) OTHER INFORMATION: / Ceres Seq. ID 1566745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atagttgtcg tctaattaat atattgttcc aaagaaaaat atgtatctac gtcttgccctc | 60  |
| taacacctct ttttcacatc acaagcatct taaaatttct taaatcactc ttttcgcgat  | 120 |
| gagacatgtc tttgtcgagg tgttggttct gatctctttg gtcattcttg agttgagcta  | 180 |
| tgcgtttgca ccaatctcat cgtatcaatg ggctgctctg tattctcaac gtttcattct  | 240 |
| tggaggcaac aagcagggtta tagtgatcaa cgacatgttc cctggaccga tccttaatgc | 300 |
| aacagcaaac gatatcattg tcgttaacat tttcaacaat ttgcccgaac ccttcctcat  | 360 |
| gacttggaat ggattgcaat tgcggaagaa ctogtggaac gatggagttc gagggacaaa  | 420 |
| ctgtcccata ctaccgggga caaattggac gtaccgtttt caggtgaagg atcaaattgg  | 480 |
| aagttacttt tattttccga cccttctact tcagaaagct gccggaggat acggtgctat  | 540 |

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tagaatctat cccccagaac ttgtcccagt cccattccct aagcccgacg aagaatacga 600
catcttgatt ggagattggt tttatctcga ccatacagtt atgagagctt cacttgacgc 660
tggtcacagt ttgccaaatc ctgatggtat tctttttaac gggcgtggcc ctgaagagac 720
cttctttgca tttgaaccag gcaaaacata taggctaaga atatcaaacg tgggtctcaa 780
aacatgctta aacttcagRa rTScaagncc acgatatgmt tctagttgag acagagggtta 840
cgtatgttca aaaacgtggt tactcgagcc tggacatcca cgtaggccaa tcatactcta 900
ttcttgtcac tgccaaaacc gacccggttg gaatttacg gtcttactac atattcgcca 960
cagctcgggt cactgattcc taccttggcg gtatagcttt aattcgatat cccggttccc 1020
cacttgaccc agtcggacaa ggtccactcg cacctgcttt gcaagatttt ggttcctcag 1080
ttgaacaagc cctttccatt agaattggacc tgaacgttgg agcagcaaga tcgaaccctc 1140
aaggttcgta ccactatgga cgaataaacg taaccagaac gataatatta cataacgacg 1200
ttatgttata gtcggggcaaa ctacgggata cgattaacgg cgtttcgttt gtctaccccg 1260
agactccggt aaagctcggt gatcattttc agctaaatga cagcataatc cctggcatgt 1320
tcccgggttta tccatccaac aaaacaccga ctcttggaac ttcagtggtc gatattcatt 1380
acaaagattt catccacatc gtgttccaga accctctatt tggattggag agttatcaca 1440
tcgatgggta caatttcttc gttgtoggat atggatttgg agcttgggtc gaaagcaaaa 1500
aagctgggata taacttagta gatgcogttt cacggccaac agttcaggtt tatccatatt 1560
cgtggacagc aatattgata gctatggata atcaaggaat gtggaacgtg agatcacaga 1620
aagcagagca atggtatctt ggtcaagagc tttatatgag agttaaaggt gaaggagaag 1680
aagatccttc gactattccg gttagagatg aaaatccgat accgggaaat gtcacccgtt 1740
gtggcaaaag tcgataataa ttaattgtct gaaataataa aaacctagaa aagtctattt 1800
taattagcaa aactaaagaa cgggtttaaag gaatgatcag agagtattag gatctgtgtt 1860
gatcttaggg tttgtggttt gattgcgatt cgaatcactt gtgtaattgc agaagacgga 1920
tggtaattta aagagatgat cttagggttt gtggtct

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1566746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

Met Arg His Val Phe Val Glu Val Leu Val Leu Ile Ser Leu Val Ile
1 5 10 15
Leu Glu Leu Ser Tyr Ala Phe Ala Pro Ile Ser Ser Tyr Gln Trp Val
20 25 30
Val Ser Tyr Ser Gln Arg Phe Ile Leu Gly Gly Asn Lys Gln Val Ile
35 40 45
Val Ile Asn Asp Met Phe Pro Gly Pro Ile Leu Asn Ala Thr Ala Asn
50 55 60
Asp Ile Ile Val Val Asn Ile Phe Asn Asn Leu Pro Glu Pro Phe Leu
65 70 75 80
Met Thr Trp Asn Gly Leu Gln Leu Arg Lys Asn Ser Trp Gln Asp Gly
85 90 95
Val Arg Gly Thr Asn Cys Pro Ile Leu Pro Gly Thr Asn Trp Thr Tyr
100 105 110
Arg Phe Gln Val Lys Asp Gln Ile Gly Ser Tyr Phe Tyr Phe Pro Thr
115 120 125
Leu Leu Leu Gln Lys Ala Ala Gly Gly Tyr Gly Ala Ile Arg Ile Tyr
130 135 140
Pro Pro Glu Leu Val Pro Val Pro Phe Pro Lys Pro Asp Glu Glu Tyr
145 150 155 160
Asp Ile Leu Ile Gly Asp Trp Phe Tyr Leu Asp His Thr Val Met Arg
165 170 175
Ala Ser Leu Asp Ala Gly His Ser Leu Pro Asn Pro Asp Gly Ile Leu
180 185 190
Phe Asn Gly Arg Gly Pro Glu Glu Thr Phe Phe Ala Phe Glu Pro Gly

```

|     |                     |                     |                     |  |     |
|-----|---------------------|---------------------|---------------------|--|-----|
|     | 195                 |                     | 200                 |  | 205 |
| Lys | Thr Tyr Arg Leu Arg | Ile Ser Asn Val Gly | Leu Lys Thr Cys Leu |  |     |
|     | 210                 | 215                 | 220                 |  |     |
| Asn | Phe Xaa Xaa Xaa Xaa | Pro Arg Tyr Xaa     | Ser Ser             |  |     |
| 225 | 230                 | 235                 |                     |  |     |

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1566747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Leu | Val | Glu | Thr | Glu | Gly | Thr | Tyr | Val | Gln | Lys | Arg | Val | Tyr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Leu | Asp | Ile | His | Val | Gly | Gln | Ser | Tyr | Ser | Ile | Leu | Val | Thr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Lys | Thr | Asp | Pro | Val | Gly | Ile | Tyr | Arg | Ser | Tyr | Tyr | Ile | Phe | Ala |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Arg | Phe | Thr | Asp | Ser | Tyr | Leu | Gly | Gly | Ile | Ala | Leu | Ile | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | Pro | Gly | Ser | Pro | Leu | Asp | Pro | Val | Gly | Gln | Gly | Pro | Leu | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Leu | Gln | Asp | Phe | Gly | Ser | Ser | Val | Glu | Gln | Ala | Leu | Ser | Ile | Arg |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Asp | Leu | Asn | Val | Gly | Ala | Ala | Arg | Ser | Asn | Pro | Gln | Gly | Ser | Tyr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Tyr | Gly | Arg | Ile | Asn | Val | Thr | Arg | Thr | Ile | Ile | Leu | His | Asn | Asp |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Met | Leu | Ser | Ser | Gly | Lys | Leu | Arg | Tyr | Thr | Ile | Asn | Gly | Val | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Val | Tyr | Pro | Glu | Thr | Pro | Leu | Lys | Leu | Val | Asp | His | Phe | Gln | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Asp | Thr | Ile | Ile | Pro | Gly | Met | Phe | Pro | Val | Tyr | Pro | Ser | Asn | Lys |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Pro | Thr | Leu | Gly | Thr | Ser | Val | Val | Asp | Ile | His | Tyr | Lys | Asp | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | His | Ile | Val | Phe | Gln | Asn | Pro | Leu | Phe | Gly | Leu | Glu | Ser | Tyr | His |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Asp | Gly | Tyr | Asn | Phe | Phe | Val | Val | Gly | Tyr | Gly | Phe | Gly | Ala | Trp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Glu | Ser | Lys | Lys | Ala | Gly | Tyr | Asn | Leu | Val | Asp | Ala | Val | Ser | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Thr | Val | Gln | Val | Tyr | Pro | Tyr | Ser | Trp | Thr | Ala | Ile | Leu | Ile | Ala |
|     |     | 245 |     |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Asp | Asn | Gln | Gly | Met | Trp | Asn | Val | Arg | Ser | Gln | Lys | Ala | Glu | Gln |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Tyr | Leu | Gly | Gln | Glu | Leu | Tyr | Met | Arg | Val | Lys | Gly | Glu | Gly | Glu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Asp | Pro | Ser | Thr | Ile | Pro | Val | Arg | Asp | Glu | Asn | Pro | Ile | Pro | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Val | Ile | Arg | Cys | Gly | Lys | Val | Arg |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..217  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566748  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Asp Leu Asn Val Gly Ala Ala Arg Ser Asn Pro Gln Gly Ser Tyr  
1 5 10 15  
His Tyr Gly Arg Ile Asn Val Thr Arg Thr Ile Ile Leu His Asn Asp  
20 25 30  
Val Met Leu Ser Ser Gly Lys Leu Arg Tyr Thr Ile Asn Gly Val Ser  
35 40 45  
Phe Val Tyr Pro Glu Thr Pro Leu Lys Leu Val Asp His Phe Gln Leu  
50 55 60  
Asn Asp Thr Ile Ile Pro Gly Met Phe Pro Val Tyr Pro Ser Asn Lys  
65 70 75 80  
Thr Pro Thr Leu Gly Thr Ser Val Val Asp Ile His Tyr Lys Asp Phe  
85 90 95  
Ile His Ile Val Phe Gln Asn Pro Leu Phe Gly Leu Glu Ser Tyr His  
100 105 110  
Ile Asp Gly Tyr Asn Phe Phe Val Val Gly Tyr Gly Phe Gly Ala Trp  
115 120 125  
Ser Glu Ser Lys Lys Ala Gly Tyr Asn Leu Val Asp Ala Val Ser Arg  
130 135 140  
Ser Thr Val Gln Val Tyr Pro Tyr Ser Trp Thr Ala Ile Leu Ile Ala  
145 150 155 160  
Met Asp Asn Gln Gly Met Trp Asn Val Arg Ser Gln Lys Ala Glu Gln  
165 170 175  
Trp Tyr Leu Gly Gln Glu Leu Tyr Met Arg Val Lys Gly Glu Gly Glu  
180 185 190  
Glu Asp Pro Ser Thr Ile Pro Val Arg Asp Glu Asn Pro Ile Pro Gly  
195 200 205  
Asn Val Ile Arg Cys Gly Lys Val Arg  
210 215

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

tatgaaattg tagataaatg gatcaaactg ttaacgtgga tgagtttcaa gagctggcca 60  
aacaggccct ccctaagatg tactatgatt tctacaatgg aggagcagag gatcaacaca 120  
ctctcaatga aaatgtccaa gctttccgta gaatcatggt taggcctagg gttcttgttg 180  
atgtgagcaa catagatatg tctacaagta tattgggtta cccaatctca gtccccatca 240  
tgattgctcc aacagcaatg cataagttgg ctcatcctaa aggagaaatc gccacagcga 300  
aagctgcagc tgcgtgtaac actatcatga tagtaccatt catgtctact tgcactattg 360  
aggaggttgc ttccagtgtg aacgctgttc ggtttcttca aatatatgtg tacaagagac 420  
gtgatgtaac agctcagatt gtgaaaagag ctgaaaaagc tggattcaag gctatagtgc 480  
taactgttga tgttcccaga cttggtagaa gggaagcaga tataaagaac aaaatgatat 540  
ccccacagct gaagaatttt gaaggcttag ttcaaccga agtccgacct aatgaaggtt 600  
caggggttga agcctttgcc tctagtgcac ttgatgcttc gttaagctgg aaggatatcg 660  
aatggttaag atctattaca aagttgccaa ttctgggtcaa agggttactc acacgtgaag 720  
acgctcttaa ggctgttgaa gccgggtgtag atggaatagt ggtatccaac cacggggctc 780

(2) INFORMATION FOR SEQ ID NO:388:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1566750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asp        | Gln        | Ile        | Val<br>5   | Asn        | Val        | Asp        | Glu        | Phe<br>10  | Gln        | Glu        | Leu        | Ala        | Lys<br>15  | Gln        |
| Ala        | Leu        | Pro        | Lys<br>20  | Met        | Tyr        | Tyr        | Asp        | Phe<br>25  | Tyr        | Asn        | Gly        | Gly<br>30  | Ala        | Glu        | Asp        |
| Gln        | His        | Thr<br>35  | Leu        | Asn        | Glu        | Asn        | Val<br>40  | Gln        | Ala        | Phe        | Arg        | Arg<br>45  | Ile        | Met        | Phe        |
| Arg        | Pro<br>50  | Arg        | Val        | Leu        | Val        | Asp<br>55  | Val        | Ser        | Asn        | Ile        | Asp<br>60  | Met        | Ser        | Thr        | Ser        |
| Ile<br>65  | Leu        | Gly        | Tyr        | Pro        | Ile<br>70  | Ser        | Ala        | Pro        | Ile        | Met<br>75  | Ile        | Ala        | Pro        | Thr        | Ala<br>80  |
| Met        | His        | Lys        | Leu        | Ala<br>85  | His        | Pro        | Lys        | Gly        | Glu<br>90  | Ile        | Ala        | Thr        | Ala<br>95  | Lys        | Ala        |
| Ala        | Ala        | Ala        | Cys<br>100 | Asn        | Thr        | Ile        | Met        | Ile<br>105 | Val        | Pro        | Phe        | Met        | Ser<br>110 | Thr        | Cys        |
| Thr        | Ile        | Glu<br>115 | Glu        | Val        | Ala        | Ser        | Ser<br>120 | Cys        | Asn        | Ala        | Val        | Arg<br>125 | Phe        | Leu        | Gln        |
| Ile        | Tyr<br>130 | Val        | Tyr        | Lys        | Arg        | Arg<br>135 | Asp        | Val        | Thr        | Ala        | Gln<br>140 | Ile        | Val        | Lys        | Arg        |
| Ala<br>145 | Glu        | Lys        | Ala        | Gly<br>150 | Phe        | Lys        | Ala        | Ile        | Val        | Leu<br>155 | Thr        | Val        | Asp        | Val        | Pro<br>160 |
| Arg        | Leu        | Gly        | Arg        | Arg<br>165 | Glu        | Ala        | Asp        | Ile        | Lys<br>170 | Asn        | Lys        | Met        | Ile        | Ser<br>175 | Pro        |
| Gln        | Leu        | Lys        | Asn<br>180 | Phe        | Glu        | Gly        | Leu<br>185 | Val        | Ser        | Thr        | Glu        | Val<br>190 | Arg        | Pro        | Asn        |
| Glu        | Gly        | Ser<br>195 | Gly        | Val        | Glu        | Ala        | Phe<br>200 | Ala        | Ser        | Ser        | Ala        | Phe<br>205 | Asp        | Ala        | Ser        |
| Leu        | Ser<br>210 | Trp        | Lys        | Asp        | Ile        | Glu<br>215 | Trp        | Leu        | Arg        | Ser        | Ile        | Thr<br>220 | Lys        | Leu        | Pro        |
| Ile<br>225 | Leu        | Val        | Lys        | Gly<br>230 | Leu        | Leu        | Thr        | Arg        | Glu        | Asp<br>235 | Ala        | Leu        | Lys        | Ala        | Val<br>240 |
| Glu        | Ala        | Gly        | Val        | Asp<br>245 | Gly        | Ile        | Val        | Val        | Ser<br>250 | Asn        | His        | Gly        | Ala<br>255 | Arg        | Gln        |
| Leu        | Asp        | Tyr        | Ser<br>260 | Pro        | Ala        | Thr        | Ile        | Thr<br>265 | Val        | Leu        | Glu        | Glu<br>270 | Val        | Val        | His        |
| Val        | Val        | Lys<br>275 | Gly        | Arg        | Ile        | Pro        | Val<br>280 | Leu        | Leu        | Asp        | Gly        | Gly<br>285 | Val        | Arg        | Arg        |
| Gly        | Thr<br>290 | Asp        | Val        | Phe        | Lys        | Ala<br>295 | Xaa        | Gly        | Ala        | Arg        | Ser<br>300 | Thr        | Ser        | Cys        | Ser        |
| Tyr<br>305 | Arg        | Glu        | Ala        | Tyr        | Ser<br>310 | Leu        | Trp        | Ala        | Cys        | Ser<br>315 |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:389:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1566751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Tyr Tyr Asp Phe Tyr Asn Gly Gly Ala Glu Asp Gln His Thr Leu  
1 5 10 15  
Asn Glu Asn Val Gln Ala Phe Arg Arg Ile Met Phe Arg Pro Arg Val  
20 25 30  
Leu Val Asp Val Ser Asn Ile Asp Met Ser Thr Ser Ile Leu Gly Tyr  
35 40 45  
Pro Ile Ser Ala Pro Ile Met Ile Ala Pro Thr Ala Met His Lys Leu  
50 55 60  
Ala His Pro Lys Gly Glu Ile Ala Thr Ala Lys Ala Ala Ala Cys  
65 70 75 80  
Asn Thr Ile Met Ile Val Pro Phe Met Ser Thr Cys Thr Ile Glu Glu  
85 90 95  
Val Ala Ser Ser Cys Asn Ala Val Arg Phe Leu Gln Ile Tyr Val Tyr  
100 105 110  
Lys Arg Arg Asp Val Thr Ala Gln Ile Val Lys Arg Ala Glu Lys Ala  
115 120 125  
Gly Phe Lys Ala Ile Val Leu Thr Val Asp Val Pro Arg Leu Gly Arg  
130 135 140  
Arg Glu Ala Asp Ile Lys Asn Lys Met Ile Ser Pro Gln Leu Lys Asn  
145 150 155 160  
Phe Glu Gly Leu Val Ser Thr Glu Val Arg Pro Asn Glu Gly Ser Gly  
165 170 175  
Val Glu Ala Phe Ala Ser Ser Ala Phe Asp Ala Ser Leu Ser Trp Lys  
180 185 190  
Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys Leu Pro Ile Leu Val Lys  
195 200 205  
Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys Ala Val Glu Ala Gly Val  
210 215 220  
Asp Gly Ile Val Val Ser Asn His Gly Ala Arg Gln Leu Asp Tyr Ser  
225 230 235 240  
Pro Ala Thr Ile Thr Val Leu Glu Glu Val Val His Val Val Lys Gly  
245 250 255  
Arg Ile Pro Val Leu Leu Asp Gly Gly Val Arg Arg Gly Thr Asp Val  
260 265 270  
Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser Cys Ser Tyr Arg Glu Ala  
275 280 285  
Tyr Ser Leu Trp Ala Cys Ser  
290 295

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1566752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

Met Phe Arg Pro Arg Val Leu Val Asp Val Ser Asn Ile Asp Met Ser
1 5 10 15
Thr Ser Ile Leu Gly Tyr Pro Ile Ser Ala Pro Ile Met Ile Ala Pro
 20 25 30
Thr Ala Met His Lys Leu Ala His Pro Lys Gly Glu Ile Ala Thr Ala
 35 40 45
Lys Ala Ala Ala Ala Cys Asn Thr Ile Met Ile Val Pro Phe Met Ser
50 55 60
Thr Cys Thr Ile Glu Glu Val Ala Ser Ser Cys Asn Ala Val Arg Phe
65 70 75 80
Leu Gln Ile Tyr Val Tyr Lys Arg Arg Asp Val Thr Ala Gln Ile Val
 85 90 95
Lys Arg Ala Glu Lys Ala Gly Phe Lys Ala Ile Val Leu Thr Val Asp
 100 105 110
Val Pro Arg Leu Gly Arg Arg Glu Ala Asp Ile Lys Asn Lys Met Ile
 115 120 125
Ser Pro Gln Leu Lys Asn Phe Glu Gly Leu Val Ser Thr Glu Val Arg
130 135 140
Pro Asn Glu Gly Ser Gly Val Glu Ala Phe Ala Ser Ser Ala Phe Asp
145 150 155 160
Ala Ser Leu Ser Trp Lys Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys
 165 170 175
Leu Pro Ile Leu Val Lys Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys
 180 185 190
Ala Val Glu Ala Gly Val Asp Gly Ile Val Val Ser Asn His Gly Ala
 195 200 205
Arg Gln Leu Asp Tyr Ser Pro Ala Thr Ile Thr Val Leu Glu Glu Val
210 215 220
Val His Val Val Lys Gly Arg Ile Pro Val Leu Leu Asp Gly Gly Val
225 230 235 240
Arg Arg Gly Thr Asp Val Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser
 245 250 255
Cys Ser Tyr Arg Glu Ala Tyr Ser Leu Trp Ala Cys Ser
 260 265

```

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```

taatttgggg tcaggggtgg gagtacccctc gacttatgat gacatttctc aatcaagagg 60
aggctacaga gatgcctaca gtttgccaca gagtgcaaca acagggaccg gatcgctttg 120
gtccagacag ccctttgagc agtttggttg agcggagagg aatgggtgctg ttggtgagga 180
gctcaggaat agatcgaatc cgatcaatat agacaacaac gcttcttcta atgttgatgc 240
agaggctaag cttcttcagt cgttcaggca ctgtattcta aagcttatta aacttgaagg 300
atccgagtggt ttgtttggac aaagcgatgg agttgatgaa gaactgattg accgggtagc 360
tgcacgagag aagtttatct atgaagctga agctcgagaa ataaaccagg tgggtcacat 420
gggggagcaa ctaatttcac cggttcctaa ctgtggagat ggttgcggtt ggagagctga 480
tttgattgtg agctttggag tttggtgcat tcacMgtgtc cttgacttgt ctctcatgga 540
gagtcggcct gagctttggg gaaagtacac ttacgttctc aaccgcctac agggagtgat 600
tgatccggcg ttctcaaagc tgcggacacc aatgacaccg tgctttttgcc ttcagattcc 660
agcgagccac cagagagcga gtccgacttc agctaaccga atgttacctc cggctgcaaa 720
accggctaaa ggcaaatgca caaccgcagt cacacttctt gatctaataa aagacgttga 780
aatggcaatc tctttagtaa aaggccgaac cggtagacgt gcaggtgatg tggctttccc 840
aaaggggaaa gagaatttgg cttcgggttt gaagcgggtat aaacgtcggg tatcgaataa 900

```

accagtaggt atgaatcagg atggacccgg ttcaagaaaa aacgtgactg cgtacggatc 960  
attgggttga agaagaagaa cattgtgaga aatctcatga tcaaagtgac gtcgagaggg 1020  
aagccgaaga atcaaaactc tcgcttttga ttgctcctct gcttcgttaa ttgtgtatta 1080  
agaaaagaag aaaaaaatg gatttttgtt gcttcagaat ttttcgctct ttttttctta 1140  
ttttggttgt aatgttatgt ttatatacat atatcttc

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1566764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Asn Leu Gly Ser Gly Val Gly Val Pro Ser Thr Tyr Asp Asp Ile Ser  
1 5 10 15  
Gln Ser Arg Gly Tyr Arg Asp Ala Tyr Ser Leu Pro Gln Ser Ala  
20 25 30  
Thr Thr Gly Thr Gly Ser Leu Trp Ser Arg Gln Pro Phe Glu Gln Phe  
35 40 45  
Val Val Ala Glu Arg Asn Gly Ala Val Gly Glu Glu Leu Arg Asn Arg  
50 55 60  
Ser Asn Pro Ile Asn Ile Asp Asn Asn Ala Ser Ser Asn Val Asp Ala  
65 70 75 80  
Glu Ala Lys Leu Leu Gln Ser Phe Arg His Cys Ile Leu Lys Leu Ile  
85 90 95  
Lys Leu Glu Gly Ser Glu Trp Leu Phe Gly Gln Ser Asp Gly Val Asp  
100 105 110  
Glu Glu Leu Ile Asp Arg Val Ala Ala Arg Glu Lys Phe Ile Tyr Glu  
115 120 125  
Ala Glu Ala Arg Glu Ile Asn Gln Val Gly His Met Gly Glu Gln Leu  
130 135 140  
Ile Ser Ser Val Pro Asn Cys Gly Asp Gly Cys Val Trp Arg Ala Asp  
145 150 155 160  
Leu Ile Val Ser Phe Gly Val Trp Cys Ile His Xaa Val Leu Asp Leu  
165 170 175  
Ser Leu Met Glu Ser Arg Pro Glu Leu Trp Gly Lys Tyr Thr Tyr Val  
180 185 190  
Leu Asn Arg Leu Gln Gly Val Ile Asp Pro Ala Phe Ser Lys Leu Arg  
195 200 205  
Thr Pro Met Thr Pro Cys Phe Cys Leu Gln Ile Pro Ala Ser His Gln  
210 215 220  
Arg Ala Ser Pro Thr Ser Ala Asn Gly Met Leu Pro Pro Ala Ala Lys  
225 230 235 240  
Pro Ala Lys Gly Lys Cys Thr Thr Ala Val Thr Leu Leu Asp Leu Ile  
245 250 255  
Lys Asp Val Glu Met Ala Ile Ser Cys Arg Lys Gly Arg Thr Gly Thr  
260 265 270  
Ala Ala Gly Asp Val Ala Phe Pro Lys Gly Lys Glu Asn Leu Ala Ser  
275 280 285  
Val Leu Lys Arg Tyr Lys Arg Arg Leu Ser Asn Lys Pro Val Gly Met  
290 295 300  
Asn Gln Asp Gly Pro Gly Ser Arg Lys Asn Val Thr Ala Tyr Gly Ser  
305 310 315 320  
Leu Gly

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..183
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1566765
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Met Gly Glu Gln Leu Ile Ser Ser Val Pro Asn Cys Gly Asp Gly Cys  
1 5 10 15  
Val Trp Arg Ala Asp Leu Ile Val Ser Phe Gly Val Trp Cys Ile His  
20 25 30  
Xaa Val Leu Asp Leu Ser Leu Met Glu Ser Arg Pro Glu Leu Trp Gly  
35 40 45  
Lys Tyr Thr Tyr Val Leu Asn Arg Leu Gln Gly Val Ile Asp Pro Ala  
50 55 60  
Phe Ser Lys Leu Arg Thr Pro Met Thr Pro Cys Phe Cys Leu Gln Ile  
65 70 75 80  
Pro Ala Ser His Gln Arg Ala Ser Pro Thr Ser Ala Asn Gly Met Leu  
85 90 95  
Pro Pro Ala Ala Lys Pro Ala Lys Gly Lys Cys Thr Thr Ala Val Thr  
100 105 110  
Leu Leu Asp Leu Ile Lys Asp Val Glu Met Ala Ile Ser Cys Arg Lys  
115 120 125  
Gly Arg Thr Gly Thr Ala Ala Gly Asp Val Ala Phe Pro Lys Gly Lys  
130 135 140  
Glu Asn Leu Ala Ser Val Leu Lys Arg Tyr Lys Arg Arg Leu Ser Asn  
145 150 155 160  
Lys Pro Val Gly Met Asn Gln Asp Gly Pro Gly Ser Arg Lys Asn Val  
165 170 175  
Thr Ala Tyr Gly Ser Leu Gly  
180

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1514 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1514
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1566766
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

atttctctac caccgttgat gttagggttt cggctgtatt ctccaccgctg ctgacggaga 60  
cgcccccgaat ccgcaattta atcttcgagg ttcgatttta gtgaagaaca agattcaata 120  
gtgatatgca gatctcatgt ctcccaattt cgattccttc gatcactcct cgaacctcaa 180  
ttccactctt accatcactc tcctcaaadc ctgcgcgcac ttccaacctc acttcacttc 240  
agagcccaaa tcaactgttt ttcaaaagat tacataaadc tcagactggg ttccagcaatc 300  
cagttttggc tgccatgaaa agagaagaag atgttgaagt cgatgattcg ttttatatga 360  
gaaagtgtgt ggagctagca aaaagagcaa ttgggtgtac aagtcctaata cctatggtag 420  
gttgtgtcat tgtcaaagat ggtgacattg ttggccaagg gtttcatccc aaagctggtc 480  
agcctcatgc tgaggtgttt gctcttagag atgctggaga gttagctgag aatgctactg 540  
cttatgttag tttggaacca tgtaatcatt acggaagaac accgccgtgt acagaagcat 600  
tgattaaggc taagggtgaga agagttgtta ttgggatggg tgatccgaat ccaattgttt 660  
tttcttcggg tatttagtcgg ttgaaagatg ctggaatcga tgttactgtg agtggtgaag 720  
aagagttatg caagaagatg aatgagggat tcatccatcg aatgttaaca gggaagcctt 780  
ttctcgccct caggtattct atgtctgtca atggttgttt gctagacaag attgggcaag 840  
gggcttcgga tagtggtgga tactactcga agctattgca ggaatatgat gcgataatac 900

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| ttttcttctc | ggtatcggat | gaactctcga | gcatttcttc  | acaagaagct | attaatgttt | 960  |
| cgatccaacc | tattcagatc | atagtagcta | gcaatgcaca  | acagtctcat | atccttgctt | 1020 |
| cttcccacac | tgtggaagaa | tcgggtccaa | aagttgtagt  | tttcaccgca | aaggaatcgg | 1080 |
| ttgcagaatc | cggaatcagt | agtagcgggg | tcgaaaaccgt | agtattggAa | aagmtaaact | 1140 |
| tggattccat | tttggattat | tgttacaacc | gtggactatg  | cagtgtcttg | ttagatttga | 1200 |
| gggggaacgt | caaagacctt | gaagttcttc | tgagagatgg  | atttgagcag | aaactattgc | 1260 |
| agaaagtaat | tattgaggtc | ttgccggaat | ggagcacaaa  | agatgagaga | cagatcgcgt | 1320 |
| cgatgaagtg | gttagaatca | aagcatgtga | aagatttgca  | gtctaagcaa | ttaggtggaa | 1380 |
| gcgttttgct | agagggctat | ttttgatgtt | ttcatgtatg  | aatgaataca | agtcatgata | 1440 |
| tttacctttt | ttaaagcata | gtattattaa | ggttttacag  | atcctattat | taatagattg | 1500 |
| ataacagatt | tttg       |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1566767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ile | Ser | Cys | Leu | Pro | Ile | Ser | Ile | Pro | Ser | Ile | Thr | Pro | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Ile | Pro | Leu | Leu | Pro | Ser | Leu | Ser | Ser | Asn | Pro | Arg | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Phe | Asn | Leu | Thr | Ser | Leu | Gln | Ser | Pro | Asn | His | Cys | Phe | Phe | Lys | Arg |
|     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | His | Lys | Ser | Gln | Thr | Gly | Phe | Ser | Asn | Pro | Val | Leu | Ala | Ala | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Glu | Glu | Asp | Val | Glu | Val | Asp | Asp | Ser | Phe | Tyr | Met | Arg | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Cys | Val | Glu | Leu | Ala | Lys | Arg | Ala | Ile | Gly | Cys | Thr | Ser | Pro | Asn | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Val | Gly | Cys | Val | Ile | Val | Lys | Asp | Gly | Asp | Ile | Val | Gly | Gln | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | His | Pro | Lys | Ala | Gly | Gln | Pro | His | Ala | Glu | Val | Phe | Ala | Leu | Arg |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Gly | Glu | Leu | Ala | Glu | Asn | Ala | Thr | Ala | Tyr | Val | Ser | Leu | Glu |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Pro | Cys | Asn | His | Tyr | Gly | Arg | Thr | Pro | Pro | Cys | Thr | Glu | Ala | Leu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Ala | Lys | Val | Arg | Arg | Val | Val | Ile | Gly | Met | Val | Asp | Pro | Asn | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Val | Phe | Ser | Ser | Gly | Ile | Ser | Arg | Leu | Lys | Asp | Ala | Gly | Ile | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Thr | Val | Ser | Val | Glu | Glu | Glu | Leu | Cys | Lys | Lys | Met | Asn | Glu | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Ile | His | Arg | Met | Leu | Thr | Gly | Lys | Pro | Phe | Leu | Ala | Leu | Arg | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Ser | Met | Ser | Val | Asn | Gly | Cys | Leu | Leu | Asp | Lys | Ile | Gly | Gln | Gly | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Asp | Ser | Gly | Gly | Tyr | Tyr | Ser | Lys | Leu | Leu | Gln | Glu | Tyr | Asp | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ile | Leu | Ser | Ser | Ser | Leu | Ser | Asp | Glu | Leu | Ser | Ser | Ile | Ser | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Glu | Ala | Ile | Asn | Val | Ser | Ile | Gln | Pro | Ile | Gln | Ile | Ile | Val | Ala |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Ser | Asn | Ala | Gln | Gln | Ser | His | Ile | Leu | Ala | Ser | Ser | His | Thr | Val | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu Ser Val Ala  
305 310 315 320  
Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val Leu Glu Lys  
325 330 335  
Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg Gly Leu Cys  
340 345 350  
Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu Glu Val Leu  
355 360 365  
Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val Ile Ile Glu  
370 375 380  
Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile Ala Ser Met  
385 390 395 400  
Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser Lys Gln Leu  
405 410 415  
Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe  
420 425

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1566768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Met Lys Arg Glu Glu Asp Val Glu Val Asp Ser Phe Tyr Met Arg  
1 5 10 15  
Lys Cys Val Glu Leu Ala Lys Arg Ala Ile Gly Cys Thr Ser Pro Asn  
20 25 30  
Pro Met Val Gly Cys Val Ile Val Lys Asp Gly Asp Ile Val Gly Gln  
35 40 45  
Gly Phe His Pro Lys Ala Gly Gln Pro His Ala Glu Val Phe Ala Leu  
50 55 60  
Arg Asp Ala Gly Glu Leu Ala Glu Asn Ala Thr Ala Tyr Val Ser Leu  
65 70 75 80  
Glu Pro Cys Asn His Tyr Gly Arg Thr Pro Pro Cys Thr Glu Ala Leu  
85 90 95  
Ile Lys Ala Lys Val Arg Arg Val Val Ile Gly Met Val Asp Pro Asn  
100 105 110  
Pro Ile Val Phe Ser Ser Gly Ile Ser Arg Leu Lys Asp Ala Gly Ile  
115 120 125  
Asp Val Thr Val Ser Val Glu Glu Leu Cys Lys Lys Met Asn Glu  
130 135 140  
Gly Phe Ile His Arg Met Leu Thr Gly Lys Pro Phe Leu Ala Leu Arg  
145 150 155 160  
Tyr Ser Met Ser Val Asn Gly Cys Leu Leu Asp Lys Ile Gly Gln Gly  
165 170 175  
Ala Ser Asp Ser Gly Gly Tyr Tyr Ser Lys Leu Leu Gln Glu Tyr Asp  
180 185 190  
Ala Ile Ile Leu Ser Ser Ser Leu Ser Asp Glu Leu Ser Ser Ile Ser  
195 200 205  
Ser Gln Glu Ala Ile Asn Val Ser Ile Gln Pro Ile Gln Ile Ile Val  
210 215 220  
Ala Ser Asn Ala Gln Gln Ser His Ile Leu Ala Ser Ser His Thr Val  
225 230 235 240  
Glu Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu Ser Val  
245 250 255  
Ala Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val Leu Glu

260 265 270  
Lys Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg Gly Leu  
275 280 285  
Cys Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu Glu Val  
290 295 300  
Leu Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val Ile Ile  
305 310 315 320  
Glu Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile Ala Ser  
325 330 335  
Met Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser Lys Gln  
340 345 350  
Leu Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe  
355 360

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1566769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Arg Lys Cys Val Glu Leu Ala Lys Arg Ala Ile Gly Cys Thr Ser  
1 5 10 15  
Pro Asn Pro Met Val Gly Cys Val Ile Val Lys Asp Gly Asp Ile Val  
20 25 30  
Gly Gln Gly Phe His Pro Lys Ala Gly Gln Pro His Ala Glu Val Phe  
35 40 45  
Ala Leu Arg Asp Ala Gly Glu Leu Ala Glu Asn Ala Thr Ala Tyr Val  
50 55 60  
Ser Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Pro Pro Cys Thr Glu  
65 70 75 80  
Ala Leu Ile Lys Ala Lys Val Arg Arg Val Ile Gly Met Val Asp  
85 90 95  
Pro Asn Pro Ile Val Phe Ser Ser Gly Ile Ser Arg Leu Lys Asp Ala  
100 105 110  
Gly Ile Asp Val Thr Val Ser Val Glu Glu Glu Leu Cys Lys Lys Met  
115 120 125  
Asn Glu Gly Phe Ile His Arg Met Leu Thr Gly Lys Pro Phe Leu Ala  
130 135 140  
Leu Arg Tyr Ser Met Ser Val Asn Gly Cys Leu Leu Asp Lys Ile Gly  
145 150 155 160  
Gln Gly Ala Ser Asp Ser Gly Gly Tyr Tyr Ser Lys Leu Leu Gln Glu  
165 170 175  
Tyr Asp Ala Ile Ile Leu Ser Ser Ser Leu Ser Asp Glu Leu Ser Ser  
180 185 190  
Ile Ser Ser Gln Glu Ala Ile Asn Val Ser Ile Gln Pro Ile Gln Ile  
195 200 205  
Ile Val Ala Ser Asn Ala Gln Gln Ser His Ile Leu Ala Ser Ser His  
210 215 220  
Thr Val Glu Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu  
225 230 235 240  
Ser Val Ala Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val  
245 250 255  
Leu Glu Lys Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg  
260 265 270  
Gly Leu Cys Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu  
275 280 285

Glu Val Leu Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val  
290 295 300  
Ile Ile Glu Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile  
305 310 315 320  
Ala Ser Met Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser  
325 330 335  
Lys Gln Leu Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe  
340 345

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1571
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

atcatctctc tcacttccac aaaactcaaa aaaatgtctc ccattccaaa accactcttc 60  
ttcttcttct tctcaacta KtgCtatctc tctcaacctc actctctctt cacctcccac 120  
tcacatctct ccctatctcc accaccacaa actctcaccg cttcaccacc tccctcctct 180  
cccggaaaaa cccatctccg tcgtctccac catacaactt ccgatcaaga ttcaaatact 240  
caatggctct aatcatctca ctcccatag gaacaccacc acaagctcaa caaatgggtc 300  
ttgacactgg aagccaactt tcttgatcc aatgtcatcg taaaaagctt cctccaaaac 360  
caaaaacatc atttgatcca tctctttctt cttctttctc aactttgcct tgctcacatc 420  
ctctttgtaa accgagaatt cccgatttta cccttcctac ttcttgtagc tccaacaggt 480  
tatgtcacta ctcttacttc tacgtgatg gaaccttcgc tgagggtaat ctggtcaaag 540  
aaaaaatcac tttctcaaat accgaaatta cccctccttt gatactaggt tgcgtacag 600  
agtcttctga tgataggggc attttgggaa tgaaccgtgg tcgtctctct tttgtttctc 660  
aagctaagat ttcgaagttc tcttattgca tccctcccaa atcaaaccgg ccggttttta 720  
ctccaaccgg ttcgttttac cttggtgata acccgaattc acacggtttc aaatacgttt 780  
ctttgttgac ttttcctgaa agtcaacgaa tgccgaatct tgatcctctt gcttacctg 840  
ttcctatgat tgggattaga tttggtttga agaagcttaa catttcagggt tcggttttca 900  
gaccgatgc aggcgggtcg ggtcaaacaa tgggtgatcc gggatccgag tttactcatt 960  
tagtagacgc agcttacgat aaagtaagag cagagataat gacacgtgta ggacgaagat 1020  
taaagaaggg ttacgtctac ggtggaacag ctgacatgtg ttccgatgga aacgtggcga 1080  
tgatccacag gttgatagga gatcttgtgt ttgtgttcac tagaggagtt gagatattg 1140  
ttccgaaaga gagggttttg gttaacgtag gaggtgggat tcattgcgtt ggaatcggac 1200  
ggtcgagtat gcttgagct gctagtaata taatcgggaa cgttcatcag caaaatcttt 1260  
gggttgagtt cgatgtgacc aatagaagag tgggtttcgc taaagctgat tgtagcagag 1320  
tagtgtgagg aaaagggttc tgctacggtt acaaacaagg gtcttatggt ggactcgggt 1380  
aaagatcgtc gttcgatgat gttaatcgga cggtagatat taaaatagca gttttgtatg 1440  
aaggaacttt tattaggggc tctgaacaat gtcctacaaa taattaaaag tgttcacgtt 1500  
agatttttat gttgtaccgt ttgtatatta tatggttcat attaacttgt tacataaaaa 1560  
tatcttttat t

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..441
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

His Leu Ser His Phe His Lys Thr Gln Lys Asn Val Ser His Ser Lys  
1 5 10 15

Thr Thr Leu Leu Leu Leu Pro Gln Leu Xaa Leu Ser Leu Ser Thr  
20 25 30  
Ser Leu Ser Leu His Leu Pro Leu Thr Ser Leu Pro Ile Ser Thr Thr  
35 40 45  
Thr Asn Ser His Arg Phe Thr Thr Ser Leu Leu Ser Arg Lys Asn Pro  
50 55 60  
Ser Pro Ser Ser Pro Pro Tyr Asn Phe Arg Ser Arg Phe Lys Tyr Ser  
65 70 75 80  
Met Ala Leu Ile Ile Ser Leu Pro Ile Gly Thr Pro Pro Gln Ala Gln  
85 90 95  
Gln Met Val Leu Asp Thr Gly Ser Gln Leu Ser Trp Ile Gln Cys His  
100 105 110  
Arg Lys Lys Leu Pro Pro Lys Pro Lys Thr Ser Phe Asp Pro Ser Leu  
115 120 125  
Ser Ser Ser Phe Ser Thr Leu Pro Cys Ser His Pro Leu Cys Lys Pro  
130 135 140  
Arg Ile Pro Asp Phe Thr Leu Pro Thr Ser Cys Asp Ser Asn Arg Leu  
145 150 155 160  
Cys His Tyr Ser Tyr Phe Tyr Ala Asp Gly Thr Phe Ala Glu Gly Asn  
165 170 175  
Leu Val Lys Glu Lys Ile Thr Phe Ser Asn Thr Glu Ile Thr Pro Pro  
180 185 190  
Leu Ile Leu Gly Cys Ala Thr Glu Ser Ser Asp Asp Arg Gly Ile Leu  
195 200 205  
Gly Met Asn Arg Gly Arg Leu Ser Phe Val Ser Gln Ala Lys Ile Ser  
210 215 220  
Lys Phe Ser Tyr Cys Ile Pro Pro Lys Ser Asn Arg Pro Gly Phe Thr  
225 230 235 240  
Pro Thr Gly Ser Phe Tyr Leu Gly Asp Asn Pro Asn Ser His Gly Phe  
245 250 255  
Lys Tyr Val Ser Leu Leu Thr Phe Pro Glu Ser Gln Arg Met Pro Asn  
260 265 270  
Leu Asp Pro Leu Ala Tyr Thr Val Pro Met Ile Gly Ile Arg Phe Gly  
275 280 285  
Leu Lys Lys Leu Asn Ile Ser Gly Ser Val Phe Arg Pro Asp Ala Gly  
290 295 300  
Gly Ser Gly Gln Thr Met Val Asp Ser Gly Ser Glu Phe Thr His Leu  
305 310 315 320  
Val Asp Ala Ala Tyr Asp Lys Val Arg Ala Glu Ile Met Thr Arg Val  
325 330 335  
Gly Arg Arg Leu Lys Lys Gly Tyr Val Tyr Gly Gly Thr Ala Asp Met  
340 345 350  
Cys Phe Asp Gly Asn Val Ala Met Ile Pro Arg Leu Ile Gly Asp Leu  
355 360 365  
Val Phe Val Phe Thr Arg Gly Val Glu Ile Phe Val Pro Lys Glu Arg  
370 375 380  
Val Leu Val Asn Val Gly Gly Gly Ile His Cys Val Gly Ile Gly Arg  
385 390 395 400  
Ser Ser Met Leu Gly Ala Ala Ser Asn Ile Ile Gly Asn Val His Gln  
405 410 415  
Gln Asn Leu Trp Val Glu Phe Asp Val Thr Asn Arg Arg Val Gly Phe  
420 425 430  
Ala Lys Ala Asp Cys Ser Arg Val Val  
435 440

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1566787

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1566788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Val Leu Asp Thr Gly Ser Gln Leu Ser Trp Ile Gln Cys His Arg  
1 5 10 15  
Lys Lys Leu Pro Pro Lys Pro Lys Thr Ser Phe Asp Pro Ser Leu Ser  
20 25 30  
Ser Ser Phe Ser Thr Leu Pro Cys Ser His Pro Leu Cys Lys Pro Arg  
35 40 45  
Ile Pro Asp Phe Thr Leu Pro Thr Ser Cys Asp Ser Asn Arg Leu Cys  
50 55 60  
His Tyr Ser Tyr Phe Tyr Ala Asp Gly Thr Phe Ala Glu Gly Asn Leu  
65 70 75 80  
Val Lys Glu Lys Ile Thr Phe Ser Asn Thr Glu Ile Thr Pro Pro Leu  
85 90 95  
Ile Leu Gly Cys Ala Thr Glu Ser Ser Asp Asp Arg Gly Ile Leu Gly  
100 105 110  
Met Asn Arg Gly Arg Leu Ser Phe Val Ser Gln Ala Lys Ile Ser Lys  
115 120 125  
Phe Ser Tyr Cys Ile Pro Pro Lys Ser Asn Arg Pro Gly Phe Thr Pro  
130 135 140  
Thr Gly Ser Phe Tyr Leu Gly Asp Asn Pro Asn Ser His Gly Phe Lys  
145 150 155 160  
Tyr Val Ser Leu Leu Thr Phe Pro Glu Ser Gln Arg Met Pro Asn Leu  
165 170 175  
Asp Pro Leu Ala Tyr Thr Val Pro Met Ile Gly Ile Arg Phe Gly Leu  
180 185 190  
Lys Lys Leu Asn Ile Ser Gly Ser Val Phe Arg Pro Asp Ala Gly Gly  
195 200 205  
Ser Gly Gln Thr Met Val Asp Ser Gly Ser Glu Phe Thr His Leu Val  
210 215 220  
Asp Ala Ala Tyr Asp Lys Val Arg Ala Glu Ile Met Thr Arg Val Gly  
225 230 235 240  
Arg Arg Leu Lys Lys Gly Tyr Val Tyr Gly Gly Thr Ala Asp Met Cys  
245 250 255  
Phe Asp Gly Asn Val Ala Met Ile Pro Arg Leu Ile Gly Asp Leu Val  
260 265 270  
Phe Val Phe Thr Arg Gly Val Glu Ile Phe Val Pro Lys Glu Arg Val  
275 280 285  
Leu Val Asn Val Gly Gly Gly Ile His Cys Val Gly Ile Gly Arg Ser  
290 295 300  
Ser Met Leu Gly Ala Ala Ser Asn Ile Ile Gly Asn Val His Gln Gln  
305 310 315 320  
Asn Leu Trp Val Glu Phe Asp Val Thr Asn Arg Arg Val Gly Phe Ala  
325 330 335  
Lys Ala Asp Cys Ser Arg Val Val  
340

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1816
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atgtttatag ttactacaag agtcactgag aaataaatta tacaaaatat gtctaatagaa | 60  |
| aattctgtaa tgtcattgat atcgcatctc tggatcatctc tgtcttcaag atgtatcaat | 120 |
| tgcgttgtaa ggtttattcc ttttcgggttg cttgcaagcg aagttaacca acaaaggcgg | 180 |



accagtacaa tggcctgtgt ttgggataac tcccagagttc ttccttcatg ttcacgatat 240  
gtttggatgg gtcacccgat gtttgacgaa aagccgagga acgtttcctt accaacgaat 300  
ctgggttagt ggatcttacg gagccatgac tagtggtcct gcaaacatcg aatacatgct 360  
caaaaccaat ttcaagaact ttcctaaagg agagttttac aaagagagat tccgtgactt 420  
actcgaagat ggtattttca atgcggatga tgaatcttg aaagaacaga gacggatcat 480  
cataacagaa atgcattcca ctgccttcgt ggatcattct ttcagacga cgagagattt 540  
gatagagagg aagcttttaa aagtgatgga gagtttctcc aagtcacaag aagcttttga 600  
tcttcaagag attccttttac ggttaacatt tgataatatc tgcacgcgg gtcttgga 660  
tgatccgggg actttggatg atgatcttcc tcacgttcca ttcgccaagg cgtttgaaga 720  
agcaacagag tctactctgt ttcggttcat gattccgcct tttgtgtgga aaccaatgaa 780  
gtttttcgt atagggtagt agaaagggtc tagggaagcg gttgagacgg ttcacaactt 840  
tatcgacaag atggtttgtg aacgaatcgc gatgcttaag gaccaaggaa cattagcgaa 900  
tagcaaatcc gatgtcctct cgaggctaata acagatcgaa agtcacaaaa gaggcgatga 960  
aaatgatcga ttcaccgcca agtttttcag acagtctctg tcaagcttca tcttagccgg 1020  
acgagacacg agttccgctg cgcttacttg gttcttcttg ttgataacaa aacaccggga 1080  
agtcgaaacc aagatccttc acgaaatcag agaaatcttg agccaaagag agaagaacaa 1140  
ctacaagctt gatgaaaccg gagaaacgga gagttctcgt cacttcacag tcaaagaact 1200  
aaacgatatg gtttatctac aagcagcatt gtcagaatct cttagactct atccaccaat 1260  
tccaatggaa atgaaacaag cgaccgagga agatgtgttt ccggatggaa ctttcttgag 1320  
aaaaggctca aggtttact tctcagtcta tgcaatggga aggatggaat cgatttgggg 1380  
aaaagactgt gaaatgttca aaccagaaag atggatacaa ggagggcaat acgtgagtga 1440  
tgatcagttt aaatacgtcg tgttcaatgc aggtccaaga ctttgtttag ggaaaacatt 1500  
tgcttacttg cagatgaaaa tgggtgctgc ttcgatcttg ctgaattact caatcaaggt 1560  
tgatcaagat catgttgttg ttccgcgagt aacaacgact ttgtatatga aacatggtct 1620  
taaggtcagg attacaccga gatctctaga agagaagaag caagattcat aaatatagaa 1680  
gaaacaaaca gctaaaactgt gaagttgtta ctgaaataca cataaataat ctttgttagt 1740  
aaaatgtaca gtgtgtgtat tatgtgtaat tcagatcaaa tgttatatac aaagaaaaaa 1800  
Attgcaatca taaggc

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Phe Gly Trp Val Thr Arg Cys Leu Thr Lys Ser Arg Gly Thr Phe  
1 5 10 15  
Pro Tyr Gln Arg Ile Trp Phe Ser Gly Ser Tyr Gly Ala Met Thr Ser  
20 25 30  
Val Pro Ala Asn Ile Glu Tyr Met Leu Lys Thr Asn Phe Lys Asn Phe  
35 40 45  
Pro Lys Gly Glu Phe Tyr Lys Glu Arg Phe Arg Asp Leu Leu Glu Asp  
50 55 60  
Gly Ile Phe Asn Ala Asp Asp Glu Ser Trp Lys Glu Gln Arg Arg Ile  
65 70 75 80  
Ile Ile Thr Glu Met His Ser Thr Arg Phe Val Asp His Ser Phe Gln  
85 90 95  
Thr Thr Arg Asp Leu Ile Glu Arg Lys Leu Leu Lys Val Met Glu Ser  
100 105 110  
Phe Ser Lys Ser Gln Glu Ala Phe Asp Leu Gln Glu Ile Leu Leu Arg  
115 120 125  
Leu Thr Phe Asp Asn Ile Cys Ile Ala Gly Leu Gly Asp Asp Pro Gly  
130 135 140  
Thr Leu Asp Asp Asp Leu Pro His Val Pro Phe Ala Lys Ala Phe Glu  
145 150 155 160  
Glu Ala Thr Glu Ser Thr Leu Phe Arg Phe Met Ile Pro Pro Phe Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Lys | Pro | Met | 165 | Lys | Phe | Phe | Asp | Ile | 170 | Gly | Tyr | Glu | Lys | Gly | 175 | Leu | Arg |
|     |     |     | 180 | Thr | Val | His | Asn | Phe | 185 | Ile | Asp | Lys | Met | 190 | Val | Val | Glu |     |
| Glu | Ala | Val | Glu | 195 | Met | Leu | Lys | Asp | 200 | Gln | Gly | Thr | Leu | Ala | Asn | Ser | Lys | Ser |
| Arg | Ile | Ala | Met | 210 | Leu | Lys | Asp | 215 | Gln | Ile | Glu | Ser | His | Lys | Arg | Gly | Asp |     |
| Asp | Val | Leu | Ser | 225 | Arg | Leu | Ile | Gln | 230 | Ile | Glu | Ser | His | Lys | Arg | Gly | Asp |     |
| Glu | Asn | Asp | Arg | 245 | Phe | Thr | Ala | Lys | 250 | Phe | Arg | Gln | Phe | Cys | Ser | Ser |     |     |
| Phe | Ile | Leu | Ala | 260 | Gly | Arg | Asp | Thr | 265 | Ser | Ser | Val | Ala | Leu | Thr | Trp | Phe |     |
| Phe | Trp | Leu | Ile | 275 | Thr | Lys | His | Pro | 280 | Glu | Val | Glu | Thr | Lys | Ile | Leu | His |     |
| Glu | Ile | Arg | Glu | 290 | Ile | Leu | Ser | Gln | 295 | Arg | Glu | Lys | Asn | Asn | Tyr | Lys | Leu |     |
| Asp | Glu | Thr | Gly | 305 | Glu | Thr | Glu | Ser | 310 | Ser | Arg | His | Phe | Thr | Val | Lys | Glu |     |
| Leu | Asn | Asp | Met | 325 | Val | Tyr | Leu | Gln | 330 | Ala | Ala | Leu | Ser | Glu | Ser | Leu | Arg |     |
| Leu | Tyr | Pro | Pro | 340 | Ile | Pro | Met | Glu | 345 | Met | Lys | Gln | Ala | Thr | Glu | Glu | Asp |     |
| Val | Phe | Pro | Asp | 355 | Gly | Thr | Phe | Leu | 360 | Arg | Lys | Gly | Ser | Arg | Val | Tyr | Phe |     |
| Ser | Val | Tyr | Ala | 370 | Met | Gly | Arg | Met | 375 | Glu | Ser | Ile | Trp | Gly | Lys | Asp | Cys |     |
| Glu | Met | Phe | Lys | 385 | Pro | Glu | Arg | Trp | 390 | Ile | Gln | Gly | Gln | Tyr | Val | Ser |     |     |
| Asp | Asp | Gln | Phe | 405 | Lys | Tyr | Val | Val | 410 | Phe | Asn | Ala | Gly | Pro | Arg | Leu | Cys |     |
| Leu | Gly | Lys | Thr | 420 | Phe | Ala | Tyr | Leu | 425 | Gln | Met | Lys | Met | Val | Ala | Ala | Ser |     |
| Ile | Leu | Leu | Asn | 435 | Tyr | Ser | Ile | Lys | 440 | Val | Asp | Gln | Asp | His | Val | Val | Val |     |
| Pro | Arg | Val | Thr | 450 | Thr | Thr | Leu | Tyr | 455 | Met | Lys | His | Gly | Leu | Lys | Val | Arg |     |
| Ile | Thr | Pro | Arg | 465 | Ser | Leu | Glu | Glu | 470 | Lys | Lys | Gln | Asp | Ser |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..448

(D) OTHER INFORMATION: / Ceres Seq. ID 1566799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Thr | Ser | Val | Pro | Ala | Asn | Ile | Glu | Tyr | Met | Leu | Lys | Thr | Asn | Phe |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |
| Lys | Asn | Phe | Pro | Lys | Gly | Glu | Phe | Tyr | Lys | Glu | Arg | Phe | Arg | Asp | Leu |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Leu | Glu | Asp | Gly | Ile | Phe | Asn | Ala | Asp | Asp | Glu | Ser | Trp | Lys | Glu | Gln |  |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |  |
| Arg | Arg | Ile | Ile | Ile | Thr | Glu | Met | His | Ser | Thr | Arg | Phe | Val | Asp | His |  |  |  |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |  |  |
| Ser | Phe | Gln | Thr | Thr | Arg | Asp | Leu | Ile | Glu | Arg | Lys | Leu | Leu | Lys | Val |  |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Ser | Phe | Ser | Lys | Ser | Gln | Glu | Ala | Phe | Asp | Leu | Gln | Glu | Ile |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Leu | Arg | Leu | Thr | Phe | Asp | Asn | Ile | Cys | Ile | Ala | Gly | Leu | Gly | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Pro | Gly | Thr | Leu | Asp | Asp | Asp | Leu | Pro | His | Val | Pro | Phe | Ala | Lys |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ala | Phe | Glu | Glu | Ala | Thr | Glu | Ser | Thr | Leu | Phe | Arg | Phe | Met | Ile | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Phe | Val | Trp | Lys | Pro | Met | Lys | Phe | Phe | Asp | Ile | Gly | Tyr | Glu | Lys |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gly | Leu | Arg | Glu | Ala | Val | Glu | Thr | Val | His | Asn | Phe | Ile | Asp | Lys | Met |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Val | Glu | Arg | Ile | Ala | Met | Leu | Lys | Asp | Gln | Gly | Thr | Leu | Ala | Asn |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Lys | Ser | Asp | Val | Leu | Ser | Arg | Leu | Ile | Gln | Ile | Glu | Ser | His | Lys |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Arg | Gly | Asp | Glu | Asn | Asp | Arg | Phe | Thr | Ala | Lys | Phe | Phe | Arg | Gln | Phe |  |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |
| Cys | Ser | Ser | Phe | Ile | Leu | Ala | Gly | Arg | Asp | Thr | Ser | Ser | Val | Ala | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |  |
| Thr | Trp | Phe | Phe | Trp | Leu | Ile | Thr | Lys | His | Pro | Glu | Val | Glu | Thr | Lys |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ile | Leu | His | Glu | Ile | Arg | Glu | Ile | Leu | Ser | Gln | Arg | Glu | Lys | Asn | Asn |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Tyr | Lys | Leu | Asp | Glu | Thr | Gly | Glu | Thr | Glu | Ser | Ser | Arg | His | Phe | Thr |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |
| Val | Lys | Glu | Leu | Asn | Asp | Met | Val | Tyr | Leu | Gln | Ala | Ala | Leu | Ser | Glu |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ser | Leu | Arg | Leu | Tyr | Pro | Pro | Ile | Pro | Met | Glu | Met | Lys | Gln | Ala | Thr |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Glu | Glu | Asp | Val | Phe | Pro | Asp | Gly | Thr | Phe | Leu | Arg | Lys | Gly | Ser | Arg |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Val | Tyr | Phe | Ser | Val | Tyr | Ala | Met | Gly | Arg | Met | Glu | Ser | Ile | Trp | Gly |  |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Lys | Asp | Cys | Glu | Met | Phe | Lys | Pro | Glu | Arg | Trp | Ile | Gln | Gly | Gly | Gln |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Tyr | Val | Ser | Asp | Asp | Gln | Phe | Lys | Tyr | Val | Val | Phe | Asn | Ala | Gly | Pro |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Arg | Leu | Cys | Leu | Gly | Lys | Thr | Phe | Ala | Tyr | Leu | Gln | Met | Lys | Met | Val |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Ala | Ala | Ser | Ile | Leu | Leu | Asn | Tyr | Ser | Ile | Lys | Val | Asp | Gln | Asp | His |  |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Val | Val | Val | Pro | Arg | Val | Thr | Thr | Thr | Leu | Tyr | Met | Lys | His | Gly | Leu |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Lys | Val | Arg | Ile | Thr | Pro | Arg | Ser | Leu | Glu | Glu | Lys | Lys | Gln | Asp | Ser |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1566800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Leu Lys Thr Asn Phe Lys Asn Phe Pro Lys Gly Glu Phe Tyr Lys

|                                                                 |     |     |  |     |  |     |
|-----------------------------------------------------------------|-----|-----|--|-----|--|-----|
| 1                                                               |     | 5   |  | 10  |  | 15  |
| Glu Arg Phe Arg Asp Leu Leu Glu Asp Gly Ile Phe Asn Ala Asp Asp |     |     |  |     |  |     |
|                                                                 | 20  |     |  | 25  |  | 30  |
| Glu Ser Trp Lys Glu Gln Arg Arg Ile Ile Ile Thr Glu Met His Ser |     |     |  |     |  |     |
|                                                                 | 35  |     |  | 40  |  | 45  |
| Thr Arg Phe Val Asp His Ser Phe Gln Thr Thr Arg Asp Leu Ile Glu |     |     |  |     |  |     |
|                                                                 | 50  |     |  | 55  |  | 60  |
| Arg Lys Leu Leu Lys Val Met Glu Ser Phe Ser Lys Ser Gln Glu Ala |     |     |  |     |  |     |
|                                                                 | 65  |     |  | 70  |  | 75  |
| Phe Asp Leu Gln Glu Ile Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys |     |     |  |     |  |     |
|                                                                 |     | 85  |  | 90  |  | 95  |
| Ile Ala Gly Leu Gly Asp Asp Pro Gly Thr Leu Asp Asp Asp Leu Pro |     |     |  |     |  |     |
|                                                                 | 100 |     |  | 105 |  | 110 |
| His Val Pro Phe Ala Lys Ala Phe Glu Glu Ala Thr Glu Ser Thr Leu |     |     |  |     |  |     |
|                                                                 | 115 |     |  | 120 |  | 125 |
| Phe Arg Phe Met Ile Pro Pro Phe Val Trp Lys Pro Met Lys Phe Phe |     |     |  |     |  |     |
|                                                                 | 130 |     |  | 135 |  | 140 |
| Asp Ile Gly Tyr Glu Lys Gly Leu Arg Glu Ala Val Glu Thr Val His |     |     |  |     |  |     |
|                                                                 | 145 |     |  | 150 |  | 155 |
| Asn Phe Ile Asp Lys Met Val Val Glu Arg Ile Ala Met Leu Lys Asp |     |     |  |     |  |     |
|                                                                 |     | 165 |  | 170 |  | 175 |
| Gln Gly Thr Leu Ala Asn Ser Lys Ser Asp Val Leu Ser Arg Leu Ile |     |     |  |     |  |     |
|                                                                 | 180 |     |  | 185 |  | 190 |
| Gln Ile Glu Ser His Lys Arg Gly Asp Glu Asn Asp Arg Phe Thr Ala |     |     |  |     |  |     |
|                                                                 | 195 |     |  | 200 |  | 205 |
| Lys Phe Phe Arg Gln Phe Cys Ser Ser Phe Ile Leu Ala Gly Arg Asp |     |     |  |     |  |     |
|                                                                 | 210 |     |  | 215 |  | 220 |
| Thr Ser Ser Val Ala Leu Thr Trp Phe Phe Trp Leu Ile Thr Lys His |     |     |  |     |  |     |
|                                                                 | 225 |     |  | 230 |  | 235 |
| Pro Glu Val Glu Thr Lys Ile Leu His Glu Ile Arg Glu Ile Leu Ser |     |     |  |     |  |     |
|                                                                 |     | 245 |  | 250 |  | 255 |
| Gln Arg Glu Lys Asn Asn Tyr Lys Leu Asp Glu Thr Gly Glu Thr Glu |     |     |  |     |  |     |
|                                                                 | 260 |     |  | 265 |  | 270 |
| Ser Ser Arg His Phe Thr Val Lys Glu Leu Asn Asp Met Val Tyr Leu |     |     |  |     |  |     |
|                                                                 | 275 |     |  | 280 |  | 285 |
| Gln Ala Ala Leu Ser Glu Ser Leu Arg Leu Tyr Pro Pro Ile Pro Met |     |     |  |     |  |     |
|                                                                 | 290 |     |  | 295 |  | 300 |
| Glu Met Lys Gln Ala Thr Glu Glu Asp Val Phe Pro Asp Gly Thr Phe |     |     |  |     |  |     |
|                                                                 | 305 |     |  | 310 |  | 315 |
| Leu Arg Lys Gly Ser Arg Val Tyr Phe Ser Val Tyr Ala Met Gly Arg |     |     |  |     |  |     |
|                                                                 |     | 325 |  | 330 |  | 335 |
| Met Glu Ser Ile Trp Gly Lys Asp Cys Glu Met Phe Lys Pro Glu Arg |     |     |  |     |  |     |
|                                                                 | 340 |     |  | 345 |  | 350 |
| Trp Ile Gln Gly Gly Gln Tyr Val Ser Asp Asp Gln Phe Lys Tyr Val |     |     |  |     |  |     |
|                                                                 | 355 |     |  | 360 |  | 365 |
| Val Phe Asn Ala Gly Pro Arg Leu Cys Leu Gly Lys Thr Phe Ala Tyr |     |     |  |     |  |     |
|                                                                 | 370 |     |  | 375 |  | 380 |
| Leu Gln Met Lys Met Val Ala Ala Ser Ile Leu Leu Asn Tyr Ser Ile |     |     |  |     |  |     |
|                                                                 | 385 |     |  | 390 |  | 395 |
| Lys Val Asp Gln Asp His Val Val Val Pro Arg Val Thr Thr Thr Leu |     |     |  |     |  |     |
|                                                                 |     | 405 |  | 410 |  | 415 |
| Tyr Met Lys His Gly Leu Lys Val Arg Ile Thr Pro Arg Ser Leu Glu |     |     |  |     |  |     |
|                                                                 | 420 |     |  | 425 |  | 430 |
| Glu Lys Lys Gln Asp Ser                                         |     |     |  |     |  |     |
|                                                                 | 435 |     |  |     |  |     |

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1370

(D) OTHER INFORMATION: / Ceres Seq. ID 1566823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| aaaaaggaaa  | aaagaaaaag | aagaagagga  | gctaaaaaaa  | cgacgctcgta | gaaggagatt  | 60   |
| cttgccatgg  | ccacacatag | tctctccttc  | ttcttcagag  | ttcttctcct  | cctctttctt  | 120  |
| actctctcag  | agagaattaa | agggcaagggt | gtgggaatca  | actacggcca  | aatagcaaac  | 180  |
| aacctcccat  | ctccggcaag | agtcgccgtg  | ctccttcgat  | cactaaacat  | cacaagagta  | 240  |
| aaactctacg  | acgcagatcc | aaacgtcctc  | ttctccttct  | caaactcaca  | agtagatttc  | 300  |
| atgatcgggt  | taggcaacga | gtatcttcaa  | aacatgtcaa  | cagatccaac  | caaagctcaa  | 360  |
| gattggttac  | aacaaagact | tgaaccacat  | atctcaaaaa  | cacgaataac  | ctcaatagtt  | 420  |
| gtcggcaacg  | aaatcttcaa | aaccaatgat  | catgtcctca  | tccaaagcct  | attaccggct  | 480  |
| atgaaatcgg  | tttacgctgc | tttaaccaat  | cttggttttag | agaaacaagt  | aaccgtaact  | 540  |
| tcagctcatt  | ctttagacat | tctttcaaca  | tcttatcctc  | cttcttcagg  | atcattcaaa  | 600  |
| gaagagttta  | ttcaatatct | tcaaccactt  | cttgattttc  | attctcaaat  | cgaatcacct  | 660  |
| ttcttgataa  | atgcttatcc | cttttttgct  | tataaagata  | gtcctaaaga  | agttccatta  | 720  |
| gagtatgttt  | tgtttcaacc | taatcaagggt | atggttgatc  | caaacactaa  | tcttcattat  | 780  |
| gacaacatgt  | tggttgctca | agttgatgag  | ctttactctg  | ccattaagac  | tttgggacat  | 840  |
| accgatatcg  | aggttcggat | atcggaaacc  | ggttggcctt  | ctaaaggaga  | tgagaatgag  | 900  |
| attggaGctt  | cgccggagaa | cgccgctttg  | tataatggga  | atttggtgaa  | gttgattcag  | 960  |
| cagaggaaaag | gaactccggc | gaagcaatct  | gttctatttg  | atgtttatgt  | gtttgctctg  | 1020 |
| tttaatgaga  | atcttaaacc | gggtccggtt  | tctgagagga  | attatggact  | tttttatccg  | 1080 |
| gatggtaaac  | cggtttacaa | tgctcggtatg | caaggttatt  | tacctgatat  | tatctatact  | 1140 |
| tcaagggcaa  | ctacaattaa | gattttgaat  | ttgtggagag  | tcgtgatggg  | tttggctgtg  | 1200 |
| gcttggttca  | tactcgatat | gggcgacaag  | atgaggatga  | gataaGcttc  | gcttggtgtct | 1260 |
| ttgtctgtcc  | ttgtaggatt | tttgtttttaa | tgtgttagtt  | gattataggt  | gaggtataca  | 1320 |
| attctttgtc  | atgtattgga | ttcacaaaaa  | ttaaaaaaat  | taattttattc |             |      |

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1566824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | His | Ser | Leu | Ser | Phe | Phe | Phe | Arg | Val | Leu | Leu | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Leu | Thr |     | Leu | Ser | Glu | Arg | Ile | Lys | Gly | Gln | Gly | Val | Gly | Ile |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     | Asn |
| Tyr | Gly | Gln | Ile | Ala | Asn | Asn | Leu | Pro | Ser | Pro | Ala | Arg | Val | Ala | Val |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Leu | Arg | Ser | Leu | Asn | Ile | Thr | Arg | Val | Lys | Leu | Tyr | Asp | Ala | Asp |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Pro | Asn | Val | Leu | Phe | Ser | Phe | Ser | Asn | Ser | Gln | Val | Asp | Phe | Met | Ile |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Gly | Leu | Gly | Asn | Glu | Tyr | Leu | Gln | Asn | Met | Ser | Thr | Asp | Pro | Thr | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Gln | Asp | Trp | Leu | Gln | Gln | Arg | Leu | Glu | Pro | His | Ile | Ser | Lys | Thr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ile | Thr | Ser | Ile | Val | Val | Gly | Asn | Glu | Ile | Phe | Lys | Thr | Asn | Asp |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| His | Val | Leu | Ile | Gln | Ser | Leu | Leu | Pro | Ala | Met | Lys | Ser | Val | Tyr | Ala |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Ala | Leu | Thr | Asn | Leu | Gly | Leu | Glu | Lys | Gln | Val | Thr | Val | Thr | Ser | Ala |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     | 160 |

His Ser Leu Asp Ile Leu Ser Thr Ser Tyr Pro Pro Ser Ser Gly Ser  
165 170 175  
Phe Lys Glu Glu Phe Ile Gln Tyr Leu Gln Pro Leu Leu Asp Phe His  
180 185 190  
Ser Gln Ile Glu Ser Pro Phe Leu Ile Asn Ala Tyr Pro Phe Phe Ala  
195 200 205  
Tyr Lys Asp Ser Pro Lys Glu Val Pro Leu Glu Tyr Val Leu Phe Gln  
210 215 220  
Pro Asn Gln Gly Met Val Asp Pro Asn Thr Asn Leu His Tyr Asp Asn  
225 230 235 240  
Met Leu Phe Ala Gln Val Asp Ala Leu Tyr Ser Ala Ile Lys Thr Leu  
245 250 255  
Gly His Thr Asp Ile Glu Val Arg Ile Ser Glu Thr Gly Trp Pro Ser  
260 265 270  
Lys Gly Asp Glu Asn Glu Ile Gly Ala Ser Pro Glu Asn Ala Ala Leu  
275 280 285  
Tyr Asn Gly Asn Leu Leu Lys Leu Ile Gln Gln Arg Lys Gly Thr Pro  
290 295 300  
Ala Lys Gln Ser Val Pro Ile Asp Val Tyr Val Phe Ala Leu Phe Asn  
305 310 315 320  
Glu Asn Leu Lys Pro Gly Pro Val Ser Glu Arg Asn Tyr Gly Leu Phe  
325 330 335  
Tyr Pro Asp Gly Lys Pro Val Tyr Asn Val Gly Met Gln Gly Tyr Leu  
340 345 350  
Pro Asp Ile Ile Tyr Thr Ser Arg Ala Thr Thr Ile Lys Ile Leu Asn  
355 360 365  
Leu Trp Arg Val Val Met Gly Leu Ala Val Ala Trp Phe Ile Leu Asp  
370 375 380  
Met Gly Asp Lys Met Arg Met Arg  
385 390

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Ile Gly Leu Gly Asn Glu Tyr Leu Gln Asn Met Ser Thr Asp Pro  
1 5 10 15  
Thr Lys Ala Gln Asp Trp Leu Gln Gln Arg Leu Glu Pro His Ile Ser  
20 25 30  
Lys Thr Arg Ile Thr Ser Ile Val Val Gly Asn Glu Ile Phe Lys Thr  
35 40 45  
Asn Asp His Val Leu Ile Gln Ser Leu Leu Pro Ala Met Lys Ser Val  
50 55 60  
Tyr Ala Ala Leu Thr Asn Leu Gly Leu Glu Lys Gln Val Thr Val Thr  
65 70 75 80  
Ser Ala His Ser Leu Asp Ile Leu Ser Thr Ser Tyr Pro Pro Ser Ser  
85 90 95  
Gly Ser Phe Lys Glu Glu Phe Ile Gln Tyr Leu Gln Pro Leu Leu Asp  
100 105 110  
Phe His Ser Gln Ile Glu Ser Pro Phe Leu Ile Asn Ala Tyr Pro Phe  
115 120 125  
Phe Ala Tyr Lys Asp Ser Pro Lys Glu Val Pro Leu Glu Tyr Val Leu  
130 135 140  
Phe Gln Pro Asn Gln Gly Met Val Asp Pro Asn Thr Asn Leu His Tyr

145 150 155 160  
Asp Asn Met Leu Phe Ala Gln Val Asp Ala Leu Tyr Ser Ala Ile Lys  
165 170 175  
Thr Leu Gly His Thr Asp Ile Glu Val Arg Ile Ser Glu Thr Gly Trp  
180 185 190  
Pro Ser Lys Gly Asp Glu Asn Glu Ile Gly Ala Ser Pro Glu Asn Ala  
195 200 205  
Ala Leu Tyr Asn Gly Asn Leu Leu Lys Leu Ile Gln Gln Arg Lys Gly  
210 215 220  
Thr Pro Ala Lys Gln Ser Val Pro Ile Asp Val Tyr Val Phe Ala Leu  
225 230 235 240  
Phe Asn Glu Asn Leu Lys Pro Gly Pro Val Ser Glu Arg Asn Tyr Gly  
245 250 255  
Leu Phe Tyr Pro Asp Gly Lys Pro Val Tyr Asn Val Gly Met Gln Gly  
260 265 270  
Tyr Leu Pro Asp Ile Ile Tyr Thr Ser Arg Ala Thr Thr Ile Lys Ile  
275 280 285  
Leu Asn Leu Trp Arg Val Val Met Gly Leu Ala Val Ala Trp Phe Ile  
290 295 300  
Leu Asp Met Gly Asp Lys Met Arg Met Arg  
305 310

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1566826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Ser Thr Asp Pro Thr Lys Ala Gln Asp Trp Leu Gln Gln Arg Leu  
1 5 10 15  
Glu Pro His Ile Ser Lys Thr Arg Ile Thr Ser Ile Val Val Gly Asn  
20 25 30  
Glu Ile Phe Lys Thr Asn Asp His Val Leu Ile Gln Ser Leu Leu Pro  
35 40 45  
Ala Met Lys Ser Val Tyr Ala Ala Leu Thr Asn Leu Gly Leu Glu Lys  
50 55 60  
Gln Val Thr Val Thr Ser Ala His Ser Leu Asp Ile Leu Ser Thr Ser  
65 70 75 80  
Tyr Pro Pro Ser Ser Gly Ser Phe Lys Glu Glu Phe Ile Gln Tyr Leu  
85 90 95  
Gln Pro Leu Leu Asp Phe His Ser Gln Ile Glu Ser Pro Phe Leu Ile  
100 105 110  
Asn Ala Tyr Pro Phe Phe Ala Tyr Lys Asp Ser Pro Lys Glu Val Pro  
115 120 125  
Leu Glu Tyr Val Leu Phe Gln Pro Asn Gln Gly Met Val Asp Pro Asn  
130 135 140  
Thr Asn Leu His Tyr Asp Asn Met Leu Phe Ala Gln Val Asp Ala Leu  
145 150 155 160  
Tyr Ser Ala Ile Lys Thr Leu Gly His Thr Asp Ile Glu Val Arg Ile  
165 170 175  
Ser Glu Thr Gly Trp Pro Ser Lys Gly Asp Glu Asn Glu Ile Gly Ala  
180 185 190  
Ser Pro Glu Asn Ala Ala Leu Tyr Asn Gly Asn Leu Leu Lys Leu Ile  
195 200 205  
Gln Gln Arg Lys Gly Thr Pro Ala Lys Gln Ser Val Pro Ile Asp Val  
210 215 220

Tyr Val Phe Ala Leu Phe Asn Glu Asn Leu Lys Pro Gly Pro Val Ser  
225 230 235 240  
Glu Arg Asn Tyr Gly Leu Phe Tyr Pro Asp Gly Lys Pro Val Tyr Asn  
245 250 255  
Val Gly Met Gln Gly Tyr Leu Pro Asp Ile Ile Tyr Thr Ser Arg Ala  
260 265 270  
Thr Thr Ile Lys Ile Leu Asn Leu Trp Arg Val Val Met Gly Leu Ala  
275 280 285  
Val Ala Trp Phe Ile Leu Asp Met Gly Asp Lys Met Arg Met Arg  
290 295 300

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1530
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| tgatattttt | tgaccagctc | gattcagaaa | tttgaaaaga | ctagcttttt | tttctctcgg  | 60   |
| gtttcacttt | ttaaaggctc | tgaaaatttg | ggaatcactg | atcaattttg | ttaatatgat  | 120  |
| ttcctgattt | agggtttctc | tgcatgcctc | tagaatcagc | aagtgtaaag | caattaccat  | 180  |
| ggtgactccg | aagcagatcg | atttctcttc | ctgtggtgtg | gtgataactc | cgacgatacc  | 240  |
| ctctcccatc | gagaatctcc | acggaatcct | tcctcaaagc | gtgctgctgc | ttccttcgca  | 300  |
| gcagaagcag | gcgaagagac | tatgaagaag | aaaaagaaga | agaagaagaa | gaatttgggt  | 360  |
| ccgccgttga | tcgtccggat | ctggaacgag | gaagatgagc | tctctatctt | aaagggatta  | 420  |
| gttgattaca | gagctaagac | aggattcaat | cccaaaattg | attgggatgc | gttttacagt  | 480  |
| ttcctcgga  | gttctatcgt | tgcgaaattc | tccaaggagc | aggttttgag | taagatcagg  | 540  |
| aagttgaaaa | ggagatttca | tgttcattgg | gagaaaatca | gtgaagggaa | tgatccgaaa  | 600  |
| tttactaggt | ctagtgtatt | tgaagccttt | ggattttctt | cgatgatttg | gggacaaggt  | 660  |
| gaatttggta | atgatgatgg | tatggataag | gagatggtga | aggagcacga | tgtaaaccga  | 720  |
| aatggcgag  | ctgaaaatgg | gactgctcga | atagcacagg | agaacgagag | tggggaggag  | 780  |
| atgttaaagg | agcatgagga | aacgttaaat | gagaatggtg | cagaggagat | aagagacaac  | 840  |
| gacgagactg | ctcgaaaagc | acagcagctc | gagagcgaga | gcgaggagga | gatgttgaag  | 900  |
| gagcatagag | aaccctttaa | tgagaatggt | gcagagaata | taagagacaa | taacgggact  | 960  |
| actcaaatag | cacagcagag | cgagagcgag | agtgaggaga | tggtgaagga | gcatgaggaa  | 1020 |
| gtggGcta   | actgaacttg | taaatgagaa | tggggcagcg | aaaacaacag | agaacggggac | 1080 |
| tactggtgga | aaagagagac | atgatgacga | tgatgatgat | gagttatgcg | ctgtgcagga  | 1140 |
| tgcatttgag | gctgtaattg | cgcaagggtt | aagtgtttat | caaaagaagt | tgcagcttga  | 1200 |
| gaagctgatg | aaccttgga  | ctggaaaaag | aagagagttg | agtgatgaat | ggaaagcggt  | 1260 |
| atgtgttgag | gaaagaagat | tgaatatcaa | gaagcttaga | ttttccgcca | agcttgcaga  | 1320 |
| ggcagcta   | gatagttaga | tgaaccaat  | aagccgttgt | agcatttggg | gttaattagg  | 1380 |
| ttcttagtaa | gccataagct | ttagtctgtt | cagtgtatat | ctttggatgt | tgtctttgtt  | 1440 |
| ctgtttgggc | aagtgtttgt | aagacattcc | agttttaact | gaagtatcca | gaagagccat  | 1500 |
| ccatgtccat | tggtggatat | aataaatttc |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Asn Leu Gly Pro Pro Leu

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1 5 10 15  
Ile Val Arg Ile Trp Asn Glu Glu Asp Glu Leu Ser Ile Leu Lys Gly  
20 25 30  
Leu Val Asp Tyr Arg Ala Lys Thr Gly Phe Asn Pro Lys Ile Asp Trp  
35 40 45  
Asp Ala Phe Tyr Ser Phe Leu Gly Ser Ser Ile Val Ala Lys Phe Ser  
50 55 60  
Lys Glu Gln Val Leu Ser Lys Ile Arg Lys Leu Lys Arg Arg Phe His  
65 70 75 80  
Val His Trp Glu Lys Ile Ser Glu Gly Asn Asp Pro Lys Phe Thr Arg  
85 90 95  
Ser Ser Asp Ser Glu Ala Phe Gly Phe Ser Ser Met Ile Trp Gly Gln  
100 105 110  
Gly Glu Phe Gly Asn Asp Asp Gly Met Asp Lys Glu Met Val Lys Glu  
115 120 125  
His Asp Val Asn Gly Asn Gly Ala Ala Glu Asn Gly Thr Ala Arg Ile  
130 135 140  
Ala Gln Glu Asn Glu Ser Gly Glu Glu Met Leu Lys Glu His Glu Glu  
145 150 155 160  
Thr Leu Asn Glu Asn Gly Ala Glu Glu Ile Arg Asp Asn Asp Glu Thr  
165 170 175  
Ala Arg Lys Ala Gln Gln Leu Glu Ser Glu Ser Glu Glu Glu Met Leu  
180 185 190  
Lys Glu His Glu Glu Pro Phe Asn Glu Asn Gly Ala Glu Asn Ile Arg  
195 200 205  
Asp Asn Asn Gly Thr Thr Gln Ile Ala Gln Gln Ser Glu Ser Glu Ser  
210 215 220  
Glu Glu Met Leu Lys Glu His Glu Glu Val Gly  
225 230 235

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ile Trp Gly Gln Gly Glu Phe Gly Asn Asp Asp Gly Met Asp Lys  
1 5 10 15  
Glu Met Val Lys Glu His Asp Val Asn Gly Asn Gly Ala Ala Glu Asn  
20 25 30  
Gly Thr Ala Arg Ile Ala Gln Glu Asn Glu Ser Gly Glu Glu Met Leu  
35 40 45  
Lys Glu His Glu Glu Thr Leu Asn Glu Asn Gly Ala Glu Glu Ile Arg  
50 55 60  
Asp Asn Asp Glu Thr Ala Arg Lys Ala Gln Gln Leu Glu Ser Glu Ser  
65 70 75 80  
Glu Glu Glu Met Leu Lys Glu His Glu Glu Pro Phe Asn Glu Asn Gly  
85 90 95  
Ala Glu Asn Ile Arg Asp Asn Asn Gly Thr Thr Gln Ile Ala Gln Gln  
100 105 110  
Ser Glu Ser Glu Ser Glu Glu Met Leu Lys Glu His Glu Glu Val Gly  
115 120 125

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1824 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1824  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566838  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

attctctttt ctctctctc tctctcacac aacacaaaca actcttgaga gagagaaaca 60  
aatctttcac ttgacacttc tctccaaatc ctcattctcat tcttcattcct aaacattttgc 120  
tcaactctcac gatgagccat aaccaaacc aacctcaccg gccagtcccg gtccatgtca 180  
caaacgccga gccaaactct aacccaaaca acctcccaa ctttctatta tccgttcgtc 240  
tcaaatacgt aaaactcggg taccactacc tgatctccaa cgetctctac atcctcctcc 300  
ttctctctct cgcgcgaaca atcgctaacc tctcttcttt caccatcaac gacctctctc 360  
tctcttaca cactctcgt ttccatttcc tctccgccac actcgccacc gcaactctga 420  
tctctctctc caccgcttac ttcaccaccc gtctctcgccg tgtcttctc ctcgacttct 480  
cgtgttacaa accagaccct tcaactgatc gcaactcgtga aacattcatg gacagatctc 540  
aacgtgtagg catcttcaca gaAgacaact TagctttcCa acaaaagatc ctcgaaaAga 600  
tccggtctag gtcagaaaaac ttacttccct gaagctcttc ttcgtgttcc tccataatcct 660  
tgtatggaag aagcgagaaa agaggcagaa acagtattgt tcggagctat tgacgcgggt 720  
cttgagaaga ccggtgtgaa acctaaagat attggaatcc ttgtggtgaa ttgtagcttg 780  
tttaatccaa caccgtcact ttctgctatg attgtgaata agtataagct tagaggcaac 840  
atcttgagct ataactcttg tggaatggga tgtagtgtcg gccttatctc cattgatctc 900  
gctaaacaga tgcttcaggt gcaaccaaac tcatacgcac tagtggtgag cacagagAAC 960  
ataaccctaa actggtactt aggcaacgac cgatcaatgc ttctatctaa ttgtatcttc 1020  
cgtatgggag gagccgcggg acttctctcg aaccgctcct ctgatcgag ccgttcaaaa 1080  
tatcagctca tccataccgt ccgtaccac aaaggagctg atgacaacgc attcgggtgc 1140  
gtttaccaac gagaagacaa caacgcagaa gaaaccggca agatcggagt ctcactctct 1200  
aaaaacotta tggcaatagc cggagaagct ctcaagacaa acatcacAAC 1260  
ctagtcttac caatgtccga acaacttctc tttttcgcga ctcttggtgc ccgaaaagtc 1320  
ttcaaagtc agaaaataaa gccttacatt cctgacttca agctagcttt cgagcatttc 1380  
tgtatccacg ctggaggtag agccgtgctt gacgagattg agaagaactt ggatttatcc 1440  
gaatggcaca tggagccatc gaggatgacg ttgaaccggg ttggtAAC 1500  
tcaatttggg atgagcttgc gtatagtga gctaaaggaa ggattaagag aggagatagg 1560  
acttggcaga ttgcttttgg atcgggtttt aagtgtAAC gtgcggtttg gaaagctttg 1620  
agaacgattg atccaatgga cgagaagact aatccatgga ttgatgagat tgatgacttt 1680  
cctgttcaag ttcttaggt cactccatt acatcgtcgt agtgttttta aattcttttg 1740  
gagaactaat ttgttatggt ttattaaatg taataactta tgtgatgtga tattttttta 1800  
ttatcttaat atatatgatt gccg

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 352 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..352  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566839  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Glu Glu Ala Arg Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile  
1 5 10 15  
Asp Ala Val Leu Glu Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile  
20 25 30  
Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala  
35 40 45  
Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Gly | Met | Gly | Cys | Ser | Ala | Gly | Leu | Ile | Ser | Ile | Asp | Leu | Ala | 65  | 70  | 75  | 80  |
| Lys | Gln | Met | Leu | Gln | Val | Gln | Pro | Asn | Ser | Tyr | Ala | Leu | Val | Val | Ser | 85  | 90  | 95  |     |
| Thr | Glu | Asn | Ile | Thr | Leu | Asn | Trp | Tyr | Leu | Gly | Asn | Asp | Arg | Ser | Met | 100 | 105 | 110 |     |
| Leu | Leu | Ser | Asn | Cys | Ile | Phe | Arg | Met | Gly | Gly | Ala | Ala | Val | Leu | Leu | 115 | 120 | 125 |     |
| Ser | Asn | Arg | Ser | Ser | Asp | Arg | Ser | Arg | Ser | Lys | Tyr | Gln | Leu | Ile | His | 130 | 135 | 140 |     |
| Thr | Val | Arg | Thr | His | Lys | Gly | Ala | Asp | Asp | Asn | Ala | Phe | Gly | Cys | Val | 145 | 150 | 155 | 160 |
| Tyr | Gln | Arg | Glu | Asp | Asn | Asn | Ala | Glu | Glu | Thr | Gly | Lys | Ile | Gly | Val | 165 | 170 | 175 |     |
| Ser | Leu | Ser | Lys | Asn | Leu | Met | Ala | Ile | Ala | Gly | Glu | Ala | Leu | Lys | Thr | 180 | 185 | 190 |     |
| Asn | Ile | Thr | Thr | Leu | Gly | Pro | Leu | Val | Leu | Pro | Met | Ser | Glu | Gln | Leu | 195 | 200 | 205 |     |
| Leu | Phe | Phe | Ala | Thr | Leu | Val | Ala | Arg | Lys | Val | Phe | Lys | Val | Lys | Lys | 210 | 215 | 220 |     |
| Ile | Lys | Pro | Tyr | Ile | Pro | Asp | Phe | Lys | Leu | Ala | Phe | Glu | His | Phe | Cys | 225 | 230 | 235 | 240 |
| Ile | His | Ala | Gly | Gly | Arg | Ala | Val | Leu | Asp | Glu | Ile | Glu | Lys | Asn | Leu | 245 | 250 | 255 |     |
| Asp | Leu | Ser | Glu | Trp | His | Met | Glu | Pro | Ser | Arg | Met | Thr | Leu | Asn | Arg | 260 | 265 | 270 |     |
| Phe | Gly | Asn | Thr | Ser | Ser | Ser | Ser | Leu | Trp | Tyr | Glu | Leu | Ala | Tyr | Ser | 275 | 280 | 285 |     |
| Glu | Ala | Lys | Gly | Arg | Ile | Lys | Arg | Gly | Asp | Arg | Thr | Trp | Gln | Ile | Ala | 290 | 295 | 300 |     |
| Phe | Gly | Ser | Gly | Phe | Lys | Cys | Asn | Ser | Ala | Val | Trp | Lys | Ala | Leu | Arg | 305 | 310 | 315 | 320 |
| Thr | Ile | Asp | Pro | Met | Asp | Glu | Lys | Thr | Asn | Pro | Trp | Ile | Asp | Glu | Ile | 325 | 330 | 335 |     |
| Asp | Asp | Phe | Pro | Val | Gln | Val | Pro | Arg | Ile | Thr | Pro | Ile | Thr | Ser | Ser | 340 | 345 | 350 |     |

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Phe | Gly | Ala | Ile | Asp | Ala | Val | Leu | Glu | Lys | Thr | Gly | Val | Lys | Pro | 1  | 5  | 10 | 15 |
| Lys | Asp | Ile | Gly | Ile | Leu | Val | Val | Asn | Cys | Ser | Leu | Phe | Asn | Pro | Thr | 20 | 25 | 30 |    |
| Pro | Ser | Leu | Ser | Ala | Met | Ile | Val | Asn | Lys | Tyr | Lys | Leu | Arg | Gly | Asn | 35 | 40 | 45 |    |
| Ile | Leu | Ser | Tyr | Asn | Leu | Gly | Gly | Met | Gly | Cys | Ser | Ala | Gly | Leu | Ile | 50 | 55 | 60 |    |
| Ser | Ile | Asp | Leu | Ala | Lys | Gln | Met | Leu | Gln | Val | Gln | Pro | Asn | Ser | Tyr | 65 | 70 | 75 | 80 |
| Ala | Leu | Val | Val | Ser | Thr | Glu | Asn | Ile | Thr | Leu | Asn | Trp | Tyr | Leu | Gly |    |    |    |    |

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(2) INFORMATION FOR SEQ ID NO:416:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..304
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566841
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:
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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Val | Asn | Lys | Tyr | Lys | Leu | Arg | Gly | Asn | Ile | Leu | Ser | Tyr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gly | Gly | Met | Gly | Cys | Ser | Ala | Gly | Leu | Ile | Ser | Ile | Asp | Leu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Gln | Met | Leu | Gln | Val | Gln | Pro | Asn | Ser | Tyr | Ala | Leu | Val | Val | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Glu | Asn | Ile | Thr | Leu | Asn | Trp | Tyr | Leu | Gly | Asn | Asp | Arg | Ser | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Ser | Asn | Cys | Ile | Phe | Arg | Met | Gly | Gly | Ala | Ala | Val | Leu | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Asn | Arg | Ser | Ser | Asp | Arg | Ser | Arg | Ser | Lys | Tyr | Gln | Leu | Ile | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Val | Arg | Thr | His | Lys | Gly | Ala | Asp | Asp | Asn | Ala | Phe | Gly | Cys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Tyr | Gln | Arg | Glu | Asp | Asn | Asn | Ala | Glu | Glu | Thr | Gly | Lys | Ile | Gly | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala Leu Lys Thr  
130 135 140  
Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu  
145 150 155 160  
Leu Phe Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys Val Lys Lys  
165 170 175  
Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys  
180 185 190  
Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu Lys Asn Leu  
195 200 205  
Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr Leu Asn Arg  
210 215 220  
Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser  
225 230 235 240  
Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Trp Gln Ile Ala  
245 250 255  
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg  
260 265 270  
Thr Ile Asp Pro Met Asp Glu Lys Thr Asn Pro Trp Ile Asp Glu Ile  
275 280 285  
Asp Asp Phe Pro Val Gln Val Pro Arg Ile Thr Pro Ile Thr Ser Ser  
290 295 300

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..998
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aatttcattt | ccatttcgat | tcgattcctc | ctttgtgtgg | gaggcctttg | ttcgggtcaac | 60  |
| ttatgtgttc | tgtttttgtc | tcttttttat | tgattaggga | ccgatctatc | aaggcttcaa  | 120 |
| gggcaaacag | aaatggacca | cgacaagaca | ggatgccaaa | gcccacctga | aggtcccaag  | 180 |
| ctatgtacta | acaactgcg  | tttctttgga | agcgtgcca  | caatgaacat | gtgttctaag  | 240 |
| tgtcacaagg | atatgttgtt | ccaacaggag | cagggcgcta | agtttgcac  | tgcagtgtct  | 300 |
| ggaacatcgt | catccagcaa | catcataaag | gaaaccttta | ccgctgcgtt | ggtcgatatt  | 360 |
| gaaaccaa   | ccgttgagcc | gatgactgtt | tctgtacagc | catcctctgt | ccaagtcgtt  | 420 |
| gcagaggtag | tagcaccaga | agaagctg   | aaaccaaagg | gaccaagccg | atgtactact  | 480 |
| tgcaataa   | gggttggcct | gactggattc | aaatgtcgct | gtgggagcct | cttctgcgga  | 540 |
| acacaccgct | atgcagacat | acatgactgc | tccttcaatt | accatgctgC | tgcgcaagag  | 600 |
| gcgatagcta | aggcaaacc  | ggttgtgaaa | gcagagaagc | ttgacaaaat | ctgaaaatct  | 660 |
| aagtaaaact | ctctggtttc | atcaggtggc | ctggtgtttc | cttctcctgt | ctgtgtctgg  | 720 |
| ttcaagtatt | ctcatgttaa | aaaggtttta | tataaggtcg | aatgaaagcg | tgcttgatct  | 780 |
| ttagogtctt | ccatctctct | gcaatatttg | tggtgtggaa | ctttctatta | tctgtgtttg  | 840 |
| caagcagaga | aacgtgctct | taaaaaaaat | gctttgtgtg | tttatctttc | tactattttt  | 900 |
| gagcactgtg | ttattgtttc | ctgtttggtc | tgtatcatat | tgagattgtc | tctgtagcta  | 960 |
| catgaagctt | atttaaaaaa | ggcctgtgtt | tgctcttc   |            |             |     |

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..173  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | His | Asp | Lys | Thr | Gly | Cys | Gln | Ser | Pro | Pro | Glu | Gly | Pro | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Cys | Thr | Asn | Asn | Cys | Gly | Phe | Phe | Gly | Ser | Ala | Ala | Thr | Met | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Cys | Ser | Lys | Cys | His | Lys | Asp | Met | Leu | Phe | Gln | Gln | Glu | Gln | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Phe | Ala | Ser | Ala | Val | Ser | Gly | Thr | Ser | Ser | Ser | Ser | Asn | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Lys | Glu | Thr | Phe | Thr | Ala | Ala | Leu | Val | Asp | Ile | Glu | Thr | Lys | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Glu | Pro | Met | Thr | Val | Ser | Val | Gln | Pro | Ser | Ser | Val | Gln | Val | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Glu | Val | Val | Ala | Pro | Glu | Glu | Ala | Ala | Lys | Pro | Lys | Gly | Pro | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Cys | Thr | Thr | Cys | Asn | Lys | Arg | Val | Gly | Leu | Thr | Gly | Phe | Lys | Cys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Cys | Gly | Ser | Leu | Phe | Cys | Gly | Thr | His | Arg | Tyr | Ala | Asp | Ile | His |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asp | Cys | Ser | Phe | Asn | Tyr | His | Ala | Ala | Ala | Gln | Glu | Ala | Ile | Ala | Lys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Asn | Pro | Val | Val | Lys | Ala | Glu | Lys | Leu | Asp | Lys | Ile |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1566911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Met | Cys | Ser | Lys | Cys | His | Lys | Asp | Met | Leu | Phe | Gln | Gln | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Gly | Ala | Lys | Phe | Ala | Ser | Ala | Val | Ser | Gly | Thr | Ser | Ser | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Ile | Lys | Glu | Thr | Phe | Thr | Ala | Ala | Leu | Val | Asp | Ile | Glu | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | Ser | Val | Glu | Pro | Met | Thr | Val | Ser | Val | Gln | Pro | Ser | Ser | Val | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Val | Ala | Glu | Val | Val | Ala | Pro | Glu | Glu | Ala | Lys | Pro | Lys | Gly |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Ser | Arg | Cys | Thr | Thr | Cys | Asn | Lys | Arg | Val | Gly | Leu | Thr | Gly | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Cys | Arg | Cys | Gly | Ser | Leu | Phe | Cys | Gly | Thr | His | Arg | Tyr | Ala | Asp |
|     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| Ile | His | Asp | Cys | Ser | Phe | Asn | Tyr | His | Ala | Ala | Ala | Gln | Glu | Ala | Ile |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Lys | Ala | Asn | Pro | Val | Val | Lys | Ala | Glu | Lys | Leu | Asp | Lys | Ile |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..141  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566912  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:  
Met Cys Ser Lys Cys His Lys Asp Met Leu Phe Gln Gln Glu Gln Gly  
1                  5                  10                  15  
Ala Lys Phe Ala Ser Ala Val Ser Gly Thr Ser Ser Ser Ser Asn Ile  
                  20                  25                  30  
Ile Lys Glu Thr Phe Thr Ala Ala Leu Val Asp Ile Glu Thr Lys Ser  
                  35                  40                  45  
Val Glu Pro Met Thr Val Ser Val Gln Pro Ser Ser Val Gln Val Val  
                  50                  55                  60  
Ala Glu Val Val Ala Pro Glu Glu Ala Ala Lys Pro Lys Gly Pro Ser  
65                  70                  75                  80  
Arg Cys Thr Thr Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys  
                  85                  90                  95  
Arg Cys Gly Ser Leu Phe Cys Gly Thr His Arg Tyr Ala Asp Ile His  
                  100                 105                 110  
Asp Cys Ser Phe Asn Tyr His Ala Ala Ala Gln Glu Ala Ile Ala Lys  
                 115                 120                 125  
Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys Ile  
130                 135                 140

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1566913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

aacgcagaaa ttaRaaaccc cttttgcctc aaaaAccctg atttcaaadc tccccaagca 60  
caacaatggc gaaatcaatg agatgcaaga ggggtgaagag attgagagca ataagaagag 120  
aaatagtggg gaaggaatca ttcactctaa cgagagaaga cgccaaatcc gccgctattg 180  
aagccgcact cgctgctccg aagttaccag ttcgtcaagc cccagtttct ccgtttatgg 240  
aagttgcgac gccttctctt gagtctgcat ctgcctccac tacaatcgcc aaaaatagtg 300  
atgaggaaaat ggatgatgag aagaaaaaca agtcgctaaa acctattggg aagaagttga 360  
agaagaagtt taagctgggg atgaagaatc gtcgtagtaa ggggtgtcct cgaggcaaac 420  
gaaactaaaa ctggtctttg ctttcttcta ctgggtttgt tttctacttg cataatztat 480  
gttctctctt aattttgggg ttcttcaatg tcttagaata tagcatcttt tgtactgtgt 540  
tttttccatg agtttcagta ctatagaaac cctg

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1566914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met Ala Lys Ser Met Arg Cys Lys Arg Val Lys Arg Leu Arg Ala Ile  
1                  5                  10                  15

Arg Arg Glu Ile Val Glu Lys Glu Ser Phe Thr Leu Thr Arg Glu Asp  
20 25 30  
Ala Lys Ser Ala Ala Ile Glu Ala Ala Leu Ala Ala Pro Lys Leu Pro  
35 40 45  
Val Arg Gln Ala Pro Val Ser Pro Phe Met Glu Val Ala Thr Pro Ser  
50 55 60  
Ser Glu Ser Ala Ser Ala Ser Thr Thr Ile Ala Lys Asn Ser Asp Glu  
65 70 75 80  
Glu Met Asp Asp Glu Lys Lys Asn Lys Ser Leu Lys Pro Ile Gly Lys  
85 90 95  
Lys Leu Lys Lys Lys Phe Lys Leu Gly Met Lys Asn Arg Arg Ser Lys  
100 105 110  
Gly Val Leu Arg Gly Lys Arg Asn  
115 120

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1566915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Met Arg Cys Lys Arg Val Lys Arg Leu Arg Ala Ile Arg Arg Glu Ile  
1 5 10 15  
Val Glu Lys Glu Ser Phe Thr Leu Thr Arg Glu Asp Ala Lys Ser Ala  
20 25 30  
Ala Ile Glu Ala Ala Leu Ala Ala Pro Lys Leu Pro Val Arg Gln Ala  
35 40 45  
Pro Val Ser Pro Phe Met Glu Val Ala Thr Pro Ser Ser Glu Ser Ala  
50 55 60  
Ser Ala Ser Thr Thr Ile Ala Lys Asn Ser Asp Glu Glu Met Asp Asp  
65 70 75 80  
Glu Lys Lys Asn Lys Ser Leu Lys Pro Ile Gly Lys Lys Leu Lys Lys  
85 90 95  
Lys Phe Lys Leu Gly Met Lys Asn Arg Arg Ser Lys Gly Val Leu Arg  
100 105 110  
Gly Lys Arg Asn  
115

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met Glu Val Ala Thr Pro Ser Ser Glu Ser Ala Ser Ala Ser Thr Thr  
1 5 10 15  
Ile Ala Lys Asn Ser Asp Glu Glu Met Asp Asp Glu Lys Lys Asn Lys  
20 25 30  
Ser Leu Lys Pro Ile Gly Lys Lys Leu Lys Lys Lys Phe Lys Leu Gly  
35 40 45  
Met Lys Asn Arg Arg Ser Lys Gly Val Leu Arg Gly Lys Arg Asn



50 55 60

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1793
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| aacatcctaa | tcgaaaaaac  | aatctatctt | ttgggtccct | aaaaaagctc | cttcctttat | 60   |
| cttgttttct | aagttatctt  | tttgtatgag | tttcaaagct | tatcattatc | tcactcttct | 120  |
| tccatagcta | tgactacttt  | aacgaagatt | caagtgtacc | cacaagtctt | ggagcaccgt | 180  |
| ctcttcttca | gagatccgat  | acgggtcggg | tcaagattga | cttgtagaga | acgtagtaat | 240  |
| agggtttatg | tgcatcggtg  | tgagaaaaaa | gttgaaagaa | agagaaaagt | tgagaaattt | 300  |
| aagggaatg  | ggtcgtggga  | ttctttgaaa | tctgggtttt | tagggtttag | taaattaggg | 360  |
| ttcttgtcta | aagatgagta  | taatcagaaa | gttgaaaact | tgagatgggt | tttctcttcg | 420  |
| gttgctgttc | aaattgcgag  | atacattgtg | acgatgacaa | gtactggagc | tattcttttg | 480  |
| attgggtttc | aattatcagg  | tggagatagt | tcgatgaact | cattggtttg | gtatagttag | 540  |
| cttggtggaa | ttatcattgg  | aaccatgact | ggtgctaaca | tggttttgga | agatcattat | 600  |
| cgagccggtc | cacggaatgt  | tgttataacc | ggaagcacta | ggggactagg | gaaagctctt | 660  |
| gctagagagt | ttcttctctc  | tgagacaga  | gtcattgtca | catctcgag  | ttctgaatct | 720  |
| gttgatatga | ctgtcaaaga  | gctagagcaa | aatctcaaag | agattatgag | taacgctagc | 780  |
| gagtcagcta | gaaagaaaact | gagtgatgct | aaggtagttg | gtattgcctg | tgatgtttgc | 840  |
| aaaccgaag  | acgttgagaa  | gctgtcgaat | ttcgtctgta | aagagcttgg | ttccatcaac | 900  |
| atatggataa | acaatgctgg  | tactaacaaa | ggttttagac | cgctactcaa | attcacggaa | 960  |
| gaagatatca | cacagattgt  | ctccacaaat | ttgattggat | caattctatg | tacacgaggg | 1020 |
| gctatagatg | tgatgagcag  | acagcacagt | ggtggacaca | tttttaacat | ggatggtgct | 1080 |
| ggctctggag | gttcaagtac  | tcctctcact | gccgtatatg | gttcaacaaa | atgtggactt | 1140 |
| aggcagtttc | atgggtctat  | agtgaagaa  | agccaaaaaa | caaacgttgg | ccttcacact | 1200 |
| gcaccccctg | gcattggtct  | gacagaactt | cttctcagtg | gttcgagcat | taaaaacaag | 1260 |
| cagatgttta | acataatctg  | tgagcttctt | gagacagtag | ctagaacttt | ggtaccacga | 1320 |
| atgcgagttg | tgaaagggtc  | gggaaaagcc | gtcaattacc | taactcctcc | tcggatattg | 1380 |
| ttagctattg | tcacttcctg  | gctaaggaga | ggccgatggt | ttgatgacca | aggacgggag | 1440 |
| ttatatgcag | cagaagcaga  | tagactaagg | aactgggag  | agaacaggac | gaggttgcg  | 1500 |
| ttaacagacg | cgatggagat  | gtatacagag | aatacttggg | tctctgtttt | ctctctttct | 1560 |
| gttgtttgcg | ctttcatcat  | cttacaagc  | acaacaccta | gctcttttcc | aggcacataa | 1620 |
| caaacatctt | cctcggatgt  | gttttaagaa | aattgtaaac | gtacatgtta | tgtataaaaa | 1680 |
| acatatatat | aacagaaccg  | attgttcat  | gtaaacactt | cttatagttg | tagaatgtgt | 1740 |
| cgttgttgaa | aacaatgaaa  | aaaAtagatt | gtaataaact | tttatcagat | tgt        |      |

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Leu | Thr | Lys | Ile | Gln | Val | Tyr | Pro | Gln | Val | Leu | Glu | His |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Leu | Phe | Phe | Arg | Asp | Pro | Ile | Arg | Val | Gly | Ser | Arg | Leu | Thr | Cys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Glu | Arg | Ser | Asn | Arg | Val | Tyr | Val | His | Arg | Cys | Glu | Lys | Lys | Val |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Lys | Arg | Lys | Val | Glu | Lys | Phe | Lys | Gly | Asn | Gly | Ser | Trp | Asp |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Lys | Ser | Gly | Phe | Leu | Gly | Phe | Ser | Lys | Leu | Gly | Phe | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asp | Glu | Tyr | Asn | Gln | Lys | Val | Glu | Asn | Leu | Glu | Met | Val | Phe | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Val | Ala | Val | Gln | Ile | Ala | Arg | Tyr | Ile | Val | Thr | Met | Thr | Ser | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ala | Ile | Leu | Leu | Ile | Gly | Phe | Gln | Leu | Ser | Gly | Gly | Asp | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Asn | Ser | Leu | Val | Trp | Tyr | Ser | Trp | Leu | Gly | Gly | Ile | Ile | Ile | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Met | Thr | Gly | Ala | Asn | Met | Val | Leu | Glu | Asp | His | Tyr | Arg | Ala | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Arg | Asn | Val | Val | Ile | Thr | Gly | Ser | Thr | Arg | Gly | Leu | Gly | Lys | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ala | Arg | Glu | Phe | Leu | Leu | Ser | Gly | Asp | Arg | Val | Ile | Val | Thr | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Ser | Glu | Ser | Val | Asp | Met | Thr | Val | Lys | Glu | Leu | Glu | Gln | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Lys | Glu | Ile | Met | Ser | Asn | Ala | Ser | Glu | Ser | Ala | Arg | Lys | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Asp | Ala | Lys | Val | Val | Gly | Ile | Ala | Cys | Asp | Val | Cys | Lys | Pro | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Val | Glu | Lys | Leu | Ser | Asn | Phe | Ala | Val | Lys | Glu | Leu | Gly | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Ile | Trp | Ile | Asn | Asn | Ala | Gly | Thr | Asn | Lys | Gly | Phe | Arg | Pro | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Lys | Phe | Thr | Glu | Glu | Asp | Ile | Thr | Gln | Ile | Val | Ser | Thr | Asn | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Gly | Ser | Ile | Leu | Cys | Thr | Arg | Gly | Ala | Ile | Asp | Val | Met | Ser | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | His | Ser | Gly | Gly | His | Ile | Phe | Asn | Met | Asp | Gly | Ala | Gly | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Ser | Ser | Thr | Pro | Leu | Thr | Ala | Val | Tyr | Gly | Ser | Thr | Lys | Cys | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Arg | Gln | Phe | His | Gly | Ser | Ile | Val | Lys | Glu | Ser | Gln | Lys | Thr | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Gly | Leu | His | Thr | Ala | Ser | Pro | Gly | Met | Val | Leu | Thr | Glu | Leu | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Ser | Gly | Ser | Ser | Ile | Lys | Asn | Lys | Gln | Met | Phe | Asn | Ile | Ile | Cys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Leu | Pro | Glu | Thr | Val | Ala | Arg | Thr | Leu | Val | Pro | Arg | Met | Arg | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Lys | Gly | Ser | Gly | Lys | Ala | Val | Asn | Tyr | Leu | Thr | Pro | Pro | Arg | Ile |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Leu | Ala | Ile | Val | Thr | Ser | Trp | Leu | Arg | Arg | Gly | Arg | Trp | Phe | Asp |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Asp | Gln | Gly | Arg | Ala | Leu | Tyr | Ala | Ala | Glu | Ala | Asp | Arg | Leu | Arg | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     | 445 |     |     |     |     |
| Trp | Ala | Glu | Asn | Arg | Thr | Arg | Leu | Ser | Leu | Thr | Asp | Ala | Met | Glu | Met |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Tyr | Thr | Glu | Asn | Thr | Trp | Val | Ser | Val | Phe | Ser | Leu | Ser | Val | Val | Cys |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ala | Phe | Ile | Ile | Leu | Gln | Ser | Thr | Thr | Pro | Ser | Ser | Phe | Pro | Gly | Thr |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |

- (2) INFORMATION FOR SEQ ID NO:427:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 404 amino acids

|            |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|------------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1   | Val | Phe | Ser | Ser<br>5 | Val | Ala | Val | Gln | Ile<br>10 | Ala | Arg | Tyr | Ile | Val<br>15 | Thr |
| Met        | Thr | Ser | Thr | Gly      | Ala | Ile | Leu | Leu | Ile       | Gly | Phe | Gln | Leu | Ser       | Gly |
|            |     |     | 20  |          |     |     |     | 25  |           |     |     |     | 30  |           |     |
| Gly        | Asp | Ser | Ser | Met      | Asn | Ser | Leu | Val | Trp       | Tyr | Ser | Trp | Leu | Gly       | Gly |
|            |     | 35  |     |          |     |     | 40  |     |           |     |     | 45  |     |           |     |
| Ile        | Ile | Ile | Gly | Thr      | Met | Thr | Gly | Ala | Asn       | Met | Val | Leu | Glu | Asp       | His |
|            | 50  |     |     |          |     | 55  |     |     |           |     | 60  |     |     |           |     |
| Tyr<br>65  | Arg | Ala | Gly | Pro      | Arg | Asn | Val | Val | Ile       | Thr | Gly | Ser | Thr | Arg       | Gly |
|            |     |     |     | 70       |     |     |     |     |           | 75  |     |     |     | 80        |     |
| Leu        | Gly | Lys | Ala | Leu      | Ala | Arg | Glu | Phe | Leu       | Leu | Ser | Gly | Asp | Arg       | Val |
|            |     |     |     | 85       |     |     |     |     | 90        |     |     |     |     | 95        |     |
| Ile        | Val | Thr | Ser | Arg      | Ser | Ser | Glu | Ser | Val       | Asp | Met | Thr | Val | Lys       | Glu |
|            |     |     | 100 |          |     |     |     | 105 |           |     |     |     | 110 |           |     |
| Leu        | Glu | Gln | Asn | Leu      | Lys | Glu | Ile | Met | Ser       | Asn | Ala | Ser | Glu | Ser       | Ala |
|            |     |     | 115 |          |     |     | 120 |     |           |     |     | 125 |     |           |     |
| Arg        | Lys | Lys | Leu | Ser      | Asp | Ala | Lys | Val | Val       | Gly | Ile | Ala | Cys | Asp       | Val |
|            | 130 |     |     |          |     | 135 |     |     |           |     | 140 |     |     |           |     |
| Cys<br>145 | Lys | Pro | Glu | Asp      | Val | Glu | Lys | Leu | Ser       | Asn | Phe | Ala | Val | Lys       | Glu |
|            |     |     |     | 150      |     |     |     |     |           | 155 |     |     |     | 160       |     |
| Leu        | Gly | Ser | Ile | Asn      | Ile | Trp | Ile | Asn | Asn       | Ala | Gly | Thr | Asn | Lys       | Gly |
|            |     |     |     | 165      |     |     |     |     | 170       |     |     |     |     | 175       |     |
| Phe        | Arg | Pro | Leu | Leu      | Lys | Phe | Thr | Glu | Glu       | Asp | Ile | Thr | Gln | Ile       | Val |
|            |     |     | 180 |          |     |     |     | 185 |           |     |     |     | 190 |           |     |
| Ser        | Thr | Asn | Leu | Ile      | Gly | Ser | Ile | Leu | Cys       | Thr | Arg | Gly | Ala | Ile       | Asp |
|            |     | 195 |     |          |     |     | 200 |     |           |     |     | 205 |     |           |     |
| Val        | Met | Ser | Arg | Gln      | His | Ser | Gly | Gly | His       | Ile | Phe | Asn | Met | Asp       | Gly |
|            | 210 |     |     |          |     | 215 |     |     |           |     | 220 |     |     |           |     |
| Ala<br>225 | Gly | Ser | Gly | Gly      | Ser | Ser | Thr | Pro | Leu       | Thr | Ala | Val | Tyr | Gly       | Ser |
|            |     |     |     | 230      |     |     |     |     |           | 235 |     |     |     | 240       |     |
| Thr        | Lys | Cys | Gly | Leu      | Arg | Gln | Phe | His | Gly       | Ser | Ile | Val | Lys | Glu       | Ser |
|            |     |     |     | 245      |     |     |     |     | 250       |     |     |     |     | 255       |     |
| Gln        | Lys | Thr | Asn | Val      | Gly | Leu | His | Thr | Ala       | Ser | Pro | Gly | Met | Val       | Leu |
|            |     |     | 260 |          |     |     |     | 265 |           |     |     |     | 270 |           |     |
| Thr        | Glu | Leu | Leu | Leu      | Ser | Gly | Ser | Ser | Ile       | Lys | Asn | Lys | Gln | Met       | Phe |
|            |     | 275 |     |          |     | 280 |     |     |           |     |     | 285 |     |           |     |
| Asn        | Ile | Ile | Cys | Glu      | Leu | Pro | Glu | Thr | Val       | Ala | Arg | Thr | Leu | Val       | Pro |
|            | 290 |     |     |          |     | 295 |     |     |           |     | 300 |     |     |           |     |
| Arg<br>305 | Met | Arg | Val | Val      | Lys | Gly | Ser | Gly | Lys       | Ala | Val | Asn | Tyr | Leu       | Thr |
|            |     |     |     | 310      |     |     |     |     |           | 315 |     |     |     | 320       |     |
| Pro        | Pro | Arg | Ile | Leu      | Leu | Ala | Ile | Val | Thr       | Ser | Trp | Leu | Arg | Arg       | Gly |
|            |     |     |     | 325      |     |     |     |     | 330       |     |     |     |     | 335       |     |
| Arg        | Trp | Phe | Asp | Asp      | Gln | Gly | Arg | Ala | Leu       | Tyr | Ala | Ala | Glu | Ala       | Asp |
|            |     |     | 340 |          |     |     |     | 345 |           |     |     |     | 350 |           |     |
| Arg        | Leu | Arg | Asn | Trp      | Ala | Glu | Asn | Arg | Thr       | Arg | Leu | Ser | Leu | Thr       | Asp |

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1566920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Thr | Gly | Ala | Ile | Leu | Leu | Ile | Gly | Phe | Gln | Leu | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Asp | Ser | Ser | Met | Asn | Ser | Leu | Val | Trp | Tyr | Ser | Trp | Leu | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Ile | Gly | Thr | Met | Thr | Gly | Ala | Asn | Met | Val | Leu | Glu | Asp | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Arg | Ala | Gly | Pro | Arg | Asn | Val | Val | Ile | Thr | Gly | Ser | Thr | Arg | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Lys | Ala | Leu | Ala | Arg | Glu | Phe | Leu | Leu | Ser | Gly | Asp | Arg | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Val | Thr | Ser | Arg | Ser | Ser | Glu | Ser | Val | Asp | Met | Thr | Val | Lys | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Gln | Asn | Leu | Lys | Glu | Ile | Met | Ser | Asn | Ala | Ser | Glu | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Lys | Lys | Leu | Ser | Asp | Ala | Lys | Val | Val | Gly | Ile | Ala | Cys | Asp | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Lys | Pro | Glu | Asp | Val | Glu | Lys | Leu | Ser | Asn | Phe | Ala | Val | Lys | Glu |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Ser | Ile | Asn | Ile | Trp | Ile | Asn | Asn | Ala | Gly | Thr | Asn | Lys | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Arg | Pro | Leu | Leu | Lys | Phe | Thr | Glu | Glu | Asp | Ile | Thr | Gln | Ile | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Thr | Asn | Leu | Ile | Gly | Ser | Ile | Leu | Cys | Thr | Arg | Gly | Ala | Ile | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Met | Ser | Arg | Gln | His | Ser | Gly | Gly | His | Ile | Phe | Asn | Met | Asp | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Gly | Ser | Gly | Gly | Ser | Ser | Thr | Pro | Leu | Thr | Ala | Val | Tyr | Gly | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Lys | Cys | Gly | Leu | Arg | Gln | Phe | His | Gly | Ser | Ile | Val | Lys | Glu | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Lys | Thr | Asn | Val | Gly | Leu | His | Thr | Ala | Ser | Pro | Gly | Met | Val | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Glu | Leu | Leu | Leu | Ser | Gly | Ser | Ser | Ile | Lys | Asn | Lys | Gln | Met | Phe |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Ile | Ile | Cys | Glu | Leu | Pro | Glu | Thr | Val | Ala | Arg | Thr | Leu | Val | Pro |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Met | Arg | Val | Val | Lys | Gly | Ser | Gly | Lys | Ala | Val | Asn | Tyr | Leu | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Pro | Arg | Ile | Leu | Leu | Ala | Ile | Val | Thr | Ser | Trp | Leu | Arg | Arg | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Trp | Phe | Asp | Asp | Gln | Gly | Arg | Ala | Leu | Tyr | Ala | Ala | Glu | Ala | Asp |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Leu | Arg | Asn | Trp | Ala | Glu | Asn | Arg | Thr | Arg | Leu | Ser | Leu | Thr | Asp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Met | Glu | Met | Tyr | Thr | Glu | Asn | Thr | Trp | Val | Ser | Val | Phe | Ser | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Val | Val | Cys | Ala | Phe | Ile | Ile | Leu | Gln | Ser | Thr | Thr | Pro | Ser | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| Phe | Pro | Gly | Thr |     |     |     |     |     |     |     |     |     |     |     |     |

2025 RELEASE UNDER E.O. 14176

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(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..681
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acataatcat cgctattctc tctctctctc tctctctctc tctctctcgc tctcatattt  | 60  |
| gcagttgaca attcgttctc tttgggaaat tagagatgca ggcatacaaga gcgcgactgt | 120 |
| ttaaagaata caaagaggta cagcgagaga aagtagcaga tcctgatatt caattgatct  | 180 |
| gtgacgatac caacatattc aaatggaccg ctcttatcaa aggaccttcg gagactcctt  | 240 |
| acgaaggcgg tgttttttcag cttgcttttt ctgttcctga accttatcct ttgcaacctc | 300 |
| ctcaagttcg attcttgacc aagatattcc atcctaattg tcatttcaag acaggagaaa  | 360 |
| tatgtctcga cattttgaag aatgcttgga gtcctgcttg gacgcttcag tctgtgtgta  | 420 |
| gagctatcat agcattgatg gctcatcctg agccggacag tcctcttaac tgcgactcag  | 480 |
| ggaatcttct aagatctggg gatgtgagag ggttcaattc aatggcacia atgtatacac  | 540 |
| gcctcgccgc tatgcctaag aaaggatgat gatgatgatg atcctcttgc tttttttttg  | 600 |
| tttttttttt tgaaatytgt aatgatattg attCtgcgag agtgaatata ttattaacga  | 660 |
| gaagaaCgat gattcttctt t                                            |     |

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ala | Ser | Arg | Ala | Arg | Leu | Phe | Glu | Tyr | Lys | Glu | Val | Gln |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Arg | Glu | Lys | Val | Ala | Asp | Pro | Asp | Ile | Gln | Leu | Ile | Cys | Asp | Asp | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Ile | Phe | Lys | Trp | Thr | Ala | Leu | Ile | Lys | Gly | Pro | Ser | Glu | Thr | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Glu | Gly | Gly | Val | Phe | Gln | Leu | Ala | Phe | Ser | Val | Pro | Glu | Pro | Tyr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Gln | Pro | Pro | Gln | Val | Arg | Phe | Leu | Thr | Lys | Ile | Phe | His | Pro |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Asn | Val | His | Phe | Lys | Thr | Gly | Glu | Ile | Cys | Leu | Asp | Ile | Leu | Lys | Asn |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |
| Ala | Trp | Ser | Pro | Ala | Trp | Thr | Leu | Gln | Ser | Val | Cys | Arg | Ala | Ile | Ile |
|     |     |     |     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |
| Ala | Leu | Met | Ala | His | Pro | Glu | Pro | Asp | Ser | Pro | Leu | Asn | Cys | Asp | Ser |
|     |     |     |     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |
| Gly | Asn | Leu | Leu | Arg | Ser | Gly | Asp | Val | Arg | Gly | Phe | Asn | Ser | Met | Ala |
|     |     |     |     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |
| Gln | Met | Tyr | Thr | Arg | Leu | Ala | Ala | Met | Pro | Lys | Lys | Gly |     |     |     |
|     |     |     |     |     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..429  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1566936  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```
aaaWacaaac aaaaaaatgc tttcaaagat aaagccggtg gttctcatgt cgttcttgc 60
tctgtttcca ttgtgttctt cggggttag agaaggccat ggagttactc acaccgacca 120
aaattcctta aacaaggttg aagagagtat tccaacgata atggattatc cggaaccagg 180
tccagaccg aaacacgata caacaaacc cggttatggt ttctctccc caccgccacc 240
gccactgtca ccgccaccgc caccgaatat gaactaagaa tcatgatgaa gcaaaaatat 300
gtaatatcgt taaatcatgc tcgtgagaag aactagtatt catgtgaagc aaaagaaaaa 360
cttaaataatg atgattctat gatatgtact atcaaagtaa tcaatcaaat ataaaagagt 420
aaaatttgg
```

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```
Xaa Thr Asn Lys Lys Met Leu Ser Lys Ile Lys Pro Val Val Leu Met
1 5 10 15
Ser Phe Leu Leu Leu Phe Pro Leu Cys Ser Ser Gly Phe Arg Glu Gly
20 25 30
His Gly Val Thr His Thr Asp Gln Asn Ser Leu Asn Lys Val Glu Glu
35 40 45
Ser Ile Pro Thr Ile Met Asp Tyr Pro Glu Pro Gly Pro Asp Pro Lys
50 55 60
His Asp Pro Thr Lys Pro Gly Tyr Gly Phe Pro Pro Pro Pro Pro
65 70 75 80
Pro Leu Ser Pro Pro Pro Pro Pro Asn Met Asn
85 90
```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..86  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```
Met Leu Ser Lys Ile Lys Pro Val Val Leu Met Ser Phe Leu Leu Leu
1 5 10 15
Phe Pro Leu Cys Ser Ser Gly Phe Arg Glu Gly His Gly Val Thr His
20 25 30
Thr Asp Gln Asn Ser Leu Asn Lys Val Glu Glu Ser Ile Pro Thr Ile
35 40 45
Met Asp Tyr Pro Glu Pro Gly Pro Asp Pro Lys His Asp Pro Thr Lys
50 55 60
Pro Gly Tyr Gly Phe Pro Pro Pro Pro Pro Pro Pro Leu Ser Pro Pro
```

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..76

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566939

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

| (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                     | Ser | Phe | Leu | Leu | Phe | Pro | Leu | Cys | Ser | Ser | Gly | Phe | Arg | Glu |     |
| 1                                       |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly                                     | His | Gly | Val | Thr | His | Thr | Asp | Gln | Asn | Ser | Leu | Asn | Lys | Val | Glu |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu                                     | Ser | Ile | Pro | Thr | Ile | Met | Asp | Tyr | Pro | Glu | Pro | Gly | Pro | Asp | Pro |
|                                         |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys                                     | His | Asp | Pro | Thr | Lys | Pro | Gly | Tyr | Gly | Phe | Pro | Pro | Pro | Pro |     |
|                                         |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro                                     | Pro | Leu | Ser | Pro | Pro | Pro | Pro | Asn | Met | Asn |     |     |     |     |     |
| 65                                      |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..716

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566946

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:101 |             |             |             |            |             |  |  |  |  |     |
|------------------------------------------|-------------|-------------|-------------|------------|-------------|--|--|--|--|-----|
| cctttgatca                               | gatagtgaaa  | gcgattctct  | atattgcaga  | tcgatctccg | agtttgctaa  |  |  |  |  | 60  |
| atcgccggga                               | aattttactga | atttggagct  | agtcattgtct | tcagatcctg | acaaaatgat  |  |  |  |  | 120 |
| gtccaaagcc                               | gacaaaatga  | caaagctcac  | gcttactaga  | tggagtgtcg | attggagagg  |  |  |  |  | 180 |
| tgtactgat                                | aacacaaata  | caccaaaaaa  | aaaaaaacag  | aaagtaacat | gagatctctc  |  |  |  |  | 240 |
| ttatttagccg                              | tgtgcctgg   | ctttgcttta  | cactgcggtg  | aagcagccgt | gtcttgcaac  |  |  |  |  | 300 |
| acggtgattg                               | cggaatttta  | cctttgctta  | tcctactgtg  | ctcaggcgcg | accgggtcca  |  |  |  |  | 360 |
| accctctgct                               | gcaacggtct  | cacaacactc  | aagagtcagg  | ctcaaacttc | tgtggaccgt  |  |  |  |  | 420 |
| caggggGtct                               | gtcgttgcac  | caaattctgct | attggaggac  | tcactctctc | tcctagaacc  |  |  |  |  | 480 |
| atccaaaatg                               | ctttggaatt  | gocctctaaa  | tgtgggtgtcg | atctccctta | caagttcagc  |  |  |  |  | 540 |
| ccttccactg                               | actgcgacag  | tatccagtga  | gacaagcaga  | aaatcttaaa | ggaagctact  |  |  |  |  | 600 |
| acaagaacta                               | taataaaccta | ataattaata  | aatgagggca  | ttggtttgct | agttgctaata |  |  |  |  | 660 |
| tgtatcagtga                              | tgtattgtca  | ttttgaatgt  | tctaatatca  | gcaggcactt | atctcc      |  |  |  |  |     |

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids

- (B) TYPE: amino acid

- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..113

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566947

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Arg Ser Leu Leu Leu Ala Val Cys Leu Val Leu Ala Leu His Cys  
1 5 10 15  
Gly Glu Ala Ala Val Ser Cys Asn Thr Val Ile Ala Asp Leu Tyr Pro  
20 25 30  
Cys Leu Ser Tyr Val Thr Gln Gly Gly Pro Val Pro Thr Leu Cys Cys  
35 40 45  
Asn Gly Leu Thr Thr Leu Lys Ser Gln Ala Gln Thr Ser Val Asp Arg  
50 55 60  
Gln Gly Val Cys Arg Cys Ile Lys Ser Ala Ile Gly Gly Leu Thr Leu  
65 70 75 80  
Ser Pro Arg Thr Ile Gln Asn Ala Leu Glu Leu Pro Ser Lys Cys Gly  
85 90 95  
Val Asp Leu Pro Tyr Lys Phe Ser Pro Ser Thr Asp Cys Asp Ser Ile  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aaaaactcct aaaccaaatt ataattgtta gtaagttaag taacagagaa caaaataata  | 60   |
| ctcgtaaactc ttgtttccaa actataacgt aacttttggt catcatcttc acagtttctg | 120  |
| tttctgtttc taaagattct aaattttgtg tttttttttt cttttttctt tcgattattt  | 180  |
| ttgattttct gatggaattc cgcaaacctt ttaagtctca tagctcgtat aaacagatta  | 240  |
| taagcaccgg aaatcaaaac gagaagacaa agaagaagaa gaaactggcg aatcttgacg  | 300  |
| atggcgacat tgctaaaact cagagctctg ggtctagttt cgatggaaac agctataagt  | 360  |
| tctggcaaga cattgcaaca gatgattata caaagagcgg gagtttcgat ttcccgcgat  | 420  |
| accgtgagga gatcacactc gatgtaaaac aagaaacaga ggaaacagag gatgtcagca  | 480  |
| acaacaacaa tttgtccggg tctaaagaaa cgagagtctc ttcaaaaata aacagttcag  | 540  |
| gaactaataa tatgtctggt tctgtacgtt cttgtacatc ttcgacttcg ttttcatcgg  | 600  |
| ccacaatgcg gttaaattta gagcagcagt tggaggatga aggagagggtg gttgtaagat | 660  |
| gttcacgcgt gaggaaaaca gagcttggtt cgaggggcga ggcgagatcg aggttgatag  | 720  |
| atccgccaca agaagaggaa caacaatact cgagctggat cgggacatcg gatcagttaa  | 780  |
| gatcagggtt acttgggaga cactctgatg atattgatga agaagatgat tcttcggctg  | 840  |
| aagaagatgt tccagtggaa tatcgaaagt tgaaaatgga cgcgataacg ttgcttcaat  | 900  |
| ggatgagctt aatcgcactc gtagtggcgt tagtggtgag tctagcgctt catacttgga  | 960  |
| gAAAAatgct actctatgga gccttcactc gtggaaatgg gaagtgggtc tgctggttct  | 1020 |
| catctgcggg aggtctggtt cgggatgcgg aatacgaatc atcgtcttct ttatcgaaag  | 1080 |
| aaacttccta ttgaggaaac gggttcttta cttcgtatac ggtgtgaaga ctgctgttca  | 1140 |
| gaactgtctc tggcttgccc tcgtgctcgt cgcttggcat ttcttggtcg acaagaaagt  | 1200 |
| agaaagggaa acacaaagcg acgttcttct tctcgtatct aaaatattag tgtgtttctt  | 1260 |
| gttgagcagc gtcttatggc tgatcaagac actgggtggg aaagttttag catcttcggt  | 1320 |
| ccacgttagt acctactttg atcggattca agaagctctg ttcatcatt acttgatcga   | 1380 |
| gacgttatct gtacctcaa tgcttgagtt aagcaggatt gaggaagagg aagatcggac   | 1440 |
| gcaagatgag atctacaagg tgcagaaagg aggagctgat ttatcacccg aactttgttc  | 1500 |
| cgctgcggtt cctcaggaaa aaagtggaag tacaatgaac atgaagtctc ctccaatcat  | 1560 |
| tccgaagacg ggtggtgata acggaatcac aatggatgat ttacacaaga tgaatcagaa  | 1620 |
| aaacgtttca gcttggaaac tgaagagact gatgaagatt gtgagaaata tttccctgac  | 1680 |
| tacgttgagc gaacaagcgc ttcaaaacac gtgtgaagat gaatccactc gacagatacg  | 1740 |
| gagcgaaaaa gaagctaaag cagctgcaag gaagattttc aagaacgtag ctcaacctgg  | 1800 |
| cacaaaacac atatacctgg aggacttgat gagatttttg cgagtagacg aggcgatgaa  | 1860 |
| gacaatgtgt ctcttcgaag ggccttagt gacaaaaaag attactaaat cagccttgaa   | 1920 |
| gaactggctg gtaaatgctt tcagagagag aagagcactt gccttaacac tcaatgacac  | 1980 |



|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| caaaacagca | gtgaacaaac | tccatcacat | gattagtttt | ctcactgcc  | ttgtcatcat | 2040 |
| agtcatatgg | ctgacccctc | ttgaaatcgc | tacttccaag | tatcttttat | ttttaacttc | 2100 |
| acaagttgta | ctcttagcct | tcatgtttgg | gaactctctc | aagaccgtct | tcgagtcaat | 2160 |
| catcttcctc | ttcatcattc | acccttaocg | tgttggtgat | cggttactca | tcgacactgt | 2220 |
| agagatggtg | gtggaggaaa | tgaacattct | cacaacagtt | ttcttgagag | ctgacaatct | 2280 |
| gaagattgtg | tatccaaata | ttcttctatg | gcagaaagcg | atccacaatt | acaaccgtag | 2340 |
| tccggatatg | ggagatgaag | ttacatgctg | tgtccacatt | actactcctc | ctgaaaagat | 2400 |
| tgctgcaatc | aaacaaagaa | tatcaagcta | cattgatagc | aagccagagt | attggtatcc | 2460 |
| aaaagctgat | atcattgtaa | aggatgtgga | agatttgaac | attgtgagga | tagcaatatg | 2520 |
| gctgtgtcat | aaaattaacc | atcaaaacat | gggagagaga | tttacaagaa | gagcgttggt | 2580 |
| gatcgaggaa | gtaatcaaaa | tcctcctcga | actcgacatt | caataccggg | ttcatccact | 2640 |
| tgatatcaat | gttaaaacca | tgccaacagt | tgtctcgagc | agagttccac | caggctgggc | 2700 |
| acaaaaccct | gattcaagg  | aattatagag | atgatgtgaa | ttgtgttatc | ttaaacttta | 2760 |
| agtgtgtttt | agtatgaggt | ttgattgttg | tatttttttt | ttcttttttt | gtaaaccggg | 2820 |
| tgttgatat  | atatgaaggt | gaaagcaaag | agtgggatca | taaacttgtg | ttatagaaac | 2880 |
| tttatgaaaa | tagaaactaa | tgatatTTTT | agtaatgatt | tttttttt   |            |      |

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1566956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Glu | Leu | Asn | Arg | Thr | Arg | Ser | Gly | Val | Ser | Val | Glu | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Tyr | Leu | Glu | Lys | Asn | Ala | Thr | Leu | Trp | Ser | Leu | His | Leu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Trp | Glu | Val | Val | Leu | Leu | Val | Leu | Ile | Cys | Gly | Arg | Leu | Val | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gly | Cys | Gly | Ile | Arg | Ile | Ile | Val | Phe | Phe | Ile | Glu | Arg | Asn | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Lys | Arg | Val | Leu | Tyr | Phe | Val | Tyr | Gly | Val | Lys | Thr | Ala | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Asn | Cys | Leu | Trp | Leu | Gly | Leu | Val | Leu | Val | Ala | Trp | His | Phe | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Asp | Lys | Lys | Val | Glu | Arg | Glu | Thr | Gln | Ser | Asp | Val | Leu | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ser | Lys | Ile | Leu | Val | Cys | Phe | Leu | Leu | Ser | Thr | Val | Leu | Trp | Leu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ile | Lys | Thr | Leu | Val | Val | Lys | Val | Leu | Ala | Ser | Ser | Phe | His | Val | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Thr | Tyr | Phe | Asp | Arg | Ile | Gln | Glu | Ala | Leu | Phe | His | His | Tyr | Leu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Thr | Leu | Ser | Val | Pro | Pro | Met | Leu | Glu | Leu | Ser | Arg | Ile | Glu | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Glu | Asp | Arg | Thr | Gln | Asp | Glu | Ile | Tyr | Lys | Val | Gln | Lys | Gly | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asp | Leu | Ser | Pro | Glu | Leu | Cys | Ser | Ala | Ala | Phe | Pro | Gln | Glu | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Gly | Ser | Thr | Met | Asn | Met | Lys | Phe | Ser | Pro | Ile | Ile | Pro | Lys | Thr |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gly | Gly | Asp | Asn | Gly | Ile | Thr | Met | Asp | Asp | Leu | His | Lys | Met | Asn | Gln |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Asn | Val | Ser | Ala | Trp | Asn | Met | Lys | Arg | Leu | Met | Lys | Ile | Val | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Ile | Ser | Leu | Thr | Thr | Leu | Asp | Glu | Gln | Ala | Leu | Gln | Asn | Thr | Cys |

260 265 270  
Glu Asp Glu Ser Thr Arg Gln Ile Arg Ser Glu Lys Glu Ala Lys Ala  
275 280 285  
Ala Ala Arg Lys Ile Phe Lys Asn Val Ala Gln Pro Gly Thr Lys His  
290 295 300  
Ile Tyr Leu Glu Asp Leu Met Arg Phe Leu Arg Val Asp Glu Ala Met  
305 310 315 320  
Lys Thr Met Cys Leu Phe Glu Gly Ala Leu Val Thr Lys Lys Ile Thr  
325 330 335  
Lys Ser Ala Leu Lys Asn Trp Leu Val Asn Ala Phe Arg Glu Arg Arg  
340 345 350  
Ala Leu Ala Leu Thr Leu Asn Asp Thr Lys Thr Ala Val Asn Lys Leu  
355 360 365  
His His Met Ile Ser Phe Leu Thr Ala Ile Val Ile Ile Val Ile Trp  
370 375 380  
Leu Ile Leu Leu Glu Ile Ala Thr Ser Lys Tyr Leu Leu Phe Leu Thr  
385 390 395 400  
Ser Gln Val Val Leu Leu Ala Phe Met Phe Gly Asn Ser Leu Lys Thr  
405 410 415  
Val Phe Glu Ser Ile Ile Phe Leu Phe Ile Ile His Pro Tyr Asp Val  
420 425 430  
Gly Asp Arg Leu Leu Ile Asp Thr Val Glu Met Val Val Glu Glu Met  
435 440 445  
Asn Ile Leu Thr Thr Val Phe Leu Arg Ala Asp Asn Leu Lys Ile Val  
450 455 460  
Tyr Pro Asn Ile Leu Leu Trp Gln Lys Ala Ile His Asn Tyr Asn Arg  
465 470 475 480  
Ser Pro Asp Met Gly Asp Glu Val Thr Cys Cys Val His Ile Thr Thr  
485 490 495  
Pro Pro Glu Lys Ile Ala Ala Ile Lys Gln Arg Ile Ser Ser Tyr Ile  
500 505 510  
Asp Ser Lys Pro Glu Tyr Trp Tyr Pro Lys Ala Asp Ile Ile Val Lys  
515 520 525  
Asp Val Glu Asp Leu Asn Ile Val Arg Ile Ala Ile Trp Leu Cys His  
530 535 540  
Lys Ile Asn His Gln Asn Met Gly Glu Arg Phe Thr Arg Arg Ala Leu  
545 550 555 560  
Leu Ile Glu Glu Val Ile Lys Ile Leu Leu Glu Leu Asp Ile Gln Tyr  
565 570 575  
Arg Phe His Pro Leu Asp Ile Asn Val Lys Thr Met Pro Thr Val Val  
580 585 590  
Ser Ser Arg Val Pro Pro Gly Trp Ser Gln Asn Pro Asp Ser Arg  
595 600 605

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..440

(D) OTHER INFORMATION: / Ceres Seq. ID 1566957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Leu Glu Leu Ser Arg Ile Glu Glu Glu Glu Asp Arg Thr Gln Asp  
1 5 10 15  
Glu Ile Tyr Lys Val Gln Lys Gly Gly Ala Asp Leu Ser Pro Glu Leu  
20 25 30  
Cys Ser Ala Ala Phe Pro Gln Glu Lys Ser Gly Ser Thr Met Asn Met  
35 40 45

```

Lys Phe Ser Pro Ile Ile Pro Lys Thr Gly Gly Asp Asn Gly Ile Thr
 50 55 60
Met Asp Asp Leu His Lys Met Asn Gln Lys Asn Val Ser Ala Trp Asn
 65 70 75 80
Met Lys Arg Leu Met Lys Ile Val Arg Asn Ile Ser Leu Thr Thr Leu
 85 90 95
Asp Glu Gln Ala Leu Gln Asn Thr Cys Glu Asp Glu Ser Thr Arg Gln
 100 105 110
Ile Arg Ser Glu Lys Glu Ala Lys Ala Ala Ala Arg Lys Ile Phe Lys
 115 120 125
Asn Val Ala Gln Pro Gly Thr Lys His Ile Tyr Leu Glu Asp Leu Met
 130 135 140
Arg Phe Leu Arg Val Asp Glu Ala Met Lys Thr Met Cys Leu Phe Glu
145 150 155 160
Gly Ala Leu Val Thr Lys Lys Ile Thr Lys Ser Ala Leu Lys Asn Trp
 165 170 175
Leu Val Asn Ala Phe Arg Glu Arg Arg Ala Leu Ala Leu Thr Leu Asn
 180 185 190
Asp Thr Lys Thr Ala Val Asn Lys Leu His His Met Ile Ser Phe Leu
 195 200 205
Thr Ala Ile Val Ile Ile Val Ile Trp Leu Ile Leu Leu Glu Ile Ala
 210 215 220
Thr Ser Lys Tyr Leu Leu Phe Leu Thr Ser Gln Val Val Leu Leu Ala
225 230 235 240
Phe Met Phe Gly Asn Ser Leu Lys Thr Val Phe Glu Ser Ile Ile Phe
 245 250 255
Leu Phe Ile Ile His Pro Tyr Asp Val Gly Asp Arg Leu Leu Ile Asp
 260 265 270
Thr Val Glu Met Val Val Glu Glu Met Asn Ile Leu Thr Thr Val Phe
 275 280 285
Leu Arg Ala Asp Asn Leu Lys Ile Val Tyr Pro Asn Ile Leu Leu Trp
 290 295 300
Gln Lys Ala Ile His Asn Tyr Asn Arg Ser Pro Asp Met Gly Asp Glu
305 310 315 320
Val Thr Cys Cys Val His Ile Thr Thr Pro Pro Glu Lys Ile Ala Ala
 325 330 335
Ile Lys Gln Arg Ile Ser Ser Tyr Ile Asp Ser Lys Pro Glu Tyr Trp
 340 345 350
Tyr Pro Lys Ala Asp Ile Ile Val Lys Asp Val Glu Asp Leu Asn Ile
 355 360 365
Val Arg Ile Ala Ile Trp Leu Cys His Lys Ile Asn His Gln Asn Met
 370 375 380
Gly Glu Arg Phe Thr Arg Arg Ala Leu Leu Ile Glu Glu Val Ile Lys
385 390 395 400
Ile Leu Leu Glu Leu Asp Ile Gln Tyr Arg Phe His Pro Leu Asp Ile
 405 410 415
Asn Val Lys Thr Met Pro Thr Val Val Ser Ser Arg Val Pro Pro Gly
 420 425 430
Trp Ser Gln Asn Pro Asp Ser Arg
 435 440

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566958

U.S. PAT. & TM. OFF.

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Met | Lys | Phe | Ser | Pro | Ile | Ile | Pro | Lys | Thr | Gly | Gly | Asp | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ile | Thr | Met | Asp | Asp | Leu | His | Lys | Met | Asn | Gln | Lys | Asn | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Trp | Asn | Met | Lys | Arg | Leu | Met | Lys | Ile | Val | Arg | Asn | Ile | Ser | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Leu | Asp | Glu | Gln | Ala | Leu | Gln | Asn | Thr | Cys | Glu | Asp | Glu | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Arg | Gln | Ile | Arg | Ser | Glu | Lys | Glu | Ala | Lys | Ala | Ala | Ala | Arg | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Phe | Lys | Asn | Val | Ala | Gln | Pro | Gly | Thr | Lys | His | Ile | Tyr | Leu | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Leu | Met | Arg | Phe | Leu | Arg | Val | Asp | Glu | Ala | Met | Lys | Thr | Met | Cys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Leu | Phe | Glu | Gly | Ala | Leu | Val | Thr | Lys | Lys | Ile | Thr | Lys | Ser | Ala | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Asn | Trp | Leu | Val | Asn | Ala | Phe | Arg | Glu | Arg | Arg | Ala | Leu | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Asn | Asp | Thr | Lys | Thr | Ala | Val | Asn | Lys | Leu | His | His | Met | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Phe | Leu | Thr | Ala | Ile | Val | Ile | Ile | Val | Ile | Trp | Leu | Ile | Leu | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ile | Ala | Thr | Ser | Lys | Tyr | Leu | Leu | Phe | Leu | Thr | Ser | Gln | Val | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Ala | Phe | Met | Phe | Gly | Asn | Ser | Leu | Lys | Thr | Val | Phe | Glu | Ser |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Ile | Phe | Leu | Phe | Ile | Ile | His | Pro | Tyr | Asp | Val | Gly | Asp | Arg | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Leu | Ile | Asp | Thr | Val | Glu | Met | Val | Val | Glu | Glu | Met | Asn | Ile | Leu | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Val | Phe | Leu | Arg | Ala | Asp | Asn | Leu | Lys | Ile | Val | Tyr | Pro | Asn | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Trp | Gln | Lys | Ala | Ile | His | Asn | Tyr | Asn | Arg | Ser | Pro | Asp | Met |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Asp | Glu | Val | Thr | Cys | Cys | Val | His | Ile | Thr | Thr | Pro | Pro | Glu | Lys |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ile | Ala | Ala | Ile | Lys | Gln | Arg | Ile | Ser | Ser | Tyr | Ile | Asp | Ser | Lys | Pro |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Glu | Tyr | Trp | Tyr | Pro | Lys | Ala | Asp | Ile | Ile | Val | Lys | Asp | Val | Glu | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Asn | Ile | Val | Arg | Ile | Ala | Ile | Trp | Leu | Cys | His | Lys | Ile | Asn | His |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gln | Asn | Met | Gly | Glu | Arg | Phe | Thr | Arg | Arg | Ala | Leu | Leu | Ile | Glu | Glu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Ile | Lys | Ile | Le  |     |     |     |     |     |     |     |     |     |     |     |

(B) LOCATION: 1..1463

(D) OTHER INFORMATION: / Ceres Seq. ID 1566971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaaaccgat | tcattttaaac | aacaaaaaac  | cacttacaga  | gttcgttcgc  | cggcggcgGc  | 60   |
| gagtcacgt  | catcaatgtc  | aaacatcggt  | gttctagaca  | acggcgggtg  | tctaataaaa  | 120  |
| gccggacaag | gcggcgagcg  | tgatcccacc  | accgtaatcc  | cgaactgtct  | ctacaaacct  | 180  |
| ctctcttcca | aaaaattcat  | ccacccatca  | ccactcacca  | ctctctccga  | cgaaatcgac  | 240  |
| ctcacctccg | ccgccgtacg  | ccgcccgaatc | gaccgtgggt  | acctcataaa  | ctccgacct   | 300  |
| caacgcgaaa | tctgggtcaca | cctattcact  | tccctcctcc  | acatagctcc  | ttcctcctcc  | 360  |
| tctctcctcc | tcaccgaagc  | accactctca  | atcccttccg  | ttcaacgaac  | caccgacgaa  | 420  |
| ctcgtcttcg | aagattttcg  | attctcttct  | ctctatatag  | ctcatcctca  | atctcttgtt  | 480  |
| catctctatg | aagctagtcg  | tcagcctgat  | tcaatcctct  | caaagactca  | gtgtagcttc  | 540  |
| gttggtgatt | gtggtttctc  | cttcactcac  | gctgttcctg  | ttcttcacaa  | tttcaactct  | 600  |
| aatcacgcca | ttaagaggat  | tgatttagga  | ggaaaagctt  | ttactaatta  | cttgaaggaa  | 660  |
| ttgggttctt | atagatctat  | taatgttatg  | gatgaaactt  | ttttagttga  | tgatgctaaa  | 720  |
| gagaagcttt | gttttgtttc  | acttgatctt  | cttcgtgatc  | tccgccttgc  | tagaaatggg  | 780  |
| aacactctta | tcaagtctac  | ttatgttctt  | cctgatgggtg | ttacacatac  | caaaggctat  | 840  |
| gttaaagacc | ctcaagctgc  | taagagggtt  | cttagtttgt  | cagagaaaaga | gtctgtgggtg | 900  |
| gtgatggata | aggttgggga  | gagaaagaag  | gctgacatga  | acaaaaatga  | gattgattta  | 960  |
| acgaatgagc | gttttcttgt  | acctgagacg  | ttattccagc  | ctgcagattt  | agggatgaat  | 1020 |
| caggcgggac | ttgcagagtg  | cattgtccga  | gctataaaact | catgccattc  | ttacttgcaa  | 1080 |
| ccagttttgt | atcaaagcat  | tatcttaact  | ggtggaagta  | cattatttcc  | acaacttaag  | 1140 |
| gagagactag | aaggagagct  | tccgaccactt | gtcccagatc  | actttgatgt  | gaagataaca  | 1200 |
| actcaggagg | accccatact  | aggtgtatgg  | agaggtgggt  | cacttttggc  | ttccagcccg  | 1260 |
| gatttcgagt | ccatgtgtgt  | caccaagggt  | gagtacgaag  | aacttggatc  | agctcgggtg  | 1320 |
| cgtagacgat | tctttcattg  | aggctaacca  | aaacaatatc  | acatgagttg  | gttgtaagtt  | 1380 |
| gaaactcttc | acattatttg  | tctgtatattg | taatgcatgt  | attgtttttc  | ttcttcctct  | 1440 |
| aatttgaaaa | acttcaaacc  | gtc         |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1566972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Ile | Val | Val | Leu | Asp | Asn | Gly | Gly | Gly | Leu | Ile | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gln | Gly | Gly | Glu | Arg | Asp | Pro | Thr | Thr | Val | Ile | Pro | Asn | Cys | Leu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Tyr | Lys | Pro | Leu | Ser | Ser | Lys | Lys | Phe | Ile | His | Pro | Ser | Pro | Leu | Thr |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Thr | Leu | Ser | Asp | Glu | Ile | Asp | Leu | Thr | Ser | Ala | Ala | Val | Arg | Arg | Pro |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Ile | Asp | Arg | Gly | Tyr | Leu | Ile | Asn | Ser | Asp | Leu | Gln | Arg | Glu | Ile | Trp |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  | 80  |
| Ser | His | Leu | Phe | Thr | Ser | Leu | Leu | His | Ile | Ala | Pro | Ser | Ser | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Leu | Thr | Glu | Ala | Pro | Leu | Ser | Ile | Pro | Ser | Val | Gln | Arg | Thr |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Thr | Asp | Glu | Leu | Val | Phe | Glu | Asp | Phe | Gly | Phe | Ser | Ser | Leu | Tyr | Ile |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Ala | His | Pro | Gln | Ser | Leu | Val | His | Leu | Tyr | Glu | Ala | Ser | Arg | Gln | Pro |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Asp | Ser | Ile | Leu | Ser | Lys | Thr | Gln | Cys | Ser | Leu | Val | Val | Asp | Cys | Gly |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 | 160 |
| Phe | Ser | Phe | Thr | His | Ala | Val | Pro | Val | Leu | His | Asn | Phe | Thr | Leu | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

His Ala Ile Lys Arg Ile Asp Leu Gly Gly Lys Ala Phe Thr Asn Tyr  
180 185 190  
Leu Lys Glu Leu Val Ser Tyr Arg Ser Ile Asn Val Met Asp Glu Thr  
195 200 205  
Phe Leu Val Asp Asp Ala Lys Glu Lys Leu Cys Phe Val Ser Leu Asp  
210 215 220  
Leu Leu Arg Asp Leu Arg Leu Ala Arg Asn Gly Asn Thr Leu Ile Lys  
225 230 235 240  
Ser Thr Tyr Val Leu Pro Asp Gly Val Thr His Thr Lys Gly Tyr Val  
245 250 255  
Lys Asp Pro Gln Ala Ala Lys Arg Phe Leu Ser Leu Ser Glu Lys Glu  
260 265 270  
Ser Val Val Val Met Asp Lys Val Gly Glu Arg Lys Lys Ala Asp Met  
275 280 285  
Asn Lys Asn Glu Ile Asp Leu Thr Asn Glu Arg Phe Leu Val Pro Glu  
290 295 300  
Thr Leu Phe Gln Pro Ala Asp Leu Gly Met Asn Gln Ala Gly Leu Ala  
305 310 315 320  
Glu Cys Ile Val Arg Ala Ile Asn Ser Cys His Ser Tyr Leu Gln Pro  
325 330 335  
Val Leu Tyr Gln Ser Ile Ile Leu Thr Gly Gly Ser Thr Leu Phe Pro  
340 345 350  
Gln Leu Lys Glu Arg Leu Glu Gly Glu Leu Arg Pro Leu Val Pro Asp  
355 360 365  
His Phe Asp Val Lys Ile Thr Thr Gln Glu Asp Pro Ile Leu Gly Val  
370 375 380  
Trp Arg Gly Gly Ser Leu Leu Ala Ser Ser Pro Asp Phe Glu Ser Met  
385 390 395 400  
Cys Val Thr Lys Ala Glu Tyr Glu Glu Leu Gly Ser Ala Arg Cys Arg  
405 410 415  
Arg Arg Phe Phe His  
420

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1566973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Asp Glu Thr Phe Leu Val Asp Asp Ala Lys Glu Lys Leu Cys Phe  
1 5 10 15  
Val Ser Leu Asp Leu Leu Arg Asp Leu Arg Leu Ala Arg Asn Gly Asn  
20 25 30  
Thr Leu Ile Lys Ser Thr Tyr Val Leu Pro Asp Gly Val Thr His Thr  
35 40 45  
Lys Gly Tyr Val Lys Asp Pro Gln Ala Ala Lys Arg Phe Leu Ser Leu  
50 55 60  
Ser Glu Lys Glu Ser Val Val Val Met Asp Lys Val Gly Glu Arg Lys  
65 70 75 80  
Lys Ala Asp Met Asn Lys Asn Glu Ile Asp Leu Thr Asn Glu Arg Phe  
85 90 95  
Leu Val Pro Glu Thr Leu Phe Gln Pro Ala Asp Leu Gly Met Asn Gln  
100 105 110  
Ala Gly Leu Ala Glu Cys Ile Val Arg Ala Ile Asn Ser Cys His Ser  
115 120 125  
Tyr Leu Gln Pro Val Leu Tyr Gln Ser Ile Ile Leu Thr Gly Gly Ser

SEQUENCE - 1566973

130 135 140  
Thr Leu Phe Pro Gln Leu Lys Glu Arg Leu Glu Gly Glu Leu Arg Pro  
145 150 155 160  
Leu Val Pro Asp His Phe Asp Val Lys Ile Thr Thr Gln Glu Asp Pro  
165 170 175  
Ile Leu Gly Val Trp Arg Gly Gly Ser Leu Leu Ala Ser Ser Pro Asp  
180 185 190  
Phe Glu Ser Met Cys Val Thr Lys Ala Glu Tyr Glu Glu Leu Gly Ser  
195 200 205  
Ala Arg Cys Arg Arg Arg Phe Phe His  
210 215

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

attctctagg cttttttata ttctgaaagt tttgattttt tgtatcttgt tttgtttctc 60  
aatcatcaat ttgtggtagt agctcactag caaacaatgg aggggaggtt gaataatatg 120  
tggaggttga ctgtgaatga gagcaaatc gttgaatctg cgttgcaatc tgagctcaga 180  
gtcgatggtc gtggccttta tgattaccgc aagcttacta ttaagtttgg caaggaatat 240  
ggcagctcac aagtccaact gggtcagact catgtaatgg cttttgtgac tgctcagcta 300  
gtacaacctt acaaagacag acctagtga ggtccttct ctatcttcac cgagttttct 360  
ccaatggctg atccatcgtt tgagccaggg catcctggtg aatctgctgt tgagcttggc 420  
cgtattatag accgtgctct acgagaaagc cgtgcagtag atacagagtc gctttgtgtt 480  
ctagccggaa agctggtttg gtctgttcgc attgatcttc acatttttga caatggaggg 540  
aacttggttg atgctgctaa tgttgctgcc ttagccgcac tcatgacttt caggagacct 600  
gattgcactg taggagggga caacagtcaa gacgtgatca tacatccacc cgaagaaagg 660  
Gaaccacttc ctttgataat acatcatctc ccaatagcct tcacgttttg attttttaat 720  
aaaggcagta tcttggtgat ggacccaact tacgttgaag aagctgttat gtgtgggaga 780  
atgactgtga cagtcaatgc caatggcgat atatgcgcaa tccaaaaacc aggagaagaa 840  
ggcgtgaacc agagtgtaat ctttcattgc ctgctgttgc cttcttcaag agcttctgca 900  
acaacaaaga taattagaga tgcagttgaa gcatacaacc gtgagaggag ctacagaag 960  
gtggagcggc atcatacttt ggctaagtct gaagtttttg gacctattgt agttgtgtag 1020  
gaagagacat aaataaaaca tttgctgtgg tgcgtgattg taaataaaga ttttagttgt 1080  
agaaatctta tcagcaacac taagtataa aaacgtcgat atgatcaaga catgttgaga 1140  
ctc

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Glu Gly Arg Leu Asn Asn Met Trp Arg Leu Thr Val Asn Glu Ser  
1 5 10 15  
Lys Phe Val Glu Ser Ala Leu Gln Ser Glu Leu Arg Val Asp Gly Arg  
20 25 30  
Gly Leu Tyr Asp Tyr Arg Lys Leu Thr Ile Lys Phe Gly Lys Glu Tyr  
35 40 45

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1566987

Trp Arg Leu Thr Val Asn Glu Ser Lys Phe V

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Arg | Leu | Thr | Val | Asn | Glu | Ser | Lys | Phe | Val | Glu | Ser | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ser | Glu | Leu | Arg | Val | Asp | Gly | Arg | Gly | Leu | Tyr | Asp | Tyr | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Ile | Lys | Phe | Gly | Lys | Glu | Tyr | Gly | Ser | Ser | Gln | Val | Gln | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gln | Thr | His | Val | Met | Ala | Phe | Val | Thr | Ala | Gln | Leu | Val | Gln | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Lys | Asp | Arg | Pro | Ser | Glu | Gly | Ser | Phe | Ser | Ile | Phe | Thr | Glu | Phe |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Pro | Met | Ala | Asp | Pro | Ser | Phe | Glu | Pro | Gly | His | Pro | Gly | Glu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Val | Glu | Leu | Gly | Arg | Ile | Ile | Asp | Arg | Ala | Leu | Arg | Glu | Ser | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Val | Asp | Thr | Glu | Ser | Leu | Cys | Val | Leu | Ala | Gly | Lys | Leu | Val | Trp |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Val | Thr | Ala | Gln | Leu | Val | Gln | Pro | Tyr | Lys | Asp | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Gly | Ser | Phe | Ser | Ile | Phe | Thr | Glu | Phe | Ser | Pro | Met | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Phe | Glu | Pro | Gly | His | Pro | Gly | Glu | Ser | Ala | Val | Glu | Leu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ile | Ile | Asp | Arg | Ala | Leu | Arg | Glu | Ser | Arg | Ala | Val | Asp | Thr | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Cys | Val | Leu | Ala | Gly | Lys | Leu | Val | Trp | Ser | Val | Arg | Ile | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | His | Ile | Leu | Asp | Asn | Gly | Gly | Asn | Leu | Val | Asp | Ala | Ala | Asn | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Leu | Ala | Ala | Leu | Met | Thr | Phe | Arg | Arg | Pro | Asp | Cys | Thr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Asp | Asn | Ser | Gln | Asp | Val | Ile | Ile | His | Pro | Pro | Glu | Glu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Pro | Leu | Pro | Leu | Ile | Ile | His | His | Leu | Pro | Ile | Ala | Phe | Thr | Phe |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Gly | Phe | Phe | Asn | Lys | Gly | Ser | Ile | Leu | Val | Met | Asp | Pro | Thr | Tyr | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Glu | Ala | Val | Met | Cys | Gly | Arg | Met | Thr | Val | Thr | Val | Asn | Ala | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Asp | Ile | Cys | Ala | Ile | Gln | Lys | Pro | Gly | Glu | Glu | Gly | Val | Asn | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Ile | Leu | His | Cys | Leu | Arg | Leu | Ala | Ser | Ser | Arg | Ala | Ser | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Thr Thr Lys Ile Ile Arg Asp Ala Val Glu Ala Tyr Asn Arg Glu Arg  
210 215 220  
Ser Ser Gln Lys Val Glu Arg His His Thr Leu Ala Lys Ser Glu Val  
225 230 235 240  
Leu Gly Pro Ile Val Val Val  
245

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

atttttctcc tacggtcgaa ctaaataccta gggcacaggt gaaatcgccg agtgacgtct 60  
agccaccgca ccgcctcctt ctccggttat ctgcgtacta atcagactat tccacagcta 120  
tgtcacaggt agacagcaga aattcatcag cagccaagcg tgctagaact gacggggggc 180  
gtagagaaga tgattggatc tgcccaagtt gtggcaatgt caacttttca ttcaggacaa 240  
cttgcaatat gcgtaattgc actcagccta gacctgcaga tcataatgga aagtctgctc 300  
ccaaacctat gcaacatcaa caaggtttct catcaccggt ggcatactta ggatctgggg 360  
gtccccctcc agtatatatg ggcgggtcac catatggatc tcctctcttt aatggatcgt 420  
ctatgcctcc ttatgacgtc ccattttctg ggggttcgcc ttaccatttt aactataata 480  
gccgaatgcc tgccggagct cattacagac cattacatat gtctggacca ccaccatacc 540  
atggcggatc tatgatggga agtgggtgga tgtatggaat gcctccacca atagacaggt 600  
atggccttgg tatggcaatg ggtcctgggt ctgccgtcgc catgatgcca agaccaaggt 660  
tttaccaga tgaaaaatca caaaagagag attcaactcg cgataatgat tggacatgtc 720  
cgaattgtgg taatgtaaac ttctcattca gaactgtatg taacatgagg aagtgcaca 780  
ctccaaagcc tggttctcag cagggtggaa gctcagataa aatatccaaa caaaatgcac 840  
cggaagggag ctggaagtgt gataactgtg gaaatataaa ctaccattc aggagcaaat 900  
gcaacaggca aaactgtgga gctgataagc ctggggatcg gtcgaatgga tctccgtccc 960  
gtgcaccaga agagaacgat caggtttgta agatgtatct atgtggtcac aactgtttgt 1020  
taataaaatg tttgcctctg aaactcgtaa atgtaacaac ctgtgtagat tttatgcctt 1080  
gtgaaagcag aggttatatg tttatgaaaa aattgactcc gaCtactgtt

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Ser Gln Val Asp Ser Arg Asn Ser Ser Ala Ala Lys Arg Ala Arg  
1 5 10 15  
Thr Asp Gly Gly Arg Arg Glu Asp Asp Trp Ile Cys Pro Ser Cys Gly  
20 25 30  
Asn Val Asn Phe Ser Phe Arg Thr Cys Asn Met Arg Asn Cys Thr  
35 40 45  
Gln Pro Arg Pro Ala Asp His Asn Gly Lys Ser Ala Pro Lys Pro Met  
50 55 60  
Gln His Gln Gln Gly Phe Ser Ser Pro Gly Ala Tyr Leu Gly Ser Gly  
65 70 75 80  
Gly Pro Pro Pro Val Tyr Met Gly Gly Ser Pro Tyr Gly Ser Pro Leu  
85 90 95

```

Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val Pro Phe Ser Gly Gly
 100 105 110
Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met Pro Ala Gly Ala His
 115 120 125
Tyr Arg Pro Leu His Met Ser Gly Pro Pro Pro Tyr His Gly Gly Ser
 130 135 140
Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro Pro Pro Ile Asp Arg
 145 150 155 160
Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser Ala Ala Ala Met Met
 165 170 175
Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser Gln Lys Arg Asp Ser
 180 185 190
Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys Gly Asn Val Asn Phe
 195 200 205
Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys Asn Thr Pro Lys Pro
 210 215 220
Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile Ser Lys Gln Asn Ala
 225 230 235 240
Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly Asn Ile Asn Tyr Pro
 245 250 255
Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly Ala Asp Lys Pro Gly
 260 265 270
Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro Glu Glu Asn Asp Gln
 275 280 285
Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys Leu Leu Ile Lys Cys
 290 295 300
Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys Val Asp Phe Met Pro
 305 310 315 320
Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys Leu Thr Pro Thr Thr
 325 330 335
Phe

```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1566991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

Met Arg Asn Cys Thr Gln Pro Arg Pro Ala Asp His Asn Gly Lys Ser
1 5 10 15
Ala Pro Lys Pro Met Gln His Gln Gln Gly Phe Ser Ser Pro Gly Ala
 20 25 30
Tyr Leu Gly Ser Gly Gly Pro Pro Pro Val Tyr Met Gly Gly Ser Pro
 35 40 45
Tyr Gly Ser Pro Leu Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val
 50 55 60
Pro Phe Ser Gly Gly Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met
 65 70 75 80
Pro Ala Gly Ala His Tyr Arg Pro Leu His Met Ser Gly Pro Pro Pro
 85 90 95
Tyr His Gly Gly Ser Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro
 100 105 110
Pro Pro Ile Asp Arg Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser
 115 120 125
Ala Ala Ala Met Met Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser

```

(2) INFORMATION FOR SEQ ID NO:451:

(A) LENGTH: 274 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1566992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | His | Gln | Gln | Gly | Phe | Ser | Ser | Pro | Gly | Ala | Tyr | Leu | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gly | Pro | Pro | Pro | Val | Tyr | Met | Gly | Gly | Ser | Pro | Tyr | Gly | Ser | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Asn | Gly | Ser | Ser | Met | Pro | Pro | Tyr | Asp | Val | Pro | Phe | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Pro | Tyr | His | Phe | Asn | Tyr | Asn | Ser | Arg | Met | Pro | Ala | Gly | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Tyr | Arg | Pro | Leu | His | Met | Ser | Gly | Pro | Pro | Pro | Tyr | His | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Met | Met | Gly | Ser | Gly | Gly | Met | Tyr | Gly | Met | Pro | Pro | Pro | Ile | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Tyr | Gly | Leu | Gly | Met | Ala | Met | Gly | Pro | Gly | Ser | Ala | Ala | Ala | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Pro | Arg | Pro | Arg | Phe | Tyr | Pro | Asp | Glu | Lys | Ser | Gln | Lys | Arg | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Thr | Arg | Asp | Asn | Asp | Trp | Thr | Cys | Pro | Asn | Cys | Gly | Asn | Val | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Phe | Arg | Thr | Val | Cys | Asn | Met | Arg | Lys | Cys | Asn | Thr | Pro | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Gly | Ser | Gln | Gln | Gly | Gly | Ser | Ser | Asp | Lys | Ile | Ser | Lys | Gln | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Pro | Glu | Gly | Ser | Trp | Lys | Cys | Asp | Asn | Cys | Gly | Asn | Ile | Asn | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Phe | Arg | Ser | Lys | Cys | Asn | Arg | Gln | Asn | Cys | Gly | Ala | Asp | Lys | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Asp | Arg | Ser | Asn | Gly | Ser | Pro | Ser | Arg | Ala | Pro | Glu | Glu | Asn | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Gln Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys Leu Leu Ile Lys  
225 230 235 240  
Cys Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys Val Asp Phe Met  
245 250 255  
Pro Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys Leu Thr Pro Thr  
260 265 270  
Thr Phe

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1717
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

aaaaaaggct tctctgtgtt gttctctgtg ttgttctctg tggtcattct tctttctttt 60  
cacttcttct tcttcttcgc tcttcttctc actgtcgggt tccatttggc gcgaaaagtt 120  
cttcactttt tccagctttt tttgttctc tgacagtttt ttttttgtt ggttacaaat 180  
aaagatgcc a gtaagtgtg cactagtttt gctgttgaca ttgagcagtg taattctgat 240  
taatgggaga agttacggcg tcggaacat atgcgatcgt ggtcggagaC cgagcgagag 300  
accacacagt gtcaaaatca ctgatttttg tgctgtggga gatgggaaaa cgttgaacac 360  
acttgcgttt caaaatgctg tcttttatct aaagtctttc gctgataaag gtggtgctca 420  
gctttatggt cctccgggac Ggtggctcac cggaagtttc aacctcacca gtcattctac 480  
tctctttctc gagaaagacg ccgtcatact tgcctcacag gatccatcgc attggcaagt 540  
cacggatgcc ttaccgtcat atgggcgggg tattgatcta ccagggaaga gatacatgag 600  
tttgataaac ggtgacatgc tacatgatgt agtagtaaca ggtgataacg gtaccataga 660  
tgggcaaggc cttgttttgt gggatcgggt taattctcat tcttttagagt acagtcgccc 720  
tcacctgtc gagtttgtct ctgccgaaaa tgtcattgta tcaaacttta cattcttgaa 780  
tgctccggct tatactatcc attcggttta ttgtcgcaat ttatacatte atagagtaac 840  
ggctaatact tgtccagaat ctcttatac catcgggtatt gtcccagatt cttctgaaaa 900  
tgtgtgtatc caagaatcta gtatcaacat ggggtatgat gccattttct ttaaaagtgg 960  
ttgggatgaa tacggtttat cgtatgcaag acctactgct aatgtccaga taagaaatgt 1020  
ttacctaga gcagcttctg gttcctccat ttccttttgt agtgaaatgt ctgggtggtat 1080  
atctgatgtt gaggtcagtg atgctcacat acacaactcg ttatccggga ttgcctttag 1140  
aacaacaaat ggaagatgtg gttatattaa ggagattgat attccaaca tccatattgt 1200  
taatgttggt actgcatttc tagccaacgg tagcttcggg actcatccgg attctggttt 1260  
cgatgaaaat gcttaccgc ttgtgagtca catcagggtta catgacattg ttggagaaaa 1320  
cataagcact gctggatatt tctttggaac gaaagagtct cctttcactt cgattttgtt 1380  
atcgaatata tctctgtcga ttaaaaactc ggcttctcct gctgattctt ggcaatgctc 1440  
atatgttgac gggctcttcg aattcgtagt cctgaaccg tgccttgagc tgaagagttt 1500  
tgatagttac tatggtagag ctgaggcctt atgaaaccaa acttcattag gaatgatgat 1560  
tcataattgt ttaagagaga gcaaatggtt ctgattcttt tcttttcccc aaaaataaac 1620  
cacagtgtgt agaattatta cctgttcctt gttggtgttg ttgtccctgt tatttgcagc 1680  
ttgtgagatt aatatatctt gtacaggttc atttctt

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

U.S. PAT. & TRADEMARK OFFICE

|       |     |     |     |       |     |     |     |     |        |     |     |     |     |        |     |
|-------|-----|-----|-----|-------|-----|-----|-----|-----|--------|-----|-----|-----|-----|--------|-----|
| Lys 1 | Lys | Ala | Ser | Leu 5 | Cys | Cys | Ser | Leu | Cys 10 | Cys | Ser | Leu | Trp | Ser 15 | Phe |
| Phe   | Phe | Leu | Phe | Thr   | Ser | Ser | Ser | Ser | Ser    | Leu | Phe | Phe | Ser | Leu    | Ser |
|       |     |     | 20  |       |     |     | 25  |     |        |     |     | 30  |     |        |     |
| Gly   | Ser | Ile | Trp | Arg   | Glu | Lys | Phe | Phe | Thr    | Phe | Ser | Ser | Phe | Phe    | Leu |
|       |     | 35  |     |       |     |     | 40  |     |        |     |     | 45  |     |        |     |
| Phe   | Ser | Asp | Ser | Phe   | Phe | Phe | Val | Trp | Leu    | Gln | Ile | Lys | Met | Pro    | Val |
|       | 50  |     |     |       |     | 55  |     |     |        |     | 60  |     |     |        |     |
| Ser   | Val | Ala | Leu | Val   | Leu | Leu | Leu | Thr | Leu    | Ser | Ser | Val | Ile | Leu    | Ile |
| 65    |     |     |     | 70    |     |     |     |     | 75     |     |     |     |     | 80     |     |
| Asn   | Gly | Arg | Ser | Tyr   | Gly | Val | Gly | Asn | Ile    | Cys | Asp | Arg | Gly | Arg    | Arg |
|       |     |     | 85  |       |     |     |     | 90  |        |     |     |     | 95  |        |     |
| Pro   | Ser | Glu | Arg | Pro   | His | Ser | Val | Lys | Ile    | Thr | Asp | Phe | Gly | Ala    | Val |
|       |     |     | 100 |       |     |     | 105 |     |        |     |     | 110 |     |        |     |
| Gly   | Asp | Gly | Lys | Thr   | Leu | Asn | Thr | Leu | Ala    | Phe | Gln | Asn | Ala | Val    | Phe |
|       |     | 115 |     |       |     |     | 120 |     |        |     |     | 125 |     |        |     |
| Tyr   | Leu | Lys | Ser | Phe   | Ala | Asp | Lys | Gly | Gly    | Ala | Gln | Leu | Tyr | Val    | Pro |
|       | 130 |     |     |       |     | 135 |     |     |        |     | 140 |     |     |        |     |
| Pro   | Gly | Arg | Trp | Leu   | Thr | Gly | Ser | Phe | Asn    | Leu | Thr | Ser | His | Leu    | Thr |
| 145   |     |     |     | 150   |     |     |     |     | 155    |     |     |     |     | 160    |     |
| Leu   | Phe | Leu | Glu | Lys   | Asp | Ala | Val | Ile | Leu    | Ala | Ser | Gln | Asp | Pro    | Ser |
|       |     |     | 165 |       |     |     |     | 170 |        |     |     |     | 175 |        |     |
| His   | Trp | Gln | Val | Thr   | Asp | Ala | Leu | Pro | Ser    | Tyr | Gly | Arg | Gly | Ile    | Asp |
|       |     |     | 180 |       |     |     |     | 185 |        |     |     |     | 190 |        |     |
| Leu   | Pro | Gly | Lys | Arg   | Tyr | Met | Ser | Leu | Ile    | Asn | Gly | Asp | Met | Leu    | His |
|       |     | 195 |     |       |     |     | 200 |     |        |     | 205 |     |     |        |     |
| Asp   | Val | Val | Val | Thr   | Gly | Asp | Asn | Gly | Thr    | Ile | Asp | Gly | Gln | Gly    | Leu |
|       | 210 |     |     |       |     | 215 |     |     |        |     | 220 |     |     |        |     |
| Val   | Trp | Trp | Asp | Arg   | Phe | Asn | Ser | His | Ser    | Leu | Glu | Tyr | Ser | Arg    | Pro |
| 225   |     |     |     | 230   |     |     |     |     |        | 235 |     |     |     |        | 240 |
| His   | Leu | Val | Glu | Phe   | Val | Ser | Ala | Glu | Asn    | Val | Ile | Val | Ser | Asn    | Leu |
|       |     |     | 245 |       |     |     |     | 250 |        |     |     |     |     | 255    |     |
| Thr   | Phe | Leu | Asn | Ala   | Pro | Ala | Tyr | Thr | Ile    | His | Ser | Val | Tyr | Cys    | Arg |
|       |     |     | 260 |       |     |     |     | 265 |        |     |     |     | 270 |        |     |
| Asn   | Leu | Tyr | Ile | His   | Arg | Val | Thr | Ala | Asn    | Thr | Cys | Pro | Glu | Ser    | Pro |
|       |     | 275 |     |       |     |     | 280 |     |        |     |     | 285 |     |        |     |
| Tyr   | Thr | Ile | Gly | Ile   | Val | Pro | Asp | Ser | Ser    | Glu | Asn | Val | Cys | Ile    | Gln |
|       | 290 |     |     |       |     | 295 |     |     |        |     | 300 |     |     |        |     |
| Glu   | Ser | Ser | Ile | Asn   | Met | Gly | Tyr | Asp | Ala    | Ile | Ser | Leu | Lys | Ser    | Gly |
| 305   |     |     |     | 310   |     |     |     |     |        | 315 |     |     |     |        | 320 |
| Trp   | Asp | Glu | Tyr | Gly   | Leu | Ser | Tyr | Ala | Arg    | Pro | Thr | Ala | Asn | Val    | Gln |
|       |     |     | 325 |       |     |     |     | 330 |        |     |     |     |     | 335    |     |
| Ile   | Arg | Asn | Val | Tyr   | Leu | Arg | Ala | Ala | Ser    | Gly | Ser | Ser | Ile | Ser    | Phe |
|       |     |     | 340 |       |     |     |     | 345 |        |     |     |     | 350 |        |     |
| Gly   | Ser | Glu | Met | Ser   | Gly | Gly | Ile | Ser | Asp    | Val | Glu | Val | Ser | Asp    | Ala |
|       |     |     |     |       |     |     |     |     |        |     |     |     |     |        |     |

(2) INFORMATION FOR SEQ ID NO:454:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1566995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Pro        | Val        | Ser        | Val<br>5   | Ala        | Leu        | Val        | Leu        | Leu<br>10  | Leu        | Thr        | Leu        | Ser        | Ser<br>15  | Val        |
| Ile        | Leu        | Ile        | Asn<br>20  | Gly        | Arg        | Ser        | Tyr        | Gly<br>25  | Val        | Gly        | Asn        | Ile        | Cys<br>30  | Asp        | Arg        |
| Gly        | Arg        | Arg<br>35  | Pro        | Ser        | Glu        | Arg        | Pro<br>40  | His        | Ser        | Val        | Lys        | Ile<br>45  | Thr        | Asp        | Phe        |
| Gly        | Ala<br>50  | Val        | Gly        | Asp        | Gly        | Lys<br>55  | Thr        | Leu        | Asn        | Thr        | Leu<br>60  | Ala        | Phe        | Gln        | Asn        |
| Ala<br>65  | Val        | Phe        | Tyr        | Leu        | Lys<br>70  | Ser        | Phe        | Ala        | Asp        | Lys<br>75  | Gly        | Gly        | Ala        | Gln        | Leu<br>80  |
| Tyr        | Val        | Pro        | Pro        | Gly<br>85  | Arg        | Trp        | Leu        | Thr        | Gly<br>90  | Ser        | Phe        | Asn        | Leu        | Thr<br>95  | Ser        |
| His        | Leu        | Thr        | Leu<br>100 | Phe        | Leu        | Glu        | Lys        | Asp<br>105 | Ala        | Val        | Ile        | Leu<br>110 | Ala        | Ser        | Gln        |
| Asp        | Pro        | Ser<br>115 | His        | Trp        | Gln        | Val        | Thr<br>120 | Asp        | Ala        | Leu        | Pro        | Ser<br>125 | Tyr        | Gly        | Arg        |
| Gly        | Ile<br>130 | Asp        | Leu        | Pro        | Gly        | Lys<br>135 | Arg        | Tyr        | Met        | Ser        | Leu<br>140 | Ile        | Asn        | Gly        | Asp        |
| Met<br>145 | Leu        | His        | Asp        | Val        | Val<br>150 | Val        | Thr        | Gly        | Asp        | Asn<br>155 | Gly        | Thr        | Ile        | Asp        | Gly<br>160 |
| Gln        | Gly        | Leu        | Val        | Trp<br>165 | Trp        | Asp        | Arg        | Phe        | Asn<br>170 | Ser        | His        | Ser        | Leu        | Glu<br>175 | Tyr        |
| Ser        | Arg        | Pro        | His<br>180 | Leu        | Val        | Glu        | Phe        | Val<br>185 | Ser        | Ala        | Glu        | Asn<br>190 | Val        | Ile        | Val        |
| Ser        | Asn<br>195 | Leu        | Thr        | Phe        | Leu        | Asn        | Ala<br>200 | Pro        | Ala        | Tyr        | Thr        | Ile<br>205 | His        | Ser        | Val        |
| Tyr        | Cys<br>210 | Arg        | Asn        | Leu        | Tyr        | Ile<br>215 | His        | Arg        | Val        | Thr        | Ala<br>220 | Asn        | Thr        | Cys        | Pro        |
| Glu<br>225 | Ser        | Pro        | Tyr        | Thr        | Ile<br>230 | Gly        | Ile        | Val        | Pro        | Asp<br>235 | Ser        | Ser        | Glu        | Asn        | Val<br>240 |
| Cys        | Ile        | Gln        | Glu        | Ser<br>245 | Ser        | Ile        | Asn        | Met        | Gly<br>250 | Tyr        | Asp        | Ala        | Ile        | Ser<br>255 | Leu        |
| Lys        | Ser        | Gly        | Trp<br>260 | Asp        | Glu        | Tyr        | Gly        | Leu<br>265 | Ser        | Tyr        | Ala        | Arg        | Pro<br>270 | Thr        | Ala        |
| Asn        | Val<br>275 | Gln        | Ile        | Arg        | Asn        | Val        | Tyr<br>280 | Leu        | Arg        | Ala        | Ala        | Ser<br>285 | Gly        | Ser        | Ser        |
| Ile        | Ser<br>290 | Phe        | Gly        | Ser        | Glu        | Met<br>295 | Ser        | Gly        | Gly        | Ile        | Ser<br>300 | Asp        | Val        | Glu        | Val        |
| Ser<br>305 | Asp        | Ala        | His        | Ile        | His<br>310 | Asn        | Ser        | Leu        | Ser        | Gly<br>315 | Ile        | Ala        | Phe        | Arg        | Thr<br>320 |
| Thr        | Asn        | Gly        | Arg        | Cys<br>325 | Gly        | Tyr        | Ile        | Lys        | Glu<br>330 | Ile        | Asp        | Ile        | Ser        | Asn<br>335 | Ile        |
| His        | Met        | Val        | Asn<br>340 | Val        | Gly        | Thr        | Ala        | Phe<br>345 | Leu        | Ala        | Asn        | Gly        | Ser<br>350 | Phe        | Gly        |
| Thr        | His<br>355 | Pro        | Asp        | Ser        | Gly        | Phe        | Asp<br>360 | Glu        | Asn        | Ala        | Tyr        | Pro<br>365 | Leu        | Val        | Ser        |

His Ile Arg Leu His Asp Ile Val Gly Glu Asn Ile Ser Thr Ala Gly  
370 375 380  
Tyr Phe Phe Gly Thr Lys Glu Ser Pro Phe Thr Ser Ile Leu Leu Ser  
385 390 395 400  
Asn Ile Ser Leu Ser Ile Lys Asn Ser Ala Ser Pro Ala Asp Ser Trp  
405 410 415  
Gln Cys Ser Tyr Val Asp Gly Ser Ser Glu Phe Val Val Pro Glu Pro  
420 425 430  
Cys Leu Glu Leu Lys Ser Phe Asp Ser Tyr Tyr Gly Arg Ala Glu Ala  
435 440 445  
Leu

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1566996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met Ser Leu Ile Asn Gly Asp Met Leu His Asp Val Val Val Thr Gly  
1 5 10 15  
Asp Asn Gly Thr Ile Asp Gly Gln Gly Leu Val Trp Trp Asp Arg Phe  
20 25 30  
Asn Ser His Ser Leu Glu Tyr Ser Arg Pro His Leu Val Glu Phe Val  
35 40 45  
Ser Ala Glu Asn Val Ile Val Ser Asn Leu Thr Phe Leu Asn Ala Pro  
50 55 60  
Ala Tyr Thr Ile His Ser Val Tyr Cys Arg Asn Leu Tyr Ile His Arg  
65 70 75 80  
Val Thr Ala Asn Thr Cys Pro Glu Ser Pro Tyr Thr Ile Gly Ile Val  
85 90 95  
Pro Asp Ser Ser Glu Asn Val Cys Ile Gln Glu Ser Ser Ile Asn Met  
100 105 110  
Gly Tyr Asp Ala Ile Ser Leu Lys Ser Gly Trp Asp Glu Tyr Gly Leu  
115 120 125  
Ser Tyr Ala Arg Pro Thr Ala Asn Val Gln Ile Arg Asn Val Tyr Leu  
130 135 140  
Arg Ala Ala Ser Gly Ser Ser Ile Ser Phe Gly Ser Glu Met Ser Gly  
145 150 155 160  
Gly Ile Ser Asp Val Glu Val Ser Asp Ala His Ile His Asn Ser Leu  
165 170 175  
Ser Gly Ile Ala Phe Arg Thr Thr Asn Gly Arg Cys Gly Tyr Ile Lys  
180 185 190  
Glu Ile Asp Ile Ser Asn Ile His Met Val Asn Val Gly Thr Ala Phe  
195 200 205  
Leu Ala Asn Gly Ser Phe Gly Thr His Pro Asp Ser Gly Phe Asp Glu  
210 215 220  
Asn Ala Tyr Pro Leu Val Ser His Ile Arg Leu His Asp Ile Val Gly  
225 230 235 240  
Glu Asn Ile Ser Thr Ala Gly Tyr Phe Phe Gly Thr Lys Glu Ser Pro  
245 250 255  
Phe Thr Ser Ile Leu Leu Ser Asn Ile Ser Leu Ser Ile Lys Asn Ser  
260 265 270  
Ala Ser Pro Ala Asp Ser Trp Gln Cys Ser Tyr Val Asp Gly Ser Ser  
275 280 285  
Glu Phe Val Val Pro Glu Pro Cys Leu Glu Leu Lys Ser Phe Asp Ser



290 295 300  
Tyr Tyr Gly Arg Ala Glu Ala Leu  
305 310

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| cttttcgcgt | ggtcgaccaa | acctaaaacc | cccaaaaaga | gaaaaatcaa | agaccattcg  | 60  |
| ctatttcgct | cgctactcag | ttgcagaaga | agatgccgac | actcacaaag | ctttattcca  | 120 |
| tggagaagc  | cgcaactcac | aacaagcaag | atgactgctg | ggtcgtcatc | gacggcaagg  | 180 |
| tctatgatgt | atcctcttat | atggatgagc | atcctggagg | agatgatgtg | cttcttgctg  | 240 |
| tcgcaggcaa | agatgcaacg | gatgattttg | aagacgcagg | gcacagcaaa | gatgctaggg  | 300 |
| aacttatgga | gaagtatttt | attggcgagc | tagatgaatc | ttctttaccg | gaaataacctg | 360 |
| agcttaagat | ctacaagaag | gaccagccac | aagactctgt | tcagaagctt | tttgacttga  | 420 |
| caaagcagta | ttgggttggt | cctgtctcca | ttatcaccat | ctctgtagcg | gttagtgtct  | 480 |
| tggtctctcg | caagacttaa | taagtagtag | tctctttctt | accttgatat | gctctgggat  | 540 |
| attgaattac | ttggggaatc | aactttacac | ccccattata | gattttttga | ataacagata  | 600 |
| tgatagagag | ataattgtta | tttttcattt | ttatcagatt | ttgagttgag | atcatgtttc  | 660 |
| aatacactta | ttactcgata | tgattatatc | atgattaatg | gatggtttgg | tttgctggc   |     |

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Ala | Trp | Ser | Thr | Lys | Pro | Lys | Thr | Pro | Lys | Lys | Arg | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Asp | His | Ser | Leu | Phe | Arg | Ser | Leu | Leu | Ser | Cys | Arg | Arg | Arg | Cys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | His | Ser | Gln | Ser | Phe | Ile | Pro | Trp | Lys | Lys | Pro | Gln | Leu | Thr | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Met | Thr | Ala | Gly | Ser | Ser | Ser | Thr | Ala | Arg | Ser | Met | Met | Tyr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Ile | Trp | Met | Ser | Ile | Leu | Glu | Glu | Met | Met | Cys | Phe | Leu | Leu |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gln | Ala | Lys | Met | Gln | Arg | Met | Ile | Leu | Lys | Thr | Gln | Gly | Thr | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Met | Leu | Gly | Asn | Leu | Trp | Arg | Ser | Ile | Leu | Leu | Ala | Ser |     |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

(2) INFORMATION FOR SEQ ID NO:459:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

(2) INFORMATION FOR SEQ ID NO:460:

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| acgacggaga | gaaaacgtct | tccaaagacg | aattgaggcg | gtggaagaag | aaaaaaaaaa | 60   |
| atcaaaatcc | aatttgatct | tcaaagtagt | gaagaaagaa | gagaagcaat | cgaaattctc | 120  |
| tgacgatgtt | gttacaaccc | caaagatcct | cttatcgatt | atcgtaattc | gtagaaaacg | 180  |
| aagcagagag | aaaatgggag | gcgaagatga | taaagataag | aaatggaatc | ctccaccacc | 240  |
| gcagcagaag | ccggactcaa | ggccttggga | agtcctcgcg | gcttttgtaa | tctgcgcaac | 300  |
| cgctactact | ttcgccgttc | atcagctgcg | aagaaatfff | gattgggtct | ataccagct  | 360  |
| aactagaaca | ccgtcggcgg | gaagaggaac | tttccgaaca | tcttttcagg | aggaagcatg | 420  |
| gagaaggtag | aacaaacgga | tgcaagagga | gtatgaggat | gagttggaga | gagtggcacg | 480  |
| tattaggcgt | atgcaaagcg | ttttcaacag | agagaggaat | aaatttagaa | ggggctacga | 540  |
| gaactggacg | gaaaatgatc | ctgGtgcaca | gcaataccat | cagcagtttc | agcgacatga | 600  |
| ttggtactgg | aaaactgagt | cttgcakag  | aaaccaaagg | accaatcacc | aggagccttc | 660  |
| agaccagaga | agagtatatc | cactatcaca | ccattactct | gttttagggc | tcagcaggtc | 720  |
| ccgagcaact | ccatacacag | aagctgagat | taagaaagca | ttcagggaaa | aggctttgga | 780  |
| attccatcca | gaccaaatac | aggataacaa | aattgtagct | gaagcaaaat | tcaaagaggt | 840  |
| gttactttca | tatgaagcta | taaaacagga | aataaaagag | aagtgatttt | ttttggtaag | 900  |
| cgagatcaat | ctcttttcca | tgcgctctaa | agaaattgga | atattgtcta | caatatcgat | 960  |
| cacaggtttt | tttgggtgtc | ttcccatttt | ataggtttat | tttaatagtc | ttgtggtttg | 1020 |
| ctttttttac | tcagttaagg | ttctttgttg | taatatgtaa | taaaaccaat | ccacagctta | 1080 |
| aatatgttga | agaggagaat | ttgggacaga | tggtccattg | attc       |            |      |

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Arg | Arg | Glu | Asn | Val | Phe | Gln | Arg | Arg | Ile | Glu | Ala | Val | Glu | Glu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Glu | Lys | Lys | Lys | Ser | Lys | Ser | Asn | Leu | Ile | Phe | Lys | Val | Val | Lys | Lys |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Glu | Glu | Lys | Gln | Ser | Lys | Phe | Ser | Asp | Asp | Val | Val | Thr | Thr | Pro | Lys |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Ile | Leu | Leu | Ser | Ile | Ile | Val | Ile | Arg | Arg | Lys | Arg | Ser | Arg | Glu | Lys |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Met | Gly | Gly | Glu | Asp | Asp | Lys | Asp | Lys | Lys | Trp | Asn | Pro | Pro | Pro | Pro |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |  |
| Gln | Gln | Lys | Pro | Asp | Ser | Arg | Pro | Trp | Glu | Val | Leu | Ala | Ala | Phe | Val |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ile | Cys | Ala | Thr | Ala | Thr | Thr | Phe | Ala | Val | His | Gln | Leu | Arg | Arg | Asn |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Asp | Trp | Val | Tyr | Thr | Gln | Leu | Thr | Arg | Thr | Pro | Ser | Ala | Gly | Arg |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Gly | Thr | Phe | Arg | Thr | Ser | Phe | Gln | Glu | Glu | Ala | Trp | Arg | Arg | Tyr | Asn |  |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |  |
| Lys | Arg | Met | Gln | Glu | Glu | Tyr | Glu | Asp | Glu | Leu | Glu | Arg | Val | Ala | Arg |  |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     | 160 |  |
| Ile | Arg | Arg | Met | Gln | Ser | Val | Phe | Asn | Arg | Glu | Arg | Asn | Lys | Phe | Arg |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Arg | Gly | Tyr | Glu | Asn | Trp | Thr | Glu | Asn | Asp | Pro | Gly | Ala | Gln | Gln | Tyr |  |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| His | Gln | Gln | Phe | Gln | Arg | His | Asp | Trp | Tyr | Trp | Lys | Thr | Glu | Ser | Ser |  |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |  |
| Xaa | Arg | Asn | Gln | Arg | Thr | Asn | His | Gln | Glu | Pro | Ser | Asp | Gln | Arg | Arg |  |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |  |
| Val | Tyr | Pro | Leu | Ser | His | His | Tyr | Ser | Val | Leu | Gly | Leu | Ser | Arg | Ser |  |

(2) INFORMATION FOR SEQ ID NO:462:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1567017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

(2) INFORMATION FOR SEQ ID NO:463:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1567018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met Gln Glu Glu Tyr Glu Asp Glu Leu Glu Arg Val Ala Arg Ile Arg  
1 5 10 15  
Arg Met Gln Ser Val Phe Asn Arg Glu Arg Asn Lys Phe Arg Arg Gly  
20 25 30  
Tyr Glu Asn Trp Thr Glu Asn Asp Pro Gly Ala Gln Gln Tyr His Gln  
35 40 45  
Gln Phe Gln Arg His Asp Trp Tyr Trp Lys Thr Glu Ser Ser Xaa Arg  
50 55 60  
Asn Gln Arg Thr Asn His Gln Glu Pro Ser Asp Gln Arg Arg Val Tyr  
65 70 75 80  
Pro Leu Ser His His Tyr Ser Val Leu Gly Leu Ser Arg Ser Arg Ala  
85 90 95  
Thr Pro Tyr Thr Glu Ala Glu Ile Lys Lys Ala Phe Arg Glu Lys Ala  
100 105 110  
Leu Glu Phe His Pro Asp Gln Asn Gln Asp Asn Lys Ile Val Ala Glu  
115 120 125  
Ala Lys Phe Lys Glu Val Leu Leu Ser Tyr Glu Ala Ile Lys Gln Glu  
130 135 140  
Ile Lys Glu Lys  
145

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

aaaaaaccaa tccttccttt gcttataaac cccaatcttc ttcgagagag agagagtga 60  
agagaagaag acgacaatgg gacacgccac gagtctctct cacttcctca tcctctcttc 120  
ctccaggttc tctcgtctcg ggtctctcac tagactactc tccaaaccca cctctctctc 180  
cggtctttaa tcttccattt cggtcaccgg acaagggttc cgatgctgtt gctccgccgc 240  
cacagatgac acttctcctt ctgtaaagaa acgtgtggtc tctggtgtcc agcctacagg 300  
ttcaattcac ttaggcaact atctcgtgtc tatcaaaaac tgggtcgctt ttcaggatac 360  
atatgaaaca ctctttatca tcgtagacca tcacgcgata acacttccat atgatacacg 420  
tcaactagga aaggcaacaa cggataccgc agcactttat ctagcatgtg aaaatgattc 480  
agttcaaaga gaaatcacgc aaggaggggg ttgagaatgc tagtgctggg ttgtttactt 540  
atcCtgatct gatgactgct gatatcctct tgtatcagtc tgattttgtc cctgttggtg 600  
aagaccaTga agcagcacat agaacttgcc cgtgaaattg cacagcgtgt gaatcattta 660  
tatggtggaa agaagtggaa gaagcttgga gggatgaaa ttttgtttgt gcatttagta 720  
tgtagtat accagtcata caagtcttta tgatctataa ttttcattgt tcttattggt 780  
ttaacttccc cttcatttgt attccctcat ccgtataaca ttgtcaattt tcattttcag 840  
ccgcggtggg tcgctcttta agataccaga accactcata ccacaagctg gagctcgtgt 900  
tatgtctctt actgatggtc tttccaagat gtccaagtct gcccttctg atcagtcgcc 960  
gattaatctc cttgactcaa aagatttgat agtggaacag ataaaacggg gcaagacaga 1020  
ctcatttgct ggccttgaat ttgacaatgc tgagagacct gaatgcaaca atctcctctc 1080  
aatatatcag attgtttcag gcaagacaaa agaggaagtg gtggaggaat gcaaagatat 1140  
gagctggggg acatttaagc ctctccttgc agatgctttg atcgatcatt tgagtccaat 1200  
ccaggtccgt tatcaggaga taatagcgga accagagtat ttggacaaaa tattgtcaga 1260  
aggtgcggat agagccgagg agttgggagc tgtcacaaat cgcaatatgt atcaagctat 1320  
gggatactat cagaggagga gatactgaga tagtagtgcc tattgatatt tgcggccggc 1380  
atTTTTgaag ttacaagaaa aaagtagaga gttacacttt gcgaaacatt tattaattct 1440  
tgagttatta ttgattataa tcttttgcaa taaccgcgac ctctcaaagt ttatcactac 1500  
gtaactgaga tagtgccc

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 145 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..145  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met Gly His Ala Thr Ser Leu Ser His Phe Leu Ile Leu Ser Ser Ser  
1                    5                    10                    15  
Arg Phe Ser Arg Leu Gly Ser Leu Thr Arg Leu Leu Ser Lys Pro Thr  
                    20                    25                    30  
Ser Leu Ser Gly Ser Leu Ser Ser Ile Ser Val Thr Gly Gln Gly Phe  
                    35                    40                    45  
Arg Cys Cys Cys Ser Ala Ala Thr Asp Asp Thr Ser Pro Ser Val Lys  
50                    55                    60  
Lys Arg Val Val Ser Gly Val Gln Pro Thr Gly Ser Ile His Leu Gly  
65                    70                    75                    80  
Asn Tyr Leu Gly Ala Ile Lys Asn Trp Val Ala Phe Gln Asp Thr Tyr  
                    85                    90                    95  
Glu Thr Leu Phe Ile Ile Val Asp His His Ala Ile Thr Leu Pro Tyr  
                    100                    105                    110  
Asp Thr Arg Gln Leu Gly Lys Ala Thr Thr Asp Thr Ala Ala Leu Tyr  
                    115                    120                    125  
Leu Ala Cys Glu Asn Asp Ser Val Gln Arg Glu Ile Thr Gln Gly Gly  
130                    135                    140  
Gly  
145

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 148 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..148  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Ser Leu Thr Asp Gly Leu Ser Lys Met Ser Lys Ser Ala Pro Ser  
1                    5                    10                    15  
Asp Gln Ser Arg Ile Asn Leu Leu Asp Ser Lys Asp Leu Ile Val Asp  
                    20                    25                    30  
Lys Ile Lys Arg Cys Lys Thr Asp Ser Phe Ala Gly Leu Glu Phe Asp  
                    35                    40                    45  
Asn Ala Glu Arg Pro Glu Cys Asn Asn Leu Leu Ser Ile Tyr Gln Ile  
50                    55                    60  
Val Ser Gly Lys Thr Lys Glu Glu Val Val Glu Cys Lys Asp Met  
65                    70                    75                    80  
Ser Trp Gly Thr Phe Lys Pro Leu Leu Ala Asp Ala Leu Ile Asp His  
                    85                    90                    95  
Leu Ser Pro Ile Gln Val Arg Tyr Gln Glu Ile Ile Ala Glu Pro Glu  
                    100                    105                    110  
Tyr Leu Asp Lys Ile Leu Ser Glu Gly Ala Asp Arg Ala Glu Glu Leu  
                    115                    120                    125  
Gly Ala Val Thr Met Arg Asn Met Tyr Gln Ala Met Gly Tyr Tyr Gln  
130                    135                    140

Arg Arg Arg Tyr  
145

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Ser | Ala | Pro | Ser | Asp | Gln | Ser | Arg | Ile | Asn | Leu | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Lys | Asp | Leu | Ile | Val | Asp | Lys | Ile | Lys | Arg | Cys | Lys | Thr | Asp | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ala | Gly | Leu | Glu | Phe | Asp | Asn | Ala | Glu | Arg | Pro | Glu | Cys | Asn | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Ser | Ile | Tyr | Gln | Ile | Val | Ser | Gly | Lys | Thr | Lys | Glu | Glu | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Glu | Glu | Cys | Lys | Asp | Met | Ser | Trp | Gly | Thr | Phe | Lys | Pro | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Asp | Ala | Leu | Ile | Asp | His | Leu | Ser | Pro | Ile | Gln | Val | Arg | Tyr | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ile | Ile | Ala | Glu | Pro | Glu | Tyr | Leu | Asp | Lys | Ile | Leu | Ser | Glu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Asp | Arg | Ala | Glu | Glu | Leu | Gly | Ala | Val | Thr | Met | Arg | Asn | Met | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ala | Met | Gly | Tyr | Tyr | Gln | Arg | Arg | Arg | Tyr |     |     |     |     |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| agaaatctaa | tgggattggt | gaggaagcta | cagaggaaga | gttgatggat | gcaacagctc | 60  |
| ttgctgattc | tactggatat | tttatatgtc | cacatactgg | tggtgcattg | acggcgttga | 120 |
| tgaagctgag | aaagtcagga | gttattggag | cgaatgatcg | gactgtggtg | gtgagtacag | 180 |
| ctcatggatt | gaagtttaca | cagagtaaga | ttgattatca | ttctaagaac | ataaaggaga | 240 |
| tggctttag  | attggcgaat | ccaccagtga | aggttaaggc | aaagtttggt | tcagttatgg | 300 |
| atgttctcaa | ggagtatttg | aagagcaatg | ataaataagc | tttgtgtggt | tgtttctcta | 360 |
| aagctcttca | cgtcctatga | tgatattggt | ggctttgtta | ttagaggaag | taatgaaatt | 420 |
| tcgtttcttt | ggacttggtg | aataaaacga | ctggGttggt | tccgt      |            |     |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1567083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Lys Ser Asn Gly Ile Val Glu Glu Ala Thr Glu Glu Glu Leu Met Asp  
1 5 10 15  
Ala Thr Ala Leu Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His Thr  
20 25 30  
Gly Val Ala Leu Thr Ala Leu Met Lys Leu Arg Lys Ser Gly Val Ile  
35 40 45  
Gly Ala Asn Asp Arg Thr Val Val Val Ser Thr Ala His Gly Leu Lys  
50 55 60  
Phe Thr Gln Ser Lys Ile Asp Tyr His Ser Lys Asn Ile Lys Glu Met  
65 70 75 80  
Ala Cys Arg Leu Ala Asn Pro Pro Val Lys Val Lys Ala Lys Phe Gly  
85 90 95  
Ser Val Met Asp Val Leu Lys Glu Tyr Leu Lys Ser Asn Asp Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1567084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Met Asp Ala Thr Ala Leu Ala Asp Ser Thr Gly Met Phe Ile Cys Pro  
1 5 10 15  
His Thr Gly Val Ala Leu Thr Ala Leu Met Lys Leu Arg Lys Ser Gly  
20 25 30  
Val Ile Gly Ala Asn Asp Arg Thr Val Val Val Ser Thr Ala His Gly  
35 40 45  
Leu Lys Phe Thr Gln Ser Lys Ile Asp Tyr His Ser Lys Asn Ile Lys  
50 55 60  
Glu Met Ala Cys Arg Leu Ala Asn Pro Pro Val Lys Val Lys Ala Lys  
65 70 75 80  
Phe Gly Ser Val Met Asp Val Leu Lys Glu Tyr Leu Lys Ser Asn Asp  
85 90 95  
Lys

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1567085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Met Phe Ile Cys Pro His Thr Gly Val Ala Leu Thr Ala Leu Met Lys  
1 5 10 15  
Leu Arg Lys Ser Gly Val Ile Gly Ala Asn Asp Arg Thr Val Val Val  
20 25 30  
Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys Ile Asp Tyr His  
35 40 45



Ser Lys Asn Ile Lys Glu Met Ala Cys Arg Leu Ala Asn Pro Pro Val  
50 55 60  
Lys Val Lys Ala Lys Phe Gly Ser Val Met Asp Val Leu Lys Glu Tyr  
65 70 75 80  
Leu Lys Ser Asn Asp Lys  
85

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1216
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

ccgtagGaaa agaaaaaggg cggtgatga agaagtgc aacagtctgc acataaggcc 60  
ctacaccttt agttactcag aactcagaac tgcaactcaa gattttgatc cttccaacaa 120  
gcttggggag ggaggatttg gacctgtttt taagggaaaa ctgaacgacg gaagagagat 180  
agccgtgaag caattgtcag ttgcatccag gcaaggaaa ggtcaatttg ttgcggagat 240  
tgcaactata tcacctgttc agcatcgcaa ccttgtaaaa ttgtatggat gctgcattga 300  
gggaaatcag cgcattgctt tatatgaata cctctcaaac aagagtctag atcaagctct 360  
attcgaggaa aagagtttgc agcttggttg gtcacagcgt ttcgagatat gcttgggagt 420  
agcaaaaggt ttagcatata tgcattgagg gtcaaatccc cgtatagtgc atagggatgt 480  
gaaggcaagc aatattcttc tggactcgga tctgggtccc aaactctcag attttgggtt 540  
ggccaaacta tatgatgata agaagaccca cataagtacc cgagttgcag ggacgatagg 600  
atatctgtca ccagagtagc tgatgcttgg acatcttacg gagaagacgg atgtgtttgc 660  
ctttggtata gtggccttgg aaattgtcag cggaaggcct aactcctctc cagaattaga 720  
tgatgacaaa caataccttc tcgaatgggc atggagccta caccaagagc agcgtgatat 780  
ggaagtagta gatccggatc tgacagaatt tgacaaggaa gaagtgaac gtgtaatagg 840  
agtagcgttc ttgtgcacac aaacagatca tgcaatacga ccaactatgt cccgagtggg 900  
aggtatgttg accggtgatg tggagataac ggaagccaat gccaaagccag ggtacgtctc 960  
tgagagaaca tttgagaatg caatgagctt catgagtggg tcaacgagct cgagctggat 1020  
attgcctgaa actccaaaag attcttccaa gtcccaagtt gaagaacatg gacgacgaca 1080  
ttgaaacttg aaaacttgtg gtttttctat tttttgttct tacataaaaa aaaagaagtc 1140  
aatatagaaa tcgttgttgg taaataacac atatacatat tcgtttgacc aaaattggat 1200  
ttgactgttt ctctctg

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Arg Arg Lys Arg Lys Arg Ala Ala Asp Glu Glu Val Leu Asn Ser Leu  
1 5 10 15  
His Ile Arg Pro Tyr Thr Phe Ser Tyr Ser Glu Leu Arg Thr Ala Thr  
20 25 30  
Gln Asp Phe Asp Pro Ser Asn Lys Leu Gly Glu Gly Gly Phe Gly Pro  
35 40 45  
Val Phe Lys Gly Lys Leu Asn Asp Gly Arg Glu Ile Ala Val Lys Gln  
50 55 60  
Leu Ser Val Ala Ser Arg Gln Gly Lys Gly Gln Phe Val Ala Glu Ile  
65 70 75 80

Ala Thr Ile Ser Pro Val Gln His Arg Asn Leu Val Lys Leu Tyr Gly  
85 90 95  
Cys Cys Ile Glu Gly Asn Gln Arg Met Leu Val Tyr Glu Tyr Leu Ser  
100 105 110  
Asn Lys Ser Leu Asp Gln Ala Leu Phe Glu Glu Lys Ser Leu Gln Leu  
115 120 125  
Gly Trp Ser Gln Arg Phe Glu Ile Cys Leu Gly Val Ala Lys Gly Leu  
130 135 140  
Ala Tyr Met His Glu Glu Ser Asn Pro Arg Ile Val His Arg Asp Val  
145 150 155 160  
Lys Ala Ser Asn Ile Leu Leu Asp Ser Asp Leu Val Pro Lys Leu Ser  
165 170 175  
Asp Phe Gly Leu Ala Lys Leu Tyr Asp Asp Lys Lys Thr His Ile Ser  
180 185 190  
Thr Arg Val Ala Gly Thr Ile Gly Tyr Leu Ser Pro Glu Tyr Val Met  
195 200 205  
Leu Gly His Leu Thr Glu Lys Thr Asp Val Phe Ala Phe Gly Ile Val  
210 215 220  
Ala Leu Glu Ile Val Ser Gly Arg Pro Asn Ser Ser Pro Glu Leu Asp  
225 230 235 240  
Asp Asp Lys Gln Tyr Leu Leu Glu Trp Ala Trp Ser Leu His Gln Glu  
245 250 255  
Gln Arg Asp Met Glu Val Val Asp Pro Asp Leu Thr Glu Phe Asp Lys  
260 265 270  
Glu Glu Val Lys Arg Val Ile Gly Val Ala Phe Leu Cys Thr Gln Thr  
275 280 285  
Asp His Ala Ile Arg Pro Thr Met Ser Arg Val Val Gly Met Leu Thr  
290 295 300  
Gly Asp Val Glu Ile Thr Glu Ala Asn Ala Lys Pro Gly Tyr Val Ser  
305 310 315 320  
Glu Arg Thr Phe Glu Asn Ala Met Ser Phe Met Ser Gly Ser Thr Ser  
325 330 335  
Ser Ser Trp Ile Leu Pro Glu Thr Pro Lys Asp Ser Ser Lys Ser Gln  
340 345 350  
Val Glu Glu His Gly Arg Arg His  
355 360

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..256

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Leu Val Tyr Glu Tyr Leu Ser Asn Lys Ser Leu Asp Gln Ala Leu  
1 5 10 15  
Phe Glu Glu Lys Ser Leu Gln Leu Gly Trp Ser Gln Arg Phe Glu Ile  
20 25 30  
Cys Leu Gly Val Ala Lys Gly Leu Ala Tyr Met His Glu Glu Ser Asn  
35 40 45  
Pro Arg Ile Val His Arg Asp Val Lys Ala Ser Asn Ile Leu Leu Asp  
50 55 60  
Ser Asp Leu Val Pro Lys Leu Ser Asp Phe Gly Leu Ala Lys Leu Tyr  
65 70 75 80  
Asp Asp Lys Lys Thr His Ile Ser Thr Arg Val Ala Gly Thr Ile Gly  
85 90 95  
Tyr Leu Ser Pro Glu Tyr Val Met Leu Gly His Leu Thr Glu Lys Thr

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Asp Val Phe Phe Gly Ile Val Ala Leu Glu Ile Val Ser Gly Arg     |     |     |
| 115                                                             | 120 | 125 |
| Pro Asn Ser Ser Pro Glu Leu Asp Asp Asp Lys Gln Tyr Leu Leu Glu |     |     |
| 130                                                             | 135 | 140 |
| Trp Ala Trp Ser Leu His Gln Glu Gln Arg Asp Met Glu Val Val Asp |     |     |
| 145                                                             | 150 | 155 |
| Pro Asp Leu Thr Glu Phe Asp Lys Glu Glu Val Lys Arg Val Ile Gly |     |     |
| 165                                                             | 170 | 175 |
| Val Ala Phe Leu Cys Thr Gln Thr Asp His Ala Ile Arg Pro Thr Met |     |     |
| 180                                                             | 185 | 190 |
| Ser Arg Val Val Gly Met Leu Thr Gly Asp Val Glu Ile Thr Glu Ala |     |     |
| 195                                                             | 200 | 205 |
| Asn Ala Lys Pro Gly Tyr Val Ser Glu Arg Thr Phe Glu Asn Ala Met |     |     |
| 210                                                             | 215 | 220 |
| Ser Phe Met Ser Gly Ser Thr Ser Ser Ser Trp Ile Leu Pro Glu Thr |     |     |
| 225                                                             | 230 | 235 |
| Pro Lys Asp Ser Ser Lys Ser Gln Val Glu Glu His Gly Arg Arg His |     |     |
| 245                                                             | 250 | 255 |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1567091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met His Glu Glu Ser Asn Pro Arg Ile Val His Arg Asp Val Lys Ala |     |
| 1                                                               | 15  |
| Ser Asn Ile Leu Leu Asp Ser Asp Leu Val Pro Lys Leu Ser Asp Phe |     |
| 20                                                              | 30  |
| Gly Leu Ala Lys Leu Tyr Asp Asp Lys Lys Thr His Ile Ser Thr Arg |     |
| 35                                                              | 45  |
| Val Ala Gly Thr Ile Gly Tyr Leu Ser Pro Glu Tyr Val Met Leu Gly |     |
| 50                                                              | 60  |
| His Leu Thr Glu Lys Thr Asp Val Phe Ala Phe Gly Ile Val Ala Leu |     |
| 65                                                              | 80  |
| Glu Ile Val Ser Gly Arg Pro Asn Ser Ser Pro Glu Leu Asp Asp Asp |     |
| 85                                                              | 95  |
| Lys Gln Tyr Leu Leu Glu Trp Ala Trp Ser Leu His Gln Glu Gln Arg |     |
| 100                                                             | 110 |
| Asp Met Glu Val Val Asp Pro Asp Leu Thr Glu Phe Asp Lys Glu Glu |     |
| 115                                                             | 125 |
| Val Lys Arg Val Ile Gly Val Ala Phe Leu Cys Thr Gln Thr Asp His |     |
| 130                                                             | 140 |
| Ala Ile Arg Pro Thr Met Ser Arg Val Val Gly Met Leu Thr Gly Asp |     |
| 145                                                             | 155 |
| Val Glu Ile Thr Glu Ala Asn Ala Lys Pro Gly Tyr Val Ser Glu Arg |     |
| 165                                                             | 175 |
| Thr Phe Glu Asn Ala Met Ser Phe Met Ser Gly Ser Thr Ser Ser Ser |     |
| 180                                                             | 190 |
| Trp Ile Leu Pro Glu Thr Pro Lys Asp Ser Ser Lys Ser Gln Val Glu |     |
| 195                                                             | 205 |
| Glu His Gly Arg Arg His                                         |     |
| 210                                                             |     |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| aaaatctctc | gctctgttac | gccattttcg  | tgagtaagaa  | gaagaaaccc  | taagagtctc  | 60   |
| tccccaaaac | ctcaaacat  | ggccgagga   | ctcgtattga  | agggcattat  | gcgcgccac   | 120  |
| accgacattg | tcacggccat | cgctacgccg  | atcgacaatt  | ccgacatcat  | cgtcacagcg  | 180  |
| tcgcgtgaca | aatcaatcat | cctctggaaa  | ctcaciaaagg | acgagaagtc  | ttacggtgtt  | 240  |
| gctcagcgta | ggctcacagg | tactctcac   | ttcgtggaag  | atgttggtct  | ctcatcggac  | 300  |
| ggtcagtttg | cactctccgg | aagttgggac  | ggtgagctcc  | gtctctggga  | tctcgccacg  | 360  |
| ggagaaacaa | ctcgtcgatt | cgttgggtcac | acgaaagatg  | tgctctctgt  | tgctttctct  | 420  |
| actgataacc | gtcagatcgt | gtctgcttct  | cgtgatcgta  | cgattaagct  | ttggaacaca  | 480  |
| cttggtgagt | gcaagtatac | catctctgaa  | ggtgatggtc  | acaaggaatg  | ggttagtgtg  | 540  |
| gttaggttta | gtcctaatac | tcttgtagca  | actattgtat  | ctgcttcttg  | ggataaaaact | 600  |
| gtgaaagtgt | ggaatctcca | gaactgtaag  | ctgaggaact  | ctcttggttg  | tcactctggt  | 660  |
| tacctcaaca | ctggtgctgt | ctcgctgat   | ggttcgctat  | gcgccagtgg  | tgggaaagat  | 720  |
| ggtgttatct | tgttggtgga | tttggtgaa   | ggaaagaagc  | tttactcgct  | tgaggctggt  | 780  |
| tcgattattc | acNtcgcttt | gcttcagtc   | taacagatac  | tggttggtgtg | ctgctactga  | 840  |
| gaatagcatt | aggatttggg | atcttgagag  | caagtctgtt  | gttgaggact  | tgaaggttga  | 900  |
| tctcaagtct | gaggcagaga | agaatgaagg  | tggtgttgga  | actggttaacc | agaagaaggt  | 960  |
| tatctactgc | acaagcttga | actggagtgc  | agatggaagc  | acattgttca  | gtggttacac  | 1020 |
| tgatggagtt | gtcaggggtc | gggggtattg  | tcgttactag  | agatcacaa   | aagatgaaga  | 1080 |
| agaagtcacg | aaatctccgg | aaaaaagtag  | ctgcttttaa  | ttttccaga   | Ctgcgtcagt  | 1140 |
| attgtattag | tctctcgcaa | acttctat    | tttggcaatt  | tggttaatt   | cc          |      |

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..244
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Gly | Leu | Val | Leu | Lys | Gly | Ile | Met | Arg | Ala | His | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Val | Thr | Ala | Ile | Ala | Thr | Pro | Ile | Asp | Asn | Ser | Asp | Ile | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Ser | Arg | Asp | Lys | Ser | Ile | Ile | Leu | Trp | Lys | Leu | Thr | Lys | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Lys | Ser | Tyr | Gly | Val | Ala | Gln | Arg | Arg | Leu | Thr | Gly | His | Ser | His |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Val | Glu | Asp | Val | Val | Leu | Ser | Ser | Asp | Gly | Gln | Phe | Ala | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ser | Trp | Asp | Gly | Glu | Leu | Arg | Leu | Trp | Asp | Leu | Ala | Thr | Gly | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Thr | Arg | Arg | Phe | Val | Gly | His | Thr | Lys | Asp | Val | Leu | Ser | Val | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Ser | Thr | Asp | Asn | Arg | Gln | Ile | Val | Ser | Ala | Ser | Arg | Asp | Arg | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Lys | Leu | Trp | Asn | Thr | Leu | Gly | Glu | Cys | Lys | Tyr | Thr | Ile | Ser | Glu |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Gly Asp Gly His Lys Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn |     |     |
| 145                                                             | 150 | 155 |
| Thr Leu Val Pro Thr Ile Val Ser Ala Ser Trp Asp Lys Thr Val Lys |     | 160 |
|                                                                 | 165 | 170 |
| Val Trp Asn Leu Gln Asn Cys Lys Leu Arg Asn Ser Leu Val Gly His |     | 175 |
|                                                                 | 180 | 185 |
| Ser Gly Tyr Leu Asn Thr Val Ala Val Ser Pro Asp Gly Ser Leu Cys |     | 190 |
|                                                                 | 195 | 200 |
| Ala Ser Gly Gly Lys Asp Gly Val Ile Leu Leu Trp Asp Leu Ala Glu |     | 205 |
|                                                                 | 210 | 215 |
| Gly Lys Lys Leu Tyr Ser Leu Glu Ala Gly Ser Ile Ile His Xaa Ala |     | 220 |
| 225                                                             | 230 | 235 |
| Leu Leu Gln Ser                                                 |     | 240 |

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1567094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Arg Ala His Thr Asp Ile Val Thr Ala Ile Ala Thr Pro Ile Asp |     |     |
| 1                                                               | 5   | 10  |
| Asn Ser Asp Ile Ile Val Thr Ala Ser Arg Asp Lys Ser Ile Ile Leu |     | 15  |
|                                                                 | 20  | 25  |
| Trp Lys Leu Thr Lys Asp Glu Lys Ser Tyr Gly Val Ala Gln Arg Arg |     | 30  |
|                                                                 | 35  | 40  |
| Leu Thr Gly His Ser His Phe Val Glu Asp Val Val Leu Ser Ser Asp |     | 45  |
|                                                                 | 50  | 55  |
| Gly Gln Phe Ala Leu Ser Gly Ser Trp Asp Gly Glu Leu Arg Leu Trp |     | 60  |
| 65                                                              | 70  | 75  |
| Asp Leu Ala Thr Gly Glu Thr Thr Arg Arg Phe Val Gly His Thr Lys |     | 80  |
|                                                                 | 85  | 90  |
| Asp Val Leu Ser Val Ala Phe Ser Thr Asp Asn Arg Gln Ile Val Ser |     | 95  |
|                                                                 | 100 | 105 |
| Ala Ser Arg Asp Arg Thr Ile Lys Leu Trp Asn Thr Leu Gly Glu Cys |     | 110 |
|                                                                 | 115 | 120 |
| Lys Tyr Thr Ile Ser Glu Gly Asp Gly His Lys Glu Trp Val Ser Cys |     | 125 |
|                                                                 | 130 | 135 |
| Val Arg Phe Ser Pro Asn Thr Leu Val Pro Thr Ile Val Ser Ala Ser |     | 140 |
| 145                                                             | 150 | 155 |
| Trp Asp Lys Thr Val Lys Val Trp Asn Leu Gln Asn Cys Lys Leu Arg |     | 160 |
|                                                                 | 165 | 170 |
| Asn Ser Leu Val Gly His Ser Gly Tyr Leu Asn Thr Val Ala Val Ser |     | 175 |
|                                                                 | 180 | 185 |
| Pro Asp Gly Ser Leu Cys Ala Ser Gly Gly Lys Asp Gly Val Ile Leu |     | 190 |
|                                                                 | 195 | 200 |
| Leu Trp Asp Leu Ala Glu Gly Lys Lys Leu Tyr Ser Leu Glu Ala Gly |     | 205 |
|                                                                 | 210 | 215 |
| Ser Ile Ile His Xaa Ala Leu Leu Gln Ser                         |     | 220 |
| 225                                                             | 230 |     |

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567095  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Met Val Arg Tyr Ala Pro Val Val Gly Lys Met Val Leu Ser Cys Cys  
1 5 10 15  
Gly Ile Trp Leu Lys Glu Arg Ser Phe Thr Arg Leu Arg Leu Val Arg  
20 25 30  
Leu Phe Xaa Ser Leu Cys Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala  
35 40 45  
Ala Thr Glu Asn Ser Ile Arg Ile Trp Asp Leu Glu Ser Lys Ser Val  
50 55 60  
Val Glu Asp Leu Lys Val Asp Leu Lys Ser Glu Ala Glu Lys Asn Glu  
65 70 75 80  
Gly Gly Val Gly Thr Gly Asn Gln Lys Lys Val Ile Tyr Cys Thr Ser  
85 90 95  
Leu Asn Trp Ser Ala Asp Gly Ser Thr Leu Phe Ser Gly Tyr Thr Asp  
100 105 110  
Gly Val Val Arg Val Trp Gly Ile Gly Arg Tyr  
115 120

(2) INFORMATION FOR SEQ ID NO:480:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1290  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

atcttaccct aaaaaccaca tttcttaact tcctcaataa aaaaaagaaa agcttcaccc 60  
tttaatttta ccttcaaccc caaaacaaaa accccttctt ccacgagggc atacagaaat 120  
atcaaagacc caatctttct ttcacttccc caatctctag atgacaatct aacgatacag 180  
ttccttttag atcgattacc aaatacaaaag gatcaatttt tcttacatga acactctgtt 240  
gtaatggcag aggagaatct agaactgagt cttttatgta cagagagcaa cgttgatgat 300  
gagggcatga ttgttgacga aactccgatt gaaatttoga ttcttcagat ggggttttct 360  
caatcggaga gtgaggagat tatcatggag atggtggaga aggagaagca gcatttgcca 420  
agtgatgatt acatcaagag acttagaagt ggagatttgg atttgaatgt tggaagaaga 480  
gatgccctca attggatttg gaaggcttgt gaagtaacac agtttggacc attgtgtttt 540  
tgcttagcaa tgaactactt ggatcgattc ttatcggttc atgatttgcc tagtggcaaa 600  
ggttggatat tgcagttggt ggctgtggct tgtttatcat tggcagccaa aattgaagaa 660  
actgaagttc caatgttgat agatcttcag gttggagatc ctcagtttgt gtttgaggct 720  
aaatcagtc aaagaatgga gcttttggtg ttgaacagat tgaaatggag attgagagca 780  
ataactccat gctcatacat aagatatttc ctgagaaaga tgagtaaagt tgatcaagaa 840  
ccatccaaca cattgatatc tagatcatta caagtgatag ccagcacacac caaaggattt 900  
gacttttttg agtttagacc ttctgaagtt gctgctgctg tggcactttc tgtttctgga 960  
gaattgcaga gactacactt tgacaactct tccttctctc ctcttttctc actacttcaa 1020  
aaggagagag tgaagaagat aggggaaatg atagagagtg atggctcaga cttattttca 1080  
caaacaccca atggggtttt agaagtatcg gcttgttgtt tcagctttaa gaccocatgat 1140  
tcttcttctt cttatacaca tcttctttaa aaaaaaaact gtttttttct tacattatta 1200  
taatcagtat gatgtctgat gagagggtga aaaaagagga caataaatca aagcaaaaaat 1260  
tttaaaataC aataaaaagtg tattaatttc

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 308 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..308
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1567097
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn  
1 5 10 15  
Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser  
20 25 30  
Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met  
35 40 45  
Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile  
50 55 60  
Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp  
65 70 75 80  
Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro  
85 90 95  
Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val  
100 105 110  
His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val  
115 120 125  
Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met  
130 135 140  
Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys  
145 150 155 160  
Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg  
165 170 175  
Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys  
180 185 190  
Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser  
195 200 205  
Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe  
210 215 220  
Arg Pro Ser Glu Val Ala Ala Val Ala Leu Ser Val Ser Gly Glu  
225 230 235 240  
Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser  
245 250 255  
Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser  
260 265 270  
Asp Gly Ser Asp Leu Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val  
275 280 285  
Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Tyr  
290 295 300  
Thr His Leu Ser  
305

- (2) INFORMATION FOR SEQ ID NO:482:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 287 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..287
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1567098
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```

Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser Ile Pro Gln Met Gly
1 5 10 15
Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met Glu Met Val Glu Lys
 20 25 30
Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile Lys Arg Leu Arg Ser
 35 40 45
Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp Ala Leu Asn Trp Ile
 50 55 60
Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro Leu Cys Phe Cys Leu
 65 70 75 80
Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val His Asp Leu Pro Ser
 85 90 95
Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val Ala Cys Leu Ser Leu
 100 105 110
Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met Leu Ile Asp Leu Gln
 115 120 125
Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys Ser Val Gln Arg Met
 130 135 140
Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg Leu Arg Ala Ile Thr
 145 150 155 160
Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys Met Ser Lys Cys Asp
 165 170 175
Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser Leu Gln Val Ile Ala
 180 185 190
Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe Arg Pro Ser Glu Val
 195 200 205
Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu Leu Gln Arg Val His
 210 215 220
Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser Leu Leu Gln Lys Glu
 225 230 235 240
Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser Asp Gly Ser Asp Leu
 245 250 255
Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val Ser Ala Cys Cys Phe
 260 265 270
Ser Phe Lys Thr His Asp Ser Ser Ser Tyr Thr His Leu Ser
 275 280 285

```

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1567099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met Glu Met Val
1 5 10 15
Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile Lys Arg Leu
 20 25 30
Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp Ala Leu Asn
 35 40 45
Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro Leu Cys Phe
 50 55 60
Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val His Asp Leu
 65 70 75 80
Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val Ala Cys Leu
 85 90 95
Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met Leu Ile Asp

```



100 105 110  
Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys Ser Val Gln  
115 120 125  
Arg Met Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg Leu Arg Ala  
130 135 140  
Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys Met Ser Lys  
145 150 155 160  
Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser Leu Gln Val  
165 170 175  
Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe Arg Pro Ser  
180 185 190  
Glu Val Ala Ala Val Ala Leu Ser Val Ser Gly Glu Leu Gln Arg  
195 200 205  
Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser Leu Leu Gln  
210 215 220  
Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser Asp Gly Ser  
225 230 235 240  
Asp Leu Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val Ser Ala Cys  
245 250 255  
Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Tyr Thr His Leu  
260 265 270  
Ser

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gagagaaaga | gagagatatg | atattattaa | gtagtagtat | aagcctctca | agaccagttt | 60   |
| cttctcaaa  | cttctctcca | cctgctgcc  | cttcaacaag | gagatctcat | tcctctgtca | 120  |
| cagtcaagt  | ctgctgttct | tccagaaggt | tggtgaagaa | tcctgagtta | aaatgttcct | 180  |
| tggagaatct | ctttgaaatc | caggctttga | ggaagtgttt | tgtttcaggg | tttgcagcta | 240  |
| ttttgcttct | ctctcaggca | ggccagggt  | tagcgttga  | tctctcatct | ggttatcaga | 300  |
| acatttgcca | actaggagg  | gctgctgct  | tgggagaaaa | caagctgact | cttccatctg | 360  |
| atggtgactc | ggaatcaatg | atgatgatga | tgatgagagg | catgactgct | aagaactttg | 420  |
| accctgttag | gtactctgga | agatggtttg | aagtagcttc | tcttaagcgt | ggatttgcag | 480  |
| gtcaaggcca | agaagactgt | cattgcactc | agggagtata | cacgtttgat | atgaaggaat | 540  |
| cagccattag | agtagataca | ttttgtgttc | atggcagccc | tgatggatat | ataacaggaa | 600  |
| tcagagggaa | agttcaatgc | gtgggagcgg | aagacctcga | gaaaagcgag | actgacttag | 660  |
| aaaagcaaga | gatgattaaa | gagaagtgtt | tcctacgatt | tcccaccatt | ccttttatcc | 720  |
| ccaagtgtcc | ttatgatgtc | atagccacag | actacgacaa | ctacgcactt | gtttctggag | 780  |
| ctaaagacaa | gggctttgtt | caggtatact | caaggacgcc | aaatccagga | cctgagttca | 840  |
| tcgcaaagta | caagaactac | ttggcacaa  | ttggctatga | cccggaaaaa | ataaaggata | 900  |
| caccacagga | ctgtgaagt  | actgatgctg | agctagcagc | catgatgtcc | atgccaggta | 960  |
| tggagcaaac | actgaccaac | cagtttccag | atcttggatt | aaAgaaagtc | agtccagttt | 1020 |
| gatcccttca | caagtgtgtt | tgaaaccttg | aagaaacttg | taccgctcta | tttcaaatag | 1080 |
| agcaagcttc | tttgctcaaa | ttcttatgta | gactataatc | actgtccata | tatacatatc | 1140 |
| ttccagaatc | aaaacactct | tctg       |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..339
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1567117
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Glu Lys Glu Arg Asp Met Ile Leu Leu Ser Ser Ser Ile Ser Leu Ser  
1 5 10 15  
Arg Pro Val Ser Ser Gln Ser Phe Ser Pro Pro Ala Ala Thr Ser Thr  
20 25 30  
Arg Arg Ser His Ser Ser Val Thr Val Lys Cys Cys Cys Ser Ser Arg  
35 40 45  
Arg Leu Leu Lys Asn Pro Glu Leu Lys Cys Ser Leu Glu Asn Leu Phe  
50 55 60  
Glu Ile Gln Ala Leu Arg Lys Cys Phe Val Ser Gly Phe Ala Ala Ile  
65 70 75 80  
Leu Leu Leu Ser Gln Ala Gly Gln Gly Ile Ala Leu Asp Leu Ser Ser  
85 90 95  
Gly Tyr Gln Asn Ile Cys Gln Leu Gly Ser Ala Ala Ala Val Gly Glu  
100 105 110  
Asn Lys Leu Thr Leu Pro Ser Asp Gly Asp Ser Glu Ser Met Met Met  
115 120 125  
Met Met Met Arg Gly Met Thr Ala Lys Asn Phe Asp Pro Val Arg Tyr  
130 135 140  
Ser Gly Arg Trp Phe Glu Val Ala Ser Leu Lys Arg Gly Phe Ala Gly  
145 150 155 160  
Gln Gly Gln Glu Asp Cys His Cys Thr Gln Gly Val Tyr Thr Phe Asp  
165 170 175  
Met Lys Glu Ser Ala Ile Arg Val Asp Thr Phe Cys Val His Gly Ser  
180 185 190  
Pro Asp Gly Tyr Ile Thr Gly Ile Arg Gly Lys Val Gln Cys Val Gly  
195 200 205  
Ala Glu Asp Leu Glu Lys Ser Glu Thr Asp Leu Glu Lys Gln Glu Met  
210 215 220  
Ile Lys Glu Lys Cys Phe Leu Arg Phe Pro Thr Ile Pro Phe Ile Pro  
225 230 235 240  
Lys Leu Pro Tyr Asp Val Ile Ala Thr Asp Tyr Asp Asn Tyr Ala Leu  
245 250 255  
Val Ser Gly Ala Lys Asp Lys Gly Phe Val Gln Val Tyr Ser Arg Thr  
260 265 270  
Pro Asn Pro Gly Pro Glu Phe Ile Ala Lys Tyr Lys Asn Tyr Leu Ala  
275 280 285  
Gln Phe Gly Tyr Asp Pro Glu Lys Ile Lys Asp Thr Pro Gln Asp Cys  
290 295 300  
Glu Val Thr Asp Ala Glu Leu Ala Ala Met Met Ser Met Pro Gly Met  
305 310 315 320  
Glu Gln Thr Leu Thr Asn Gln Phe Pro Asp Leu Gly Leu Lys Lys Val  
325 330 335  
Ser Pro Val

- (2) INFORMATION FOR SEQ ID NO:486:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 334 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..334
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1567118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met Ile Leu Leu Ser Ser Ser Ile Ser Leu Ser Arg Pro Val Ser Ser  
1 5 10 15  
Gln Ser Phe Ser Pro Pro Ala Ala Thr Ser Thr Arg Arg Ser His Ser  
20 25 30  
Ser Val Thr Val Lys Cys Cys Cys Ser Ser Arg Arg Leu Leu Lys Asn  
35 40 45  
Pro Glu Leu Lys Cys Ser Leu Glu Asn Leu Phe Glu Ile Gln Ala Leu  
50 55 60  
Arg Lys Cys Phe Val Ser Gly Phe Ala Ala Ile Leu Leu Leu Ser Gln  
65 70 75 80  
Ala Gly Gln Gly Ile Ala Leu Asp Leu Ser Ser Gly Tyr Gln Asn Ile  
85 90 95  
Cys Gln Leu Gly Ser Ala Ala Ala Val Gly Glu Asn Lys Leu Thr Leu  
100 105 110  
Pro Ser Asp Gly Asp Ser Glu Ser Met Met Met Met Met Met Arg Gly  
115 120 125  
Met Thr Ala Lys Asn Phe Asp Pro Val Arg Tyr Ser Gly Arg Trp Phe  
130 135 140  
Glu Val Ala Ser Leu Lys Arg Gly Phe Ala Gly Gln Gly Gln Glu Asp  
145 150 155 160  
Cys His Cys Thr Gln Gly Val Tyr Thr Phe Asp Met Lys Glu Ser Ala  
165 170 175  
Ile Arg Val Asp Thr Phe Cys Val His Gly Ser Pro Asp Gly Tyr Ile  
180 185 190  
Thr Gly Ile Arg Gly Lys Val Gln Cys Val Gly Ala Glu Asp Leu Glu  
195 200 205  
Lys Ser Glu Thr Asp Leu Glu Lys Gln Glu Met Ile Lys Glu Lys Cys  
210 215 220  
Phe Leu Arg Phe Pro Thr Ile Pro Phe Ile Pro Lys Leu Pro Tyr Asp  
225 230 235 240  
Val Ile Ala Thr Asp Tyr Asp Asn Tyr Ala Leu Val Ser Gly Ala Lys  
245 250 255  
Asp Lys Gly Phe Val Gln Val Tyr Ser Arg Thr Pro Asn Pro Gly Pro  
260 265 270  
Glu Phe Ile Ala Lys Tyr Lys Asn Tyr Leu Ala Gln Phe Gly Tyr Asp  
275 280 285  
Pro Glu Lys Ile Lys Asp Thr Pro Gln Asp Cys Glu Val Thr Asp Ala  
290 295 300  
Glu Leu Ala Ala Met Met Ser Met Pro Gly Met Glu Gln Thr Leu Thr  
305 310 315 320  
Asn Gln Phe Pro Asp Leu Gly Leu Lys Lys Val Ser Pro Val  
325 330

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1567119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

Met Met Met Met Met Arg Gly Met Thr Ala Lys Asn Phe Asp Pro  
1 5 10 15  
Val Arg Tyr Ser Gly Arg Trp Phe Glu Val Ala Ser Leu Lys Arg Gly  
20 25 30  
Phe Ala Gly Gln Gly Gln Glu Asp Cys His Cys Thr Gln Gly Val Tyr  
35 40 45

Thr Phe Asp Met Lys Glu Ser Ala Ile Arg Val Asp Thr Phe Cys Val  
50 55 60  
His Gly Ser Pro Asp Gly Tyr Ile Thr Gly Ile Arg Gly Lys Val Gln  
65 70 75 80  
Cys Val Gly Ala Glu Asp Leu Glu Lys Ser Glu Thr Asp Leu Glu Lys  
85 90 95  
Gln Glu Met Ile Lys Glu Lys Cys Phe Leu Arg Phe Pro Thr Ile Pro  
100 105 110  
Phe Ile Pro Lys Leu Pro Tyr Asp Val Ile Ala Thr Asp Tyr Asp Asn  
115 120 125  
Tyr Ala Leu Val Ser Gly Ala Lys Asp Lys Gly Phe Val Gln Val Tyr  
130 135 140  
Ser Arg Thr Pro Asn Pro Gly Pro Glu Phe Ile Ala Lys Tyr Lys Asn  
145 150 155 160  
Tyr Leu Ala Gln Phe Gly Tyr Asp Pro Glu Lys Ile Lys Asp Thr Pro  
165 170 175  
Gln Asp Cys Glu Val Thr Asp Ala Glu Leu Ala Ala Met Met Ser Met  
180 185 190  
Pro Gly Met Glu Gln Thr Leu Thr Asn Gln Phe Pro Asp Leu Gly Leu  
195 200 205  
Lys Lys Val Ser Pro Val  
210

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| gaccacatca attctGstca tatctctctc tcacttttoga atatattctta agataacaga | 60   |
| gacacatact cttaaagtttg gtgaagaata agaagacaat gacgaaggaa gtgggttggtg | 120  |
| ataagagatc tttctccggg aaagactatc aagaccacc acctgaacct ctattcgacg    | 180  |
| ctactgagct tgggaagtgg tctttctaca gagctctcat cgctgagttc atagccatc    | 240  |
| tccttttccct ctatgtcaact attatgactg tcatcggtta caagagccag accgatccag | 300  |
| ccctgaatcc tgaccagtgt acaggcggtg gcgctccttg tategcatgg gccttttggtg  | 360  |
| gcatgatctt catcctcgtc tactgcaccg ccggcatctc tgggtgggcat attaatccgg  | 420  |
| cagtgacttt tgggctggtg ttggctcgga aagtgcagtt ggtgagagca gtgatgtaca   | 480  |
| tgggtggctca gtgcctcggg gccatttggt gtgtggcttt ggtcaaggcc ttccagtcg   | 540  |
| cttacttcac ccgctacggt ggtggcgcaa atggtctctc tgacggttac agcatcggca   | 600  |
| ccggtgttgc agccgagatc attggtacat tcgtcttagt ctacaccgtc ttctctgcca   | 660  |
| ctgatcccaa gaggagtgcg cgtgactctc acgttccgtg attggctcca ttgccaattg   | 720  |
| gatttgcagt gttcatcggt cacttagcta caatcccaat cacgggcact ggtatcaacc   | 780  |
| ctgcaagaag tctcggagct gcaatcatct acaacaagga caaagcttgg gaccatcatt   | 840  |
| ggatattctg ggtgggtccg tttgctggtg cagccatcgc agctttctac catcagtttg   | 900  |
| tgttgagggc tgggtgcgatt aaggcgctcg ggtctttcag gagccagcct cacgtttaac  | 960  |
| tttgatatgc tcttccttga gtacatcaaa gagagaaaaa gagaagataa taagagaggc   | 1020 |
| ttgtaatttt atcttggtga gacggttgga gccaaagtgc gtgtagtact agtatcta     | 1080 |
| ttctagcttt ggtgaggaga gatattttga agtgctcgtt gcggggccaa tttgaattgc   | 1140 |
| tacttctatg attaaatcta tgtctctact ccttgactat taagattgct ctatttatta   | 1200 |
| gtactaaata ttccttatat atg                                           |      |

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..286  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567121  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Met Thr Lys Glu Val Val Gly Asp Lys Arg Ser Phe Ser Gly Lys Asp  
1                  5                  10                  15  
Tyr Gln Asp Pro Pro Pro Glu Pro Leu Phe Asp Ala Thr Glu Leu Gly  
                  20                  25                  30  
Lys Trp Ser Phe Tyr Arg Ala Leu Ile Ala Glu Phe Ile Ala Thr Leu  
                  35                  40                  45  
Leu Phe Leu Tyr Val Thr Ile Met Thr Val Ile Gly Tyr Lys Ser Gln  
50                  55                  60  
Thr Asp Pro Ala Leu Asn Pro Asp Gln Cys Thr Gly Val Gly Val Leu  
65                  70                  75                  80  
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ile Leu Val Tyr Cys  
                  85                  90                  95  
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly  
                  100                  105                  110  
Leu Leu Leu Ala Arg Lys Val Thr Leu Val Arg Ala Val Met Tyr Met  
                  115                  120                  125  
Val Ala Gln Cys Leu Gly Ala Ile Cys Gly Val Ala Leu Val Lys Ala  
130                  135                  140  
Phe Gln Ser Ala Tyr Phe Thr Arg Tyr Gly Gly Gly Ala Asn Gly Leu  
145                  150                  155                  160  
Ser Asp Gly Tyr Ser Ile Gly Thr Gly Val Ala Ala Glu Ile Ile Gly  
                  165                  170                  175  
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Pro Lys Arg  
                  180                  185                  190  
Ser Ala Arg Asp Ser His Val Pro Val Leu Ala Pro Leu Pro Ile Gly  
                  195                  200                  205  
Phe Ala Val Phe Ile Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr  
210                  215                  220  
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys  
225                  230                  235                  240  
Asp Lys Ala Trp Asp His His Trp Ile Phe Trp Val Gly Pro Phe Ala  
                  245                  250                  255  
Gly Ala Ala Ile Ala Ala Phe Tyr His Gln Phe Val Leu Arg Ala Gly  
                  260                  265                  270  
Ala Ile Lys Ala Leu Gly Ser Phe Arg Ser Gln Pro His Val  
275                  280                  285

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 231 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..231  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567122  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Thr Val Ile Gly Tyr Lys Ser Gln Thr Asp Pro Ala Leu Asn Pro  
1                  5                  10                  15  
Asp Gln Cys Thr Gly Val Gly Val Leu Gly Ile Ala Trp Ala Phe Gly  
                  20                  25                  30  
Gly Met Ile Phe Ile Leu Val Tyr Cys Thr Ala Gly Ile Ser Gly Gly  
                  35                  40                  45  
His Ile Asn Pro Ala Val Thr Phe Gly Leu Leu Leu Ala Arg Lys Val

[illegible]

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

|                                                                       |      |
|-----------------------------------------------------------------------|------|
| aaaatttcgc aaactaatttt tttcactttc ttcttogggtg atctctctga aagcttctct   | 60   |
| tcttcttctc accatgtctg gttatcctcc atcaagccaa ggttacgggtt acggcggtaa    | 120  |
| tccaccacct cctcagccac cgtacggatc aaccggcaat aaccctcctc cgtgcggatc     | 180  |
| atccggcagc aatcctcctc ctccgtacgg atcatcagcc tcttcaccgt acgcagttcc     | 240  |
| ctacggagct cagcccgtc cttacgggtgc accaccgtca gcaccgtacg cgtctcctcc     | 300  |
| aggagacatc aataagccgc acaaagagaa acctcacggc gcctcctacg gatctccatc     | 360  |
| tcccgggtggc tacgggtgctc atccatcgctc tggaccttcc gactacgggtg gttacggagg | 420  |
| agcgcgcgag cagtctggac atggaggagg ttacggagga gcgcgcgagc agtctggaca     | 480  |
| tggaggagggt tacggagctc ctccctccga agcttcttat ggaagtccgt ttgcgtctct    | 540  |
| ggttccgtcg gcgtttcctc ccggaacaga tccgaacatt gtggcttggt tccaagctgc     | 600  |
| ggatcgggac aatagtggat tcatcgatga taaggagctt caaggagctc tatcttcgta     | 660  |
| taatcagagc ttcagcataa gaactgttca tctccttatg tatctattca ccaacagcaa     | 720  |
| tgtcaggaag attggaccaa aagagtttac ttcacttttc Tkkagtcttc agaattggag     | 780  |
| gtctatcttt gagaggtttg ataaggacag aagcggtaga atagatacaa acgagctgag     | 840  |
| agatgcactc atgagccttg ggttttctgt gtctcctgtg attttggatc tgctggtttc     | 900  |
| aaagtttgac aaaagcggag gcaggaacag ggctatcgaa tatgacaatt tcatcgagtg     | 960  |
| ttgtttgact gtaaaggggc tcaccgagaa gttcaaggag aaggatacgg cgttatcagg     | 1020 |
| ctcagctact ttcaattacg agaacttcat gctcactgtt ttaccattcc tcgtcgcttg     | 1080 |
| agtgattggt tttttttttt ttgttgaccA aasagattgt tttctaactc tattttcttt     | 1140 |
| gtgagctttt ggatatttta tttgttgtct tttt                                 |      |

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Phe Arg Lys Leu Ile Phe Ser Leu Ser Ser Ser Leu Ile Ser Leu |  |
| 1 5 10 15                                                       |  |
| Lys Ala Ser Leu Leu Leu Thr Met Ser Gly Tyr Pro Pro Ser Ser     |  |
| 20 25 30                                                        |  |
| Gln Gly Tyr Gly Tyr Gly Gly Asn Pro Pro Pro Pro Gln Pro Pro Tyr |  |
| 35 40 45                                                        |  |
| Gly Ser Thr Gly Asn Asn Pro Pro Pro Cys Gly Ser Ser Gly Ser Asn |  |
| 50 55 60                                                        |  |
| Pro Pro Pro Pro Tyr Gly Ser Ser Ala Ser Ser Pro Tyr Ala Val Pro |  |
| 65 70 75 80                                                     |  |
| Tyr Gly Ala Gln Pro Ala Pro Tyr Gly Ala Pro Pro Ser Ala Pro Tyr |  |
| 85 90 95                                                        |  |
| Ala Ser Pro Pro Gly Asp His Asn Lys Pro His Lys Glu Lys Pro His |  |
| 100 105 110                                                     |  |
| Gly Ala Ser Tyr Gly Ser Pro Ser Pro Gly Gly Tyr Gly Ala His Pro |  |
| 115 120 125                                                     |  |
| Ser Ser Gly Pro Ser Asp Tyr Gly Gly Tyr Gly Gly Ala Pro Gln Gln |  |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Ser Gly His Gly Gly Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His |     |     |
| 145                                                             | 150 | 155 |
| Gly Gly Gly Tyr Gly Ala Pro Pro Pro Gln Ala Ser Tyr Gly Ser Pro |     |     |
|                                                                 | 165 | 170 |
| Phe Ala Ser Leu Val Pro Ser Ala Phe Pro Pro Gly Thr Asp Pro Asn |     |     |
|                                                                 | 180 | 185 |
| Ile Val Ala Cys Phe Gln Ala Ala Asp Arg Asp Asn Ser Gly Phe Ile |     |     |
|                                                                 | 195 | 200 |
| Asp Asp Lys Glu Leu Gln Gly Ala Leu Ser Ser Tyr Asn Gln Ser Phe |     |     |
| 210                                                             | 215 | 220 |
| Ser Ile Arg Thr Val His Leu Leu Met Tyr Leu Phe Thr Asn Ser Asn |     |     |
| 225                                                             | 230 | 235 |
| Val Arg Lys Ile Gly Pro Lys Glu Phe Thr Ser Leu Phe Xaa Ser Leu |     |     |
|                                                                 | 245 | 250 |
| Gln Asn Trp Arg Ser Ile Phe Glu Arg Phe Asp Lys Asp Arg Ser Gly |     |     |
|                                                                 | 260 | 265 |
| Arg Ile Asp Thr Asn Glu Leu Arg Asp Ala Leu Met Ser Leu Gly Phe |     |     |
|                                                                 | 275 | 280 |
| Ser Val Ser Pro Val Ile Leu Asp Leu Leu Val Ser Lys Phe Asp Lys |     |     |
| 290                                                             | 295 | 300 |
| Ser Gly Gly Arg Asn Arg Ala Ile Glu Tyr Asp Asn Phe Ile Glu Cys |     |     |
| 305                                                             | 310 | 315 |
| Cys Leu Thr Val Lys Gly Leu Thr Glu Lys Phe Lys Glu Lys Asp Thr |     |     |
|                                                                 | 325 | 330 |
| Ala Leu Ser Gly Ser Ala Thr Phe Asn Tyr Glu Asn Phe Met Leu Thr |     |     |
|                                                                 | 340 | 345 |
| Val Leu Pro Phe Leu Val Ala                                     |     | 350 |
| 355                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Ser Gly Tyr Pro Pro Ser Ser Gln Gly Tyr Gly Tyr Gly Gly Asn |     |
| 1                                                               | 15  |
| Pro Pro Pro Pro Gln Pro Pro Tyr Gly Ser Thr Gly Asn Asn Pro Pro |     |
| 20                                                              | 30  |
| Pro Cys Gly Ser Ser Gly Ser Asn Pro Pro Pro Tyr Gly Ser Ser     |     |
| 35                                                              | 45  |
| Ala Ser Ser Pro Tyr Ala Val Pro Tyr Gly Ala Gln Pro Ala Pro Tyr |     |
| 50                                                              | 60  |
| Gly Ala Pro Pro Ser Ala Pro Tyr Ala Ser Pro Pro Gly Asp His Asn |     |
| 65                                                              | 80  |
| Lys Pro His Lys Glu Lys Pro His Gly Ala Ser Tyr Gly Ser Pro Ser |     |
| 85                                                              | 95  |
| Pro Gly Gly Tyr Gly Ala His Pro Ser Ser Gly Pro Ser Asp Tyr Gly |     |
| 100                                                             | 110 |
| Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His Gly Gly Gly Tyr Gly |     |
| 115                                                             | 125 |
| Gly Ala Pro Gln Gln Ser Gly His Gly Gly Gly Tyr Gly Ala Pro Pro |     |
| 130                                                             | 140 |
| Pro Gln Ala Ser Tyr Gly Ser Pro Phe Ala Ser Leu Val Pro Ser Ala |     |
| 145                                                             | 155 |
|                                                                 | 160 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Pro | Gly | Thr | Asp | Pro | Asn | Ile | Val | Ala | Cys | Phe | Gln | Ala | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Arg | Asp | Asn | Ser | Gly | Phe | Ile | Asp | Asp | Lys | Glu | Leu | Gln | Gly | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ser | Ser | Tyr | Asn | Gln | Ser | Phe | Ser | Ile | Arg | Thr | Val | His | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Met | Tyr | Leu | Phe | Thr | Asn | Ser | Asn | Val | Arg | Lys | Ile | Gly | Pro | Lys | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Thr | Ser | Leu | Phe | Xaa | Ser | Leu | Gln | Asn | Trp | Arg | Ser | Ile | Phe | Glu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Phe | Asp | Lys | Asp | Arg | Ser | Gly | Arg | Ile | Asp | Thr | Asn | Glu | Leu | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Ala | Leu | Met | Ser | Leu | Gly | Phe | Ser | Val | Ser | Pro | Val | Ile | Leu | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Val | Ser | Lys | Phe | Asp | Lys | Ser | Gly | Gly | Arg | Asn | Arg | Ala | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Tyr | Asp | Asn | Phe | Ile | Glu | Cys | Cys | Leu | Thr | Val | Lys | Gly | Leu | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Lys | Phe | Lys | Glu | Lys | Asp | Thr | Ala | Leu | Ser | Gly | Ser | Ala | Thr | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Tyr | Glu | Asn | Phe | Met | Leu | Thr | Val | Leu | Pro | Phe | Leu | Val | Ala |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| ctctctctct  | ctctcacttc | atctatggct | tcttcttctc  | tgcagtctct | cttctctctg  | 60   |
| ttttgccttg  | ctctgtttct | tcttctctct | atcgctctct  | ccatcggcct | caactatggc  | 120  |
| caggctcgct  | acaaccttcc | tccccctaaa | aacgtcatcc  | ctctctctca | gtctgtggga  | 180  |
| gctacaaag   | tcaagctcta | tgacgcccgt | ccacaagccc  | tacgtgcctt | cgccggctcc  | 240  |
| ggcttcgagc  | tcaccgtggc | cctcggtaac | gagtagcttg  | ctcagatgag | cgaccctatt  | 300  |
| aaagcccaag  | gctgggtgaa | ggagaacgtc | caagcttacc  | tcccaaacac | caagatcggt  | 360  |
| gccatcgtag  | tgggaaacga | agTcctcacc | tcaaaccagt  | cagccctcac | ggcagccctc  | 420  |
| ttcccggcta  | tgcaaagcat | ccacgggtgt | ctgggtggatt | gtggcctaaa | caagcagatc  | 480  |
| tttgtgaoga  | cggctcactc | actagccatc | ttggatgtat  | cctaccctcc | ctcggccact  | 540  |
| tccttccgcc  | gcgacctoct | cggctccctc | actcccattc  | tggacttcca | cgtcaagact  | 600  |
| ggctcaccaa  | tcctcatcaa | cgcctacctt | ttcttcgcct  | acgaagaaaa | ccccaaacac  | 660  |
| gtttctctcg  | acttcgtact | cttccaacca | aatcaaggct  | tcaccgatcc | tggctctaata | 720  |
| ttccactaog  | acaacatgct | cttcgctcag | gtcgacgcag  | tctatcacgc | tcttgacgct  | 780  |
| gtcggcatca  | gctacaagaa | agttccattt | gtcgtctccg  | agaccggatg | gccttccaac  | 840  |
| ggtgacccgc  | aagaagtcgg | agccacctgc | gacaatgtct  | gcaagtacaa | tgggaatctg  | 900  |
| atcaagatga  | tgatgagcaa | gaagatgagg | acgcctattc  | gacctgagt  | cgatctcacc  | 960  |
| atcttcgtct  | ttgctctctt | taacgagaac | atgaagcctg  | Gaccaacctc | cgagaggaac  | 1020 |
| tacggtctct  | tcaaccctga | cggaaactcc | gtttactcac  | ttgggatcaa | gacctcttcc  | 1080 |
| actcatagta  | gtggtagtgg | tagcagcaac | tccactgggt  | gtagtagcag | tggcgggtggc | 1140 |
| ggtaaacactg | gtggctcttc | cagcgggtgt | ggcatctatc  | agccagtcac | gggtaaccca  | 1200 |
| tcaccggatt  | acatgtccat | ttcctccgcc | gggggaaaa   | gcagattcgt | tgagtgtgtg  | 1260 |
| ttgttcttct  | tcttgctttg | catcatcaag | cttcggttgt  | aaaagcttct | ccactagatc  | 1320 |
| tcgtcggctt  | tgtactttta | cgcgggtgtg | gacgtgatat  | agcccccaaa | tttaatttaa  | 1380 |
| ttagttttgt  | gttggtgttt | tggtcggagg | atgatttagg  | agacatacca | tctttgttgt  | 1440 |
| gccgacctcc  | tctccaactc | ttttcttttt | tccattccat  | cctccttttt | cttggtttaag | 1500 |
| catagattat  | ttaaataatg | aatcttagtt | gattagattt  | ttctaaagaa | gatgatgatt  | 1560 |
| ttcgataaaa  | gc         |            |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1567134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Ser | Leu | Thr | Ser | Ser | Met | Ala | Ser | Ser | Ser | Leu | Gln | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Phe | Ser | Leu | Phe | Cys | Leu | Ala | Leu | Phe | Ser | Leu | Pro | Leu | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ile | Gly | Ile | Asn | Tyr | Gly | Gln | Val | Ala | Asn | Asn | Leu | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Lys | Asn | Val | Ile | Pro | Leu | Lys | Ser | Val | Gly | Ala | Thr | Lys | Val |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Leu | Tyr | Asp | Ala | Asp | Pro | Gln | Ala | Leu | Arg | Ala | Phe | Ala | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Phe | Glu | Leu | Thr | Val | Ala | Leu | Gly | Asn | Glu | Tyr | Leu | Ala | Gln | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Asp | Pro | Ile | Lys | Ala | Gln | Gly | Trp | Val | Lys | Glu | Asn | Val | Gln | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Leu | Pro | Asn | Thr | Lys | Ile | Val | Ala | Ile | Val | Val | Gly | Asn | Glu | Val |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Ser | Asn | Gln | Ser | Ala | Leu | Thr | Ala | Ala | Leu | Phe | Pro | Ala | Met |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gln | Ser | Ile | His | Gly | Ala | Leu | Val | Asp | Cys | Gly | Leu | Asn | Lys | Gln | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Val | Thr | Thr | Ala | His | Ser | Leu | Ala | Ile | Leu | Asp | Val | Ser | Tyr | Pro |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |
| Pro | Ser | Ala | Thr | Ser | Phe | Arg | Arg | Asp | Leu | Leu | Gly | Ser | Leu | Thr | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Asp | Phe | His | Val | Lys | Thr | Gly | Ser | Pro | Ile | Leu | Ile | Asn | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Pro | Phe | Phe | Ala | Tyr | Glu | Glu | Asn | Pro | Lys | His | Val | Ser | Leu | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Val | Leu | Phe | Gln | Pro | Asn | Gln | Gly | Phe | Thr | Asp | Pro | Gly | Ser | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | His | Tyr | Asp | Asn | Met | Leu | Phe | Ala | Gln | Val | Asp | Ala | Val | Tyr | His |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Asp | Ala | Val | Gly | Ile | Ser | Tyr | Lys | Lys | Val | Pro | Ile | Val | Val |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     | 270 |     |     |
| Ser | Glu | Thr | Gly | Trp | Pro | Ser | Asn | Gly | Asp | Pro | Gln | Glu | Val | Gly | Ala |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Cys | Asp | Asn | Ala | Arg | Lys | Tyr | Asn | Gly | Asn | Leu | Ile | Lys | Met | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Ser | Lys | Lys | Met | Arg | Thr | Pro | Ile | Arg | Pro | Glu | Cys | Asp | Leu | Thr |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Phe | Val | Phe | Ala | Leu | Phe | Asn | Glu | Asn | Met | Lys | Pro | Gly | Pro | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Glu | Arg | Asn | Tyr | Gly | Leu | Phe | Asn | Pro | Asp | Gly | Thr | Pro | Val | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Leu | Gly | Ile | Lys | Thr | Ser | Ser | Thr | His | Ser | Ser | Gly | Ser | Gly | Ser |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Asn | Ser | Thr | Gly | Gly | Ser | Ser | Ser | Gly | Gly | Gly | Gly | Asn | Thr | Gly |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Ser | Ser | Ser | Gly | Gly | Gly | Ile | Tyr | Gln | Pro | Val | Thr | Gly | Asn | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Pro | Asp | Tyr | Met | Ser | Ile | Ser | Ser | Ala | Gly | Gly | Lys | Gly | Arg | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Val | Glu | Cys | Val | Leu | Phe | Phe | Phe | Leu | Leu | Cys | Ile | Ile | Lys | Leu | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..425

(D) OTHER INFORMATION: / Ceres Seq. ID 1567135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Ser | Leu | Gln | Ser | Leu | Phe | Ser | Leu | Phe | Cys | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Phe | Ser | Leu | Pro | Leu | Ile | Val | Ser | Ser | Ile | Gly | Ile | Asn | Tyr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Val | Ala | Asn | Asn | Leu | Pro | Pro | Pro | Lys | Asn | Val | Ile | Pro | Leu | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Ser | Val | Gly | Ala | Thr | Lys | Val | Lys | Leu | Tyr | Asp | Ala | Asp | Pro | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Arg | Ala | Phe | Ala | Gly | Ser | Gly | Phe | Glu | Leu | Thr | Val | Ala | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly | Asn | Glu | Tyr | Leu | Ala | Gln | Met | Ser | Asp | Pro | Ile | Lys | Ala | Gln | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Val | Lys | Glu | Asn | Val | Gln | Ala | Tyr | Leu | Pro | Asn | Thr | Lys | Ile | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ile | Val | Val | Gly | Asn | Glu | Val | Leu | Thr | Ser | Asn | Gln | Ser | Ala | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Ala | Ala | Leu | Phe | Pro | Ala | Met | Gln | Ser | Ile | His | Gly | Ala | Leu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Cys | Gly | Leu | Asn | Lys | Gln | Ile | Phe | Val | Thr | Thr | Ala | His | Ser | Leu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Ala | Ile | Leu | Asp | Val | Ser | Tyr | Pro | Pro | Ser | Ala | Thr | Ser | Phe | Arg | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Leu | Leu | Gly | Ser | Leu | Thr | Pro | Ile | Leu | Asp | Phe | His | Val | Lys | Thr |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Ser | Pro | Ile | Leu | Ile | Asn | Ala | Tyr | Pro | Phe | Phe | Ala | Tyr | Glu | Glu |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asn | Pro | Lys | His | Val | Ser | Leu | Asp | Phe | Val | Leu | Phe | Gln | Pro | Asn | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Phe | Thr | Asp | Pro | Gly | Ser | Asn | Phe | His | Tyr | Asp | Asn | Met | Leu | Phe |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ala | Gln | Val | Asp | Ala | Val | Tyr | His | Ala | Leu | Asp | Ala | Val | Gly | Ile | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Tyr | Lys | Lys | Val | Pro | Ile | Val | Val | Ser | Glu | Thr | Gly | Trp | Pro | Ser | Asn |
|     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Gly | Asp | Pro | Gln | Glu | Val | Gly | Ala | Thr | Cys | Asp | Asn | Ala | Arg | Lys | Tyr |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Asn | Gly | Asn | Leu | Ile | Lys | Met | Met | Met | Ser | Lys | Lys | Met | Arg | Thr | Pro |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Arg | Pro | Glu | Cys | Asp | Leu | Thr | Ile | Phe | Val | Phe | Ala | Leu | Phe | Asn |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Glu | Asn | Met | Lys | Pro | Gly | Pro | Thr | Ser | Glu | Arg | Asn | Tyr | Gly | Leu | Phe |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |

Asn Pro Asp Gly Thr Pro Val Tyr Ser Leu Gly Ile Lys Thr Ser Ser  
340 345 350  
Thr His Ser Ser Gly Ser Gly Ser Ser Asn Ser Thr Gly Gly Ser Ser  
355 360 365  
Ser Gly Gly Gly Gly Asn Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile  
370 375 380  
Tyr Gln Pro Val Thr Gly Asn Pro Ser Pro Asp Tyr Met Ser Ile Ser  
385 390 395 400  
Ser Ala Gly Gly Lys Gly Arg Phe Val Glu Cys Val Leu Phe Phe Phe  
405 410 415  
Leu Leu Cys Ile Ile Lys Leu Arg Leu  
420 425

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1567136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Ser Asp Pro Ile Lys Ala Gln Gly Trp Val Lys Glu Asn Val Gln  
1 5 10 15  
Ala Tyr Leu Pro Asn Thr Lys Ile Val Ala Ile Val Val Gly Asn Glu  
20 25 30  
Val Leu Thr Ser Asn Gln Ser Ala Leu Thr Ala Ala Leu Phe Pro Ala  
35 40 45  
Met Gln Ser Ile His Gly Ala Leu Val Asp Cys Gly Leu Asn Lys Gln  
50 55 60  
Ile Phe Val Thr Thr Ala His Ser Leu Ala Ile Leu Asp Val Ser Tyr  
65 70 75 80  
Pro Pro Ser Ala Thr Ser Phe Arg Arg Asp Leu Leu Gly Ser Leu Thr  
85 90 95  
Pro Ile Leu Asp Phe His Val Lys Thr Gly Ser Pro Ile Leu Ile Asn  
100 105 110  
Ala Tyr Pro Phe Phe Ala Tyr Glu Glu Asn Pro Lys His Val Ser Leu  
115 120 125  
Asp Phe Val Leu Phe Gln Pro Asn Gln Gly Phe Thr Asp Pro Gly Ser  
130 135 140  
Asn Phe His Tyr Asp Asn Met Leu Phe Ala Gln Val Asp Ala Val Tyr  
145 150 155 160  
His Ala Leu Asp Ala Val Gly Ile Ser Tyr Lys Lys Val Pro Ile Val  
165 170 175  
Val Ser Glu Thr Gly Trp Pro Ser Asn Gly Asp Pro Gln Glu Val Gly  
180 185 190  
Ala Thr Cys Asp Asn Ala Arg Lys Tyr Asn Gly Asn Leu Ile Lys Met  
195 200 205  
Met Met Ser Lys Lys Met Arg Thr Pro Ile Arg Pro Glu Cys Asp Leu  
210 215 220  
Thr Ile Phe Val Phe Ala Leu Phe Asn Glu Asn Met Lys Pro Gly Pro  
225 230 235 240  
Thr Ser Glu Arg Asn Tyr Gly Leu Phe Asn Pro Asp Gly Thr Pro Val  
245 250 255  
Tyr Ser Leu Gly Ile Lys Thr Ser Ser Thr His Ser Ser Gly Ser Gly  
260 265 270  
Ser Ser Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Gly Asn Thr  
275 280 285  
Gly Gly Ser Ser Ser Gly Gly Gly Ile Tyr Gln Pro Val Thr Gly Asn

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 290                                                             | 295 | 300 |
| Pro Ser Pro Asp Tyr Met Ser Ile Ser Ser Ala Gly Gly Lys Gly Arg |     |     |
| 305                                                             | 310 | 315 |
| Phe Val Glu Cys Val Leu Phe Phe Phe Leu Leu Cys Ile Ile Lys Leu |     |     |
|                                                                 | 325 | 330 |
|                                                                 |     | 335 |

Arg Leu

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atcactaacc caaaaacaaa acaaaaaatg ggtttcattg gtaagagtgt attagtgagt | 60  |
| ctcgtagcac tttggtgctt cacttcctct gtcttcactg aagaagtga ccataagact  | 120 |
| caaaccctt ctctagctcc tggaaaggat acggcggtag aggtggcggt ggaggatgta  | 180 |
| ctatggattg taagaagaag tgtatcgctt attgttaaga tataataaag atcacatcat | 240 |
| ctttataata tatagtcatt atgatgggta tgtattttct atgttatagc ctatagatta | 300 |
| tgagatcatg aggatccttt tgtcttgatt cgattttag cagttttata tgcataatat  | 360 |
| atgggttgta tgaataaatg agggaacttt actgttttct ctattgtatg tttgtgtaag | 420 |
| agattctaag ttaaAttgtg                                             |     |

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Ile Thr Asn Pro Lys Thr Lys Gln Lys Met Gly Phe Ile Gly Lys Ser |    |
| 1                                                               | 5  |
| Val Leu Val Ser Leu Val Ala Leu Trp Cys Phe Thr Ser Ser Val Phe | 10 |
|                                                                 | 20 |
| Thr Glu Glu Val Asn His Lys Thr Gln Thr Pro Ser Leu Ala Pro Gly | 25 |
|                                                                 | 30 |
| Lys Asp Thr Ala Val Glu Val Ala Val Glu Asp Val Leu Trp Ile Val | 35 |
|                                                                 | 40 |
| Arg Arg Ser Val Ser Leu Ile Val Lys Ile                         | 45 |
| 65                                                              | 70 |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Met Gly Phe Ile Gly Lys Ser Val Leu Val Ser Leu Val Ala Leu Trp  
1 5 10 15  
Cys Phe Thr Ser Ser Val Phe Thr Glu Val Asn His Lys Thr Gln  
20 25 30  
Thr Pro Ser Leu Ala Pro Gly Lys Asp Thr Ala Val Glu Val Ala Val  
35 40 45  
Glu Asp Val Leu Trp Ile Val Arg Arg Ser Val Ser Leu Ile Val Lys  
50 55 60  
Ile  
65

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1560
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

aaaagctctg ttattcaaga ttattccgat aatgcagtca ctctccaccc cacacaccat 60  
ctctcttctt ctccccagaa cctctccgtc tcgtctttct cctctcttc actcccttgc 120  
tttccccact cgattacggg ctcttttcta ttctttctcaa acgtcgatcc tccccgatgc 180  
cggcgatgat ttcatgtgct gtgactgtct cgtctacgag gacggcgtct tcgaagaccc 240  
ttaccttgat aaggagggtca ctcaggttgc gaagcaggag cgcaagaaga atcggcgtgg 300  
cggggctaag agattagatg aatccgagat tgagcccag aacctcgtgc cagaggaatg 360  
gagggatatt caggcggagg tgaatctgac gaagaaggac aagcgcaaaa tagcgagga 420  
gatggagtgc ggggttcggg tggagaagaa gaggcaaggg ctaattccgc tgaggaaaagt 480  
tgacttgaat gacttttcta cgtacaagga agccaagttg gctcaattga ggcctgtcat 540  
tctcgataaaa cggggaaatt tctccgacga cagtggagcg tcaagcgatg gagagaccgc 600  
tgtatcatct cccagcgagc gagtggctcc taagaaccct agatgggcag tttacggaaa 660  
gggattcgac cacgttgcca agttcttcaa tagcgacaag tacgatccca gcgacaagaa 720  
atccgacggc cctcgaaagc tgcttttcaa agaagagaag tttatgctca atagccggaa 780  
tcttgacctt gccgttgcca catcaaaaaa atggcttctt cttcacacac tggcagcatg 840  
tgagagagtt tatctggttg attccttgc taaagcacaat cttgatatca atgcaaccga 900  
tgtgggcggc ttgacagtac ttaccgagc aatcattggg aagaagcagg ctattactaa 960  
ctacctgctg agggaaatcg caaatccatt tgttcttgat gacgaagggt cgaccttgat 1020  
gcactatgct gtgcaaacag catcagctcc cacaataaaa cttctcctac tgtataacgc 1080  
tgatataaac gctcaggaca gggacgggtg gactccactg cacgttgcat tacaggccag 1140  
aagaagcgac attgtaaagc ttcttttgat aaaaggggcg gacatagaag tgaagaacaa 1200  
ggatgggtta actccgcttg ggctttgcct ctaccttgga agagagataa ggacgtatgC 1260  
aggatgatgaa gctgttgaaa gagtttccac ttagcagaca caagaagaga ttggttaacaa 1320  
cagCatgaag atattgaata gtcctttcaa tttcagcttg aagtacactc acttatgaga 1380  
acctgagaaa aggagatgga ggtaaagggt atgattaggg cattggaacc tcggagtcgg 1440  
agtgggtcca ctgtctcact tccttaaatt tggtttgctg ttagtcttat ccatcgattt 1500  
tggatattta tcacaacttg atccattctt aaagaaaata tctgaaaata aataaaaagt 1560

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..430
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```

Lys Ala Leu Leu Phe Lys Ile Ile Pro Ile Met Gln Ser Leu Ser Thr
1 5 10 15
Pro His Thr Ile Ser Leu Leu Leu Pro Arg Thr Ser Pro Ser Arg Leu
20 25 30
Ser Pro Ser Leu His Ser Leu Ala Phe Pro Thr Arg Leu Arg Ser Leu
35 40 45
Ser Tyr Ser Ser Gln Thr Ser Ile Leu Pro Asp Ala Gly Asp Asp Phe
50 55 60
Ile Val Gly Asp Cys Leu Val Tyr Glu Asp Gly Val Phe Glu Asp Pro
65 70 75 80
Tyr Leu Asp Lys Glu Val Thr Gln Val Ala Lys Gln Glu Arg Lys Lys
85 90 95
Asn Arg Arg Gly Gly Ala Lys Arg Leu Asp Glu Ser Glu Ile Glu Pro
100 105 110
Glu Asn Leu Val Pro Glu Glu Trp Arg Asp Ile Gln Ala Glu Val Asn
115 120 125
Leu Thr Lys Lys Asp Lys Arg Lys Ile Ala Gln Glu Met Glu Phe Gly
130 135 140
Val Arg Val Glu Lys Lys Arg Gln Gly Leu Ile Pro Leu Arg Lys Val
145 150 155 160
Asp Leu Asn Asp Phe Leu Thr Tyr Lys Glu Ala Lys Leu Ala Gln Leu
165 170 175
Arg Pro Val Ile Leu Asp Lys Pro Gly Asn Phe Ser Asp Asp Ser Gly
180 185 190
Ala Ser Ser Asp Gly Glu Thr Ala Val Ser Ser Pro Ser Glu Arg Val
195 200 205
Ala Pro Lys Asn Pro Arg Trp Ala Val Tyr Gly Lys Gly Phe Asp His
210 215 220
Val Ala Lys Phe Phe Asn Ser Asp Lys Tyr Asp Pro Ser Asp Lys Lys
225 230 235 240
Ser Asp Gly Pro Arg Lys Leu Leu Ser Lys Glu Glu Lys Phe Met Leu
245 250 255
Asn Ser Arg Asn Pro Asp Leu Ala Val Ala Thr Ser Lys Lys Trp Leu
260 265 270
Pro Leu His Thr Leu Ala Ala Cys Gly Glu Phe Tyr Leu Val Asp Ser
275 280 285
Leu Leu Lys His Asn Leu Asp Ile Asn Ala Thr Asp Val Gly Gly Leu
290 295 300
Thr Val Leu His Arg Ala Ile Ile Gly Lys Lys Gln Ala Ile Thr Asn
305 310 315 320
Tyr Leu Leu Arg Glu Ser Ala Asn Pro Phe Val Leu Asp Asp Glu Gly
325 330 335
Ala Thr Leu Met His Tyr Ala Val Gln Thr Ala Ser Ala Pro Thr Ile
340 345 350
Lys Leu Leu Leu Leu Tyr Asn Ala Asp Ile Asn Ala Gln Asp Arg Asp
355 360 365
Gly Trp Thr Pro Leu His Val Ala Val Gln Ala Arg Arg Ser Asp Ile
370 375 380
Val Lys Leu Leu Leu Ile Lys Gly Ala Asp Ile Glu Val Lys Asn Lys
385 390 395 400
Asp Gly Leu Thr Pro Leu Gly Leu Cys Leu Tyr Leu Gly Arg Glu Ile
405 410 415
Arg Thr Tyr Ala Gly Asp Glu Ala Val Glu Arg Val Ser Thr
420 425 430

```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1567166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Met Gln Ser Leu Ser Thr Pro His Thr Ile Ser Leu Leu Leu Pro Arg  
1 5 10 15  
Thr Ser Pro Ser Arg Leu Ser Pro Ser Leu His Ser Leu Ala Phe Pro  
20 25 30  
Thr Arg Leu Arg Ser Leu Ser Tyr Ser Ser Gln Thr Ser Ile Leu Pro  
35 40 45  
Asp Ala Gly Asp Asp Phe Ile Val Gly Asp Cys Leu Val Tyr Glu Asp  
50 55 60  
Gly Val Phe Glu Asp Pro Tyr Leu Asp Lys Glu Val Thr Gln Val Ala  
65 70 75 80  
Lys Gln Glu Arg Lys Lys Asn Arg Arg Gly Gly Ala Lys Arg Leu Asp  
85 90 95  
Glu Ser Glu Ile Glu Pro Glu Asn Leu Val Pro Glu Glu Trp Arg Asp  
100 105 110  
Ile Gln Ala Glu Val Asn Leu Thr Lys Lys Asp Lys Arg Lys Ile Ala  
115 120 125  
Gln Glu Met Glu Phe Gly Val Arg Val Glu Lys Lys Arg Gln Gly Leu  
130 135 140  
Ile Pro Leu Arg Lys Val Asp Leu Asn Asp Phe Leu Thr Tyr Lys Glu  
145 150 155 160  
Ala Lys Leu Ala Gln Leu Arg Pro Val Ile Leu Asp Lys Pro Gly Asn  
165 170 175  
Phe Ser Asp Asp Ser Gly Ala Ser Ser Asp Gly Glu Thr Ala Val Ser  
180 185 190  
Ser Pro Ser Glu Arg Val Ala Pro Lys Asn Pro Arg Trp Ala Val Tyr  
195 200 205  
Gly Lys Gly Phe Asp His Val Ala Lys Phe Phe Asn Ser Asp Lys Tyr  
210 215 220  
Asp Pro Ser Asp Lys Lys Ser Asp Gly Pro Arg Lys Leu Leu Ser Lys  
225 230 235 240  
Glu Glu Lys Phe Met Leu Asn Ser Arg Asn Pro Asp Leu Ala Val Ala  
245 250 255  
Thr Ser Lys Lys Trp Leu Pro Leu His Thr Leu Ala Ala Cys Gly Glu  
260 265 270  
Phe Tyr Leu Val Asp Ser Leu Leu Lys His Asn Leu Asp Ile Asn Ala  
275 280 285  
Thr Asp Val Gly Gly Leu Thr Val Leu His Arg Ala Ile Ile Gly Lys  
290 295 300  
Lys Gln Ala Ile Thr Asn Tyr Leu Leu Arg Glu Ser Ala Asn Pro Phe  
305 310 315 320  
Val Leu Asp Asp Glu Gly Ala Thr Leu Met His Tyr Ala Val Gln Thr  
325 330 335  
Ala Ser Ala Pro Thr Ile Lys Leu Leu Leu Leu Tyr Asn Ala Asp Ile  
340 345 350  
Asn Ala Gln Asp Arg Asp Gly Trp Thr Pro Leu His Val Ala Val Gln  
355 360 365  
Ala Arg Arg Ser Asp Ile Val Lys Leu Leu Leu Ile Lys Gly Ala Asp  
370 375 380  
Ile Glu Val Lys Asn Lys Asp Gly Leu Thr Pro Leu Gly Leu Cys Leu  
385 390 395 400  
Tyr Leu Gly Arg Glu Ile Arg Thr Tyr Ala Gly Asp Glu Ala Val Glu  
405 410 415  
Arg Val Ser Thr  
420

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..290
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1567167
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```

Met Glu Phe Gly Val Arg Val Glu Lys Lys Arg Gln Gly Leu Ile Pro
1 5 10 15
Leu Arg Lys Val Asp Leu Asn Asp Phe Leu Thr Tyr Lys Glu Ala Lys
20 25 30
Leu Ala Gln Leu Arg Pro Val Ile Leu Asp Lys Pro Gly Asn Phe Ser
35 40 45
Asp Asp Ser Gly Ala Ser Ser Asp Gly Glu Thr Ala Val Ser Ser Pro
50 55 60
Ser Glu Arg Val Ala Pro Lys Asn Pro Arg Trp Ala Val Tyr Gly Lys
65 70 75 80
Gly Phe Asp His Val Ala Lys Phe Phe Asn Ser Asp Lys Tyr Asp Pro
85 90 95
Ser Asp Lys Lys Ser Asp Gly Pro Arg Lys Leu Leu Ser Lys Glu Glu
100 105 110
Lys Phe Met Leu Asn Ser Arg Asn Pro Asp Leu Ala Val Ala Thr Ser
115 120 125
Lys Lys Trp Leu Pro Leu His Thr Leu Ala Ala Cys Gly Glu Phe Tyr
130 135 140
Leu Val Asp Ser Leu Leu Lys His Asn Leu Asp Ile Asn Ala Thr Asp
145 150 155 160
Val Gly Gly Leu Thr Val Leu His Arg Ala Ile Ile Gly Lys Lys Gln
165 170 175
Ala Ile Thr Asn Tyr Leu Leu Arg Glu Ser Ala Asn Pro Phe Val Leu
180 185 190
Asp Asp Glu Gly Ala Thr Leu Met His Tyr Ala Val Gln Thr Ala Ser
195 200 205
Ala Pro Thr Ile Lys Leu Leu Leu Tyr Asn Ala Asp Ile Asn Ala
210 215 220
Gln Asp Arg Asp Gly Trp Thr Pro Leu His Val Ala Val Gln Ala Arg
225 230 235 240
Arg Ser Asp Ile Val Lys Leu Leu Leu Ile Lys Gly Ala Asp Ile Glu
245 250 255
Val Lys Asn Lys Asp Gly Leu Thr Pro Leu Gly Leu Cys Leu Tyr Leu
260 265 270
Gly Arg Glu Ile Arg Thr Tyr Ala Gly Asp Glu Ala Val Glu Arg Val
275 280 285
Ser Thr
290

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(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1257 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1257
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1567168
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

agattctttc ttctaaaccc attcgctctc tccgatcaac acaacatttg atctaacggt

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| ttaatttttct | cgagaaaccg | aagGaaaaca | aacagagcaa | tggcgtcgat  | gggacgggtgc | 120  |
| ctgagctgaa  | attgagagtc | gaagaagatt | ccgataatgg | tgattatctg  | aaattgagag  | 180  |
| gaggatcaaa  | tgaagaagat | gaaggatcat | cggcggaatc | atcgagatgt  | ccgataggat  | 240  |
| cggttacttc  | tgtctggttc | tgggtgaaat | tgatctcctt | ggtcgtttgt  | ttgggttcac  | 300  |
| tggcctttgt  | tatcatcaaa | tgggttggtc | cctttttgat | tgaaaaggag  | ctgattccat  | 360  |
| ttataaattg  | ggtgagaaac | acattcagca | taccggttct | cggctcttcta | ctatttgcct  | 420  |
| cagtggcatt  | gtttccaagc | attcttcttc | cttcttcccc | ttccatgtgg  | atggctggtc  | 480  |
| ttacatttgg  | ttatggaaaa | gggtttcttc | tgattttatc | agctgcttcc  | atcgggtgta  | 540  |
| ctcttccttt  | cttaattgga | catctcttcc | tccacaagat | gcaagaatgg  | ttgaagaaat  | 600  |
| accctaaaaa  | agcagccata | cttagagctg | ctggtgaagg | aacctggttt  | catcagtttc  | 660  |
| aagcagtcac  | actaatccgt | gtctctccat | ttccttacat | catttacaac  | tactgcgctt  | 720  |
| tagcgactgg  | agttcattat | ggtccttata | tcttaggctc | tcttggttga  | atggttcctg  | 780  |
| agatctttgt  | ctcaatttac | acgggtataa | tgctaaggac | actagcagtt  | gcatcagaca  | 840  |
| cgagacacac  | actttcgggt | gtggagatag | tcgtgaatgt | tcttggtctc  | tgtgtaactg  | 900  |
| cgagcgcgac  | tatagtctgc | acaatctatg | cgaagaagaa | gctaagtgcg  | atgcaatcag  | 960  |
| aggacgtaga  | gacattacaa | aatccaatac | tttattaact | cttttcacca  | tgaccacaac  | 1020 |
| ataccatcat  | ctaacacgat | cttgaaattg | ataatatata | atgttttttt  | tttttttttg  | 1080 |
| ttattcttat  | tcatttgaaa | atgaatattt | atgtcttttt | ctcttgata   | tatgatatgt  | 1140 |
| atcaattgaa  | ttttgaaaat | ttccaatgta | tatttattag | atcatctaag  | tctttttctt  | 1200 |
| tccttgcata  | taatccacct | tatgtatcat | ggaacaatgt | cttggtgggt  | tttggttc    |      |

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1567169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Met | Ala | Gly | Leu | Thr | Phe | Gly | Tyr | Gly | Lys | Gly | Phe | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Leu | Ser | Ala | Ala | Ser | Ile | Gly | Val | Thr | Leu | Pro | Phe | Leu | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| His | Leu | Phe | Leu | His | Lys | Met | Gln | Glu | Trp | Leu | Lys | Lys | Tyr | Pro | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ala | Ala | Ile | Leu | Arg | Ala | Ala | Gly | Glu | Gly | Thr | Trp | Phe | His | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Gln | Ala | Val | Thr | Leu | Ile | Arg | Val | Ser | Pro | Phe | Pro | Tyr | Ile | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Asn | Tyr | Cys | Ala | Leu | Ala | Thr | Gly | Val | His | Tyr | Gly | Pro | Tyr | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Gly | Ser | Leu | Val | Gly | Met | Val | Pro | Glu | Ile | Phe | Val | Ser | Ile | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Thr | Gly | Ile | Met | Leu | Arg | Thr | Leu | Ala | Val | Ala | Ser | Asp | Thr | Arg | His |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Leu | Ser | Val | Val | Glu | Ile | Val | Val | Asn | Val | Leu | Gly | Phe | Cys | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Thr | Ala | Ser | Ala | Thr | Ile | Val | Cys | Thr | Ile | Tyr | Ala | Lys | Lys | Lys | Leu |
|     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ala | Met | Gln | Ser | Glu | Asp | Val | Glu | Thr | Leu | Gln | Asn | Pro | Ile | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |

Tyr

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Leu | Thr | Phe | Gly | Tyr | Gly | Lys | Gly | Phe | Leu | Leu | Ile | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ala | Ala | Ser | Ile | Gly | Val | Thr | Leu | Pro | Phe | Leu | Ile | Gly | His | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Leu | His | Lys | Met | Gln | Glu | Trp | Leu | Lys | Lys | Tyr | Pro | Lys | Lys | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ile | Leu | Arg | Ala | Ala | Gly | Glu | Gly | Thr | Trp | Phe | His | Gln | Phe | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Val | Thr | Leu | Ile | Arg | Val | Ser | Pro | Phe | Pro | Tyr | Ile | Ile | Tyr | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Cys | Ala | Leu | Ala | Thr | Gly | Val | His | Tyr | Gly | Pro | Tyr | Ile | Leu | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Val | Gly | Met | Val | Pro | Glu | Ile | Phe | Val | Ser | Ile | Tyr | Thr | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Met | Leu | Arg | Thr | Leu | Ala | Val | Ala | Ser | Asp | Thr | Arg | His | Thr | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Val | Glu | Ile | Val | Val | Asn | Val | Leu | Gly | Phe | Cys | Val | Thr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ala | Thr | Ile | Val | Cys | Thr | Ile | Tyr | Ala | Lys | Lys | Lys | Leu | Ser | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Gln | Ser | Glu | Asp | Val | Glu | Thr | Leu | Gln | Asn | Pro | Ile | Leu | Tyr |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 139 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1567171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Glu | Trp | Leu | Lys | Lys | Tyr | Pro | Lys | Lys | Ala | Ala | Ile | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Gly | Glu | Gly | Thr | Trp | Phe | His | Gln | Phe | Gln | Ala | Val | Thr | Leu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Arg | Val | Ser | Pro | Phe | Pro | Tyr | Ile | Ile | Tyr | Asn | Tyr | Cys | Ala | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ala | Thr | Gly | Val | His | Tyr | Gly | Pro | Tyr | Ile | Leu | Gly | Ser | Leu | Val | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Val | Pro | Glu | Ile | Phe | Val | Ser | Ile | Tyr | Thr | Gly | Ile | Met | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Leu | Ala | Val | Ala | Ser | Asp | Thr | Arg | His | Thr | Leu | Ser | Val | Val | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Val | Val | Asn | Val | Leu | Gly | Phe | Cys | Val | Thr | Ala | Ser | Ala | Thr | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Cys | Thr | Ile | Tyr | Ala | Lys | Lys | Lys | Leu | Ser | Ala | Met | Gln | Ser | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asp | Val | Glu | Thr | Leu | Gln | Asn | Pro | Ile | Leu | Tyr |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1592  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567172  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

gtagtctctc tttttataac cacttctcga aaactgaaac cttttagtag agaaccata 60  
gttcgataaa acattctttt tgcaactgag acttggaac ttggttttac tcaaagtaag 120  
atttcttctt gttgatggtg ataagttcaa tatgatgaaa agtttggcta gtgcggttgg 180  
agggaagacg gcgagggcat gtgatagctg cgtgaagagg cgggcacgtt ggtattgcgc 240  
aGctgatgat gcctttcttt gccatgcttg tgacggttcg gtccactcgg caaacctct 300  
tgctcgtaga cacgagagag ttcgcttgaa atcggttagc gccggaaaat atcgccatgc 360  
ctcgccgcct caccaagcca cgtggcatca gggatttaca cgtaaagctc ggacccacg 420  
tgagggcaag aagagccaca cgatggtttt tcatgatctt gtgccggaga tgagcacgga 480  
ggatcaagcg gagagttacg aggtggaaga gcagctcata tttgaggtgc cggatgatgaa 540  
ctcgatggtt gaggagcaat gctttaacca atccctggag aaacagaatg agtttccaat 600  
gatgccctta agtttcaaga gtagtgacga agaagatgac gacaacgctg agagttgtct 660  
gaatggtttg ttoccaaccg acatggaact agctcagttc acagctgacg tggagactct 720  
actcggtgga ggggatcgag agtttcattc catagaagaa ctagggttag gtgagatggt 780  
aaagatcgaa aaagaggagg tggaggaaga ggaaggagtt gtgacaagag aagtgcata 840  
tcaagatgaa ggtgatgaga catccccatt tgaataaagc tttgactacg agtacacaca 900  
caagaccaca ttogatgaag gagaagaaga tgagaaagaa gacgtgatga agaattgtgat 960  
ggagatggga gtgaatgaga tgagtggtag gattaaagaa gagaagaagg agaaggctct 1020  
tatgcttaga ttggactatg aatcagtcct ttccacttgg ggaggccaag ggatcccatg 1080  
gaccgcccgg gtgccatctg aaatagacct cgacatggtt tgtttcccaa cccataccat 1140  
gggtgaaagt ggagcagagg ctcacatca caaccacttc cgcggcctaG ggttacacct 1200  
aggagatgct ggggatggag gaagagaggc tagggtttca agataccgag agaaaaggag 1260  
gacaagggtt ttctccaaga agataaggta cgaggtagct aaattgaatg cagataaaag 1320  
gcctcgcatg aaaggaaggt tcgtcaagag atcttcaatt ggtgttgctc actaaagaac 1380  
ttaattaatt atggatatta aattactttg ctctcatctt gcttttttgt tgctatagtt 1440  
ttgggtgatt ttagctttct tttctgcat tcatagagaa ttttgcacgt tttgtgagc 1500  
tacgtatgta cataaatata tcacaaaaaa atgtgactat cttgtaagca ctgatttata 1560  
tagtcgatat aacgtgaatt ttgattgctg gt

- (2) INFORMATION FOR SEQ ID NO:511:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 407 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..407  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567173  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

Met Met Lys Ser Leu Ala Ser Ala Val Gly Gly Lys Thr Ala Arg Ala  
1 5 10 15  
Cys Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp  
20 25 30  
Asp Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn  
35 40 45  
Pro Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala  
50 55 60  
Gly Lys Tyr Arg His Ala Ser Pro Pro His Gln Ala Thr Trp His Gln  
65 70 75 80  
Gly Phe Thr Arg Lys Ala Arg Thr Pro Arg Gly Gly Lys Lys Ser His  
85 90 95

```

Thr Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln
 100 105 110
Ala Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val
 115 120 125
Met Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys
 130 135 140
Gln Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu
 145 150 155 160
Glu Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr
 165 170 175
Asp Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly
 180 185 190
Gly Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu
 195 200 205
Met Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Glu Gly Val Val
 210 215 220
Thr Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe
 225 230 235 240
Glu Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu
 245 250 255
Gly Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met
 260 265 270
Gly Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys
 275 280 285
Ala Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly
 290 295 300
Gly Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu
 305 310 315 320
Asp Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu
 325 330 335
Ala His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp
 340 345 350
Ala Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys
 355 360 365
Arg Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys
 370 375 380
Leu Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg
 385 390 395 400
Ser Ser Ile Gly Val Ala His
 405

```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1567174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

Met Lys Ser Leu Ala Ser Ala Val Gly Gly Lys Thr Ala Arg Ala Cys
1 5 10 15
Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp Asp
 20 25 30
Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn Pro
 35 40 45
Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala Gly
 50 55 60
Lys Tyr Arg His Ala Ser Pro Pro His Gln Ala Thr Trp His Gln Gly

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Thr | Arg | Lys | Ala | Arg | Thr | Pro | Arg | Gly | Gly | Lys | Lys | Ser | His | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Val | Phe | His | Asp | Leu | Val | Pro | Glu | Met | Ser | Thr | Glu | Asp | Gln | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ser | Tyr | Glu | Val | Glu | Glu | Gln | Leu | Ile | Phe | Glu | Val | Pro | Val | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ser | Met | Val | Glu | Glu | Gln | Cys | Phe | Asn | Gln | Ser | Leu | Glu | Lys | Gln |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Glu | Phe | Pro | Met | Met | Pro | Leu | Ser | Phe | Lys | Ser | Ser | Asp | Glu | Glu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Asp | Asp | Asn | Ala | Glu | Ser | Cys | Leu | Asn | Gly | Leu | Phe | Pro | Thr | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Glu | Leu | Ala | Gln | Phe | Thr | Ala | Asp | Val | Glu | Thr | Leu | Leu | Gly | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asp | Arg | Glu | Phe | His | Ser | Ile | Glu | Glu | Leu | Gly | Leu | Gly | Glu | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Lys | Ile | Glu | Lys | Glu | Glu | Val | Glu | Glu | Glu | Glu | Gly | Val | Val | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Arg | Glu | Val | His | Asp | Gln | Asp | Glu | Gly | Asp | Glu | Thr | Ser | Pro | Phe | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Ser | Phe | Asp | Tyr | Glu | Tyr | Thr | His | Lys | Thr | Thr | Phe | Asp | Glu | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Glu | Asp | Glu | Lys | Glu | Asp | Val | Met | Lys | Asn | Val | Met | Glu | Met | Gly |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Asn | Glu | Met | Ser | Gly | Gly | Ile | Lys | Glu | Glu | Lys | Lys | Glu | Lys | Ala |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Leu | Met | Leu | Arg | Leu | Asp | Tyr | Glu | Ser | Val | Ile | Ser | Thr | Trp | Gly | Gly |
|     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |     |
| Gln | Gly | Ile | Pro | Trp | Thr | Ala | Arg | Val | Pro | Ser | Glu | Ile | Asp | Leu | Asp |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |
| Met | Val | Cys | Phe | Pro | Thr | His | Thr | Met | Gly | Glu | Ser | Gly | Ala | Glu | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | His | His | Asn | His | Phe | Arg | Gly | Leu | Gly | Leu | His | Leu | Gly | Asp | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Asp | Gly | Gly | Arg | Glu | Ala | Arg | Val | Ser | Arg | Tyr | Arg | Glu | Lys | Arg |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Arg | Thr | Arg | Leu | Phe | Ser | Lys | Ile | Arg | Tyr | Glu | Val | Arg | Lys | Leu |     |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Asn | Ala | Asp | Lys | Arg | Pro | Arg | Met | Lys | Gly | Arg | Phe | Val | Lys | Arg | Ser |
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     |     | 400 |
| Ser | Ile | Gly | Val | Ala | His |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 405 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1567175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | His | Asp | Leu | Val | Pro | Glu | Met | Ser | Thr | Glu | Asp | Gln | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Glu | Ser | Tyr | Glu | Val | Glu | Glu | Gln | Leu | Ile | Phe | Glu | Val | Pro | Val | Met |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Ser | Met | Val | Glu | Glu | Gln | Cys | Phe | Asn | Gln | Ser | Leu | Glu | Lys | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu Glu  
50 55 60  
Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr Asp  
65 70 75 80  
Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly Gly  
85 90 95  
Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu Met  
100 105 110  
Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Glu Gly Val Val Thr  
115 120 125  
Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu  
130 135 140  
Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly  
145 150 155 160  
Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly  
165 170 175  
Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys Ala  
180 185 190  
Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly  
195 200 205  
Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp  
210 215 220  
Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala  
225 230 235 240  
His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala  
245 250 255  
Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg  
260 265 270  
Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu  
275 280 285  
Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser  
290 295 300  
Ser Ile Gly Val Ala His  
305 310

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1071
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atttgtttag | tggtaatcaa | atccggtgaa | aatggagcgg | aGccgagtga  | ccagagaagc  | 60  |
| accgaccgga | accaggatcc | tgcttgcttc | actctctgcg | atgggtgcag  | agtcagttac  | 120 |
| gtttccgatt | gatctcacia | agactagaat | gcagctccat | ggttcgggat  | ccgcttctgg  | 180 |
| tgcgcatcgg | attggcgctt | tcggagtcgt | atcggagatt | gcgagaaagg  | aaggagtgat  | 240 |
| tggtctctac | aaaggtctat | ctccggcgat | tatcagacac | ctgttctaca  | cgcctatcag  | 300 |
| aatcattgga | tacgagaatt | tgaaaggact | catcgtcaga | tctgaaacta  | acaatagcga  | 360 |
| gtctcttctc | ctcgccacaa | aggctctcgt | cggaggattt | tctggtgtta  | tagctcaggt  | 420 |
| agtggctagt | ccagctgatt | tggtcaaagt | gagaatgcaa | gcagatggta  | gattgggtgag | 480 |
| ccaaggcctg | aaaccgaggt | actcgggacc | aatcgaggct | tttaccaaaa  | tcctacaatc  | 540 |
| agaaggagta | aaagggttat | ggaaagggtg | tcttccaaac | atccagagag  | catttctagt  | 600 |
| gaatatggga | gaactagctt | gctatgatca | cgccaaacac | tttgtcatcg  | ataagaagat  | 660 |
| tgctgaggat | aacatttttg | cgcacactct | tgcttctata | atgtccgggtc | ttgcttcgac  | 720 |
| aagtttgagt | tgtccagctg | atgtggtgaa | gacgaggatg | atgaaccagg  | gtgaaaatgc  | 780 |
| tgtgtacaga | aattcttacg | actgtttggt | gaagacggtt | aagtttgaag  | gaataagagc  | 840 |
| tttgtgga   | ggtttcttcc | cgacatgggc | aaggcttgga | ccgtggcagt  | tcgtgttttg  | 900 |

gggtctcctat gagaagttta gactgctggc aggaatctct tccttctaga cctgagaaac 960  
tggaagaaagca aatttgagat ttgtgttctt tagttcttac ttgttagttg ttacacattt 1020  
tgtaagaacc ttgagaagta gcatcagttt ctgattaacg cgagaagagt t

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1567184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Glu Arg Ser Arg Val Thr Arg Glu Ala Pro Thr Gly Thr Arg Ile  
1 5 10 15  
Leu Leu Ala Ser Leu Ser Ala Met Val Ala Glu Ser Val Thr Phe Pro  
20 25 30  
Ile Asp Leu Thr Lys Thr Arg Met Gln Leu His Gly Ser Gly Ser Ala  
35 40 45  
Ser Gly Ala His Arg Ile Gly Ala Phe Gly Val Val Ser Glu Ile Ala  
50 55 60  
Arg Lys Glu Gly Val Ile Gly Leu Tyr Lys Gly Leu Ser Pro Ala Ile  
65 70 75 80  
Ile Arg His Leu Phe Tyr Thr Pro Ile Arg Ile Ile Gly Tyr Glu Asn  
85 90 95  
Leu Lys Gly Leu Ile Val Arg Ser Glu Thr Asn Asn Ser Glu Ser Leu  
100 105 110  
Pro Leu Ala Thr Lys Ala Leu Val Gly Gly Phe Ser Gly Val Ile Ala  
115 120 125  
Gln Val Val Ala Ser Pro Ala Asp Leu Val Lys Val Arg Met Gln Ala  
130 135 140  
Asp Gly Arg Leu Val Ser Gln Gly Leu Lys Pro Arg Tyr Ser Gly Pro  
145 150 155 160  
Ile Glu Ala Phe Thr Lys Ile Leu Gln Ser Glu Gly Val Lys Gly Leu  
165 170 175  
Trp Lys Gly Val Leu Pro Asn Ile Gln Arg Ala Phe Leu Val Asn Met  
180 185 190  
Gly Glu Leu Ala Cys Tyr Asp His Ala Lys His Phe Val Ile Asp Lys  
195 200 205  
Lys Ile Ala Glu Asp Asn Ile Phe Ala His Thr Leu Ala Ser Ile Met  
210 215 220  
Ser Gly Leu Ala Ser Thr Ser Leu Ser Cys Pro Ala Asp Val Val Lys  
225 230 235 240  
Thr Arg Met Met Asn Gln Gly Glu Asn Ala Val Tyr Arg Asn Ser Tyr  
245 250 255  
Asp Cys Leu Val Lys Thr Val Lys Phe Glu Gly Ile Arg Ala Leu Trp  
260 265 270  
Lys Gly Phe Phe Pro Thr Trp Ala Arg Leu Gly Pro Trp Gln Phe Val  
275 280 285  
Phe Trp Val Ser Tyr Glu Lys Phe Arg Leu Leu Ala Gly Ile Ser Ser  
290 295 300  
Phe  
305

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..282  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567185  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Met Val Ala Glu Ser Val Thr Phe Pro Ile Asp Leu Thr Lys Thr Arg  
1                    5                    10                    15  
Met Gln Leu His Gly Ser Gly Ser Ala Ser Gly Ala His Arg Ile Gly  
                    20                    25                    30  
Ala Phe Gly Val Val Ser Glu Ile Ala Arg Lys Glu Gly Val Ile Gly  
                    35                    40                    45  
Leu Tyr Lys Gly Leu Ser Pro Ala Ile Ile Arg His Leu Phe Tyr Thr  
50                    55                    60  
Pro Ile Arg Ile Ile Gly Tyr Glu Asn Leu Lys Gly Leu Ile Val Arg  
65                    70                    75                    80  
Ser Glu Thr Asn Asn Ser Glu Ser Leu Pro Leu Ala Thr Lys Ala Leu  
                    85                    90                    95  
Val Gly Gly Phe Ser Gly Val Ile Ala Gln Val Val Ala Ser Pro Ala  
                    100                    105                    110  
Asp Leu Val Lys Val Arg Met Gln Ala Asp Gly Arg Leu Val Ser Gln  
115                    120                    125  
Gly Leu Lys Pro Arg Tyr Ser Gly Pro Ile Glu Ala Phe Thr Lys Ile  
130                    135                    140  
Leu Gln Ser Glu Gly Val Lys Gly Leu Trp Lys Gly Val Leu Pro Asn  
145                    150                    155                    160  
Ile Gln Arg Ala Phe Leu Val Asn Met Gly Glu Leu Ala Cys Tyr Asp  
                    165                    170                    175  
His Ala Lys His Phe Val Ile Asp Lys Lys Ile Ala Glu Asp Asn Ile  
180                    185                    190  
Phe Ala His Thr Leu Ala Ser Ile Met Ser Gly Leu Ala Ser Thr Ser  
195                    200                    205  
Leu Ser Cys Pro Ala Asp Val Val Lys Thr Arg Met Met Asn Gln Gly  
210                    215                    220  
Glu Asn Ala Val Tyr Arg Asn Ser Tyr Asp Cys Leu Val Lys Thr Val  
225                    230                    235                    240  
Lys Phe Glu Gly Ile Arg Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp  
                    245                    250                    255  
Ala Arg Leu Gly Pro Trp Gln Phe Val Phe Trp Val Ser Tyr Glu Lys  
260                    265                    270  
Phe Arg Leu Leu Ala Gly Ile Ser Ser Phe  
275                    280

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 266 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..266  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567186  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Gln Leu His Gly Ser Gly Ser Ala Ser Gly Ala His Arg Ile Gly  
1                    5                    10                    15  
Ala Phe Gly Val Val Ser Glu Ile Ala Arg Lys Glu Gly Val Ile Gly  
                    20                    25                    30  
Leu Tyr Lys Gly Leu Ser Pro Ala Ile Ile Arg His Leu Phe Tyr Thr  
35                    40                    45  
Pro Ile Arg Ile Ile Gly Tyr Glu Asn Leu Lys Gly Leu Ile Val Arg

50 55 60  
Ser Glu Thr Asn Asn Ser Glu Ser Leu Pro Leu Ala Thr Lys Ala Leu  
65 70 75 80  
Val Gly Gly Phe Ser Gly Val Ile Ala Gln Val Val Ala Ser Pro Ala  
85 90 95  
Asp Leu Val Lys Val Arg Met Gln Ala Asp Gly Arg Leu Val Ser Gln  
100 105 110  
Gly Leu Lys Pro Arg Tyr Ser Gly Pro Ile Glu Ala Phe Thr Lys Ile  
115 120 125  
Leu Gln Ser Glu Gly Val Lys Gly Leu Trp Lys Gly Val Leu Pro Asn  
130 135 140  
Ile Gln Arg Ala Phe Leu Val Asn Met Gly Glu Leu Ala Cys Tyr Asp  
145 150 155 160  
His Ala Lys His Phe Val Ile Asp Lys Lys Ile Ala Glu Asp Asn Ile  
165 170 175  
Phe Ala His Thr Leu Ala Ser Ile Met Ser Gly Leu Ala Ser Thr Ser  
180 185 190  
Leu Ser Cys Pro Ala Asp Val Val Lys Thr Arg Met Met Asn Gln Gly  
195 200 205  
Glu Asn Ala Val Tyr Arg Asn Ser Tyr Asp Cys Leu Val Lys Thr Val  
210 215 220  
Lys Phe Glu Gly Ile Arg Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp  
225 230 235 240  
Ala Arg Leu Gly Pro Trp Gln Phe Val Phe Trp Val Ser Tyr Glu Lys  
245 250 255  
Phe Arg Leu Leu Ala Gly Ile Ser Ser Phe  
260 265

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| gtcgtgtcat | cgttttctca  | gattcctgaa | taatcattcc | cttccgattc | caaaatcccc | 60   |
| aaacctcatc | cactcctcca  | tctcccggat | tcggattccc | agaatcatgc | ccatggagaa | 120  |
| cgacaatggc | ccacacgttg  | gcaacgtcgt | cgtcaccgct | gagcaagcga | ccaagattaa | 180  |
| cgagactgat | ggacggttgc  | cggagaatcg | gcagaccggt | gttgtctctg | acaccggaag | 240  |
| tggtagcgag | agaggagagc  | aaggggttgg | agagtcggca | gttgctgtgg | cggtgccggt | 300  |
| ggaggagagc | ggatcgattt  | cggtgggaga | gctacctgct | ccccgatctt | cctctgctag | 360  |
| agttccgttt | actaatctaa  | gccaaattga | tgcggatctt | gctcttgctc | gcacactcca | 420  |
| agaacaggag | cgggcgtata  | tgatgttgac | catgaatagt | gaaatcagtg | actatgggag | 480  |
| ctgggaaact | ggaagctatg  | tatacgatga | ggatgagttt | gatgaccccg | agaatgagga | 540  |
| tgaggatgat | gatgaagatg  | aatatgaaac | agatgatgat | cctcaggaag | atgggcttga | 600  |
| tgtcaatgtg | cacgccaatg  | aagatgatca | agaagatgac | ggtAactctg | acattgaaga | 660  |
| agttgcttat | acagatgatg  | aggcctatgc | tagagctctt | caagaagctg | aagaaaggga | 720  |
| tatggctgct | agattgtctg  | ccttatctgg | gttagcaaac | cgggtgggtt | aagatctaga | 780  |
| ggatgagagt | catactttctc | aggatgccag | ggatgagatg | gatcctgatg | agctttcata | 840  |
| tgaggagttg | cttgcacttg  | gcgacattgt | gggaaccgaa | agtagaggat | tgtctgctga | 900  |
| tacaattgca | tctttgcctt  | caaaaagata | taaagaagga | gacaatcaga | acggaaccaa | 960  |
| tgagtcagt  | gttatatgtc  | gtttagacta | tgaggatgac | gaagacctga | tactgctccc | 1020 |
| atgcaaacat | tcttaccact  | cggagtgcac | aaacaactgg | ttgaagataa | ataaggtttg | 1080 |
| ccccgtatgc | agtgcagaag  | tttcaacttc | gacctctgga | caaagctgat | gaggcaaagg | 1140 |
| aagaaagatt | cagaaagaat  | cataagctaa | gaacttcaaa | accttagctg | cctgtttgta | 1200 |
| cacttcttat | aaacaaaata  | acatcatcag | atttccttgg | atccttttaa | aaatctcaaa | 1260 |
| gattgg     |             |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1567210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Cys | His | Arg | Phe | Leu | Arg | Phe | Leu | Asn | Asn | His | Ser | Leu | Pro | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Lys | Ser | Pro | Asn | Leu | Ile | His | Ser | Ser | Ile | Ser | Arg | Ile | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | Ile | Met | Pro | Met | Glu | Asn | Asp | Asn | Gly | Pro | His | Val | Gly | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Val | Thr | Ala | Glu | Gln | Ala | Thr | Lys | Ile | Asn | Glu | Thr | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Pro | Glu | Asn | Arg | Gln | Thr | Gly | Val | Val | Ser | Asp | Thr | Gly | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly | Ser | Glu | Arg | Gly | Glu | Gln | Gly | Val | Gly | Glu | Ser | Ala | Val | Ala | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Val | Pro | Val | Glu | Glu | Ser | Gly | Ser | Ile | Ser | Val | Gly | Glu | Leu | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Pro | Arg | Ser | Ser | Ser | Ala | Arg | Val | Pro | Phe | Thr | Asn | Leu | Ser | Gln |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Asp | Ala | Asp | Leu | Ala | Leu | Ala | Arg | Thr | Leu | Gln | Glu | Gln | Glu | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Tyr | Met | Met | Leu | Thr | Met | Asn | Ser | Glu | Ile | Ser | Asp | Tyr | Gly | Ser |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Trp | Glu | Thr | Gly | Ser | Tyr | Val | Tyr | Asp | Glu | Asp | Glu | Phe | Asp | Asp | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Asn | Glu | Asp | Glu | Asp | Asp | Asp | Glu | Asp | Glu | Tyr | Glu | Thr | Asp | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Pro | Gln | Glu | Asp | Gly | Leu | Asp | Val | Asn | Val | His | Ala | Asn | Glu | Asp |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Asp | Gln | Glu | Asp | Asp | Gly | Asn | Ser | Asp | Ile | Glu | Glu | Val | Ala | Tyr | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Asp | Glu | Ala | Tyr | Ala | Arg | Ala | Leu | Gln | Glu | Ala | Glu | Glu | Arg | Asp |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Met | Ala | Ala | Arg | Leu | Ser | Ala | Leu | Ser | Gly | Leu | Ala | Asn | Arg | Val | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Glu | Asp | Leu | Glu | Asp | Glu | Ser | His | Thr | Ser | Gln | Asp | Ala | Arg | Asp | Glu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Met | Asp | Pro | Asp | Glu | Leu | Ser | Tyr | Glu | Glu | Leu | Leu | Ala | Leu | Gly | Asp |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ile | Val | Gly | Thr | Glu | Ser | Arg | Gly | Leu | Ser | Ala | Asp | Thr | Ile | Ala | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Pro | Ser | Lys | Arg | Tyr | Lys | Glu | Gly | Asp | Asn | Gln | Asn | Gly | Thr | Asn |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Glu | Ser | Cys | Val | Ile | Cys | Arg | Leu | Asp | Tyr | Glu | Asp | Asp | Glu | Asp | Leu |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ile | Leu | Leu | Pro | Cys | Lys | His | Ser | Tyr | His | Ser | Glu | Cys | Ile | Asn | Asn |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Trp | Leu | Lys | Ile | Asn | Lys | Val | Cys | Pro | Val | Cys | Ser | Ala | Glu | Val | Ser |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     |     | 365 |     |     |
| Thr | Ser | Thr | Ser | Gly | Gln | Ser |     |     |     |     |     |     |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:520:

(2) INFORMATION FOR SEQ ID NO:521:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..338
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1567212
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Glu Asn Asp Asn Gly Pro His Val Gly Asn Val Val Val Thr Ala  
1 5 10 15  
Glu Gln Ala Thr Lys Ile Asn Glu Thr Asp Gly Arg Leu Pro Glu Asn  
20 25 30  
Arg Gln Thr Gly Val Val Ser Asp Thr Gly Ser Gly Ser Glu Arg Gly  
35 40 45  
Glu Gln Gly Val Gly Glu Ser Ala Val Ala Val Ala Val Pro Val Glu  
50 55 60  
Glu Ser Gly Ser Ile Ser Val Gly Glu Leu Pro Ala Pro Arg Ser Ser  
65 70 75 80  
Ser Ala Arg Val Pro Phe Thr Asn Leu Ser Gln Ile Asp Ala Asp Leu  
85 90 95  
Ala Leu Ala Arg Thr Leu Gln Glu Gln Glu Arg Ala Tyr Met Met Leu  
100 105 110  
Thr Met Asn Ser Glu Ile Ser Asp Tyr Gly Ser Trp Glu Thr Gly Ser  
115 120 125  
Tyr Val Tyr Asp Glu Asp Glu Phe Asp Asp Pro Glu Asn Glu Asp Glu  
130 135 140  
Asp Asp Asp Glu Asp Glu Tyr Glu Thr Asp Asp Asp Pro Gln Glu Asp  
145 150 155 160  
Gly Leu Asp Val Asn Val His Ala Asn Glu Asp Asp Gln Glu Asp Asp  
165 170 175  
Gly Asn Ser Asp Ile Glu Glu Val Ala Tyr Thr Asp Asp Glu Ala Tyr  
180 185 190  
Ala Arg Ala Leu Gln Glu Ala Glu Glu Arg Asp Met Ala Ala Arg Leu  
195 200 205  
Ser Ala Leu Ser Gly Leu Ala Asn Arg Val Val Glu Asp Leu Glu Asp  
210 215 220  
Glu Ser His Thr Ser Gln Asp Ala Arg Asp Glu Met Asp Pro Asp Glu  
225 230 235 240  
Leu Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp Ile Val Gly Thr Glu  
245 250 255  
Ser Arg Gly Leu Ser Ala Asp Thr Ile Ala Ser Leu Pro Ser Lys Arg  
260 265 270  
Tyr Lys Glu Gly Asp Asn Gln Asn Gly Thr Asn Glu Ser Cys Val Ile  
275 280 285  
Cys Arg Leu Asp Tyr Glu Asp Asp Glu Asp Leu Ile Leu Leu Pro Cys  
290 295 300  
Lys His Ser Tyr His Ser Glu Cys Ile Asn Asn Trp Leu Lys Ile Asn  
305 310 315 320  
Lys Val Cys Pro Val Cys Ser Ala Glu Val Ser Thr Ser Thr Ser Gly  
325 330 335  
Gln Ser

- (2) INFORMATION FOR SEQ ID NO:522:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1665 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..1665
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1567213

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| gttaagagat  | ccttctccct  | cttcgaagat  | gagcggtagc | gtgaaggata | tcgtttcaaa  | 60   |
| ggcggaGctt  | gataaacttg  | gccagagcgg  | cgcaccagtc | gtgccttact | tctgggcttc  | 120  |
| ttggtgtgat  | gcttcgaagc  | agatggatca  | agttttctct | catctcgcta | ctgatttccc  | 180  |
| tctgtctcac  | ttctttaggg  | ttgaagctga  | ggaacatcct | gagatatctg | aggettactc  | 240  |
| tgttgctgct  | gtgccttatt  | tctgtcttct  | caaggatgg  | aaaactgtgg | atacacttga  | 300  |
| gggtgcagat  | ccatcaagtt  | tagctaataa  | ggttggcaaa | gttgctgggt | ctagtacttc  | 360  |
| tgcggaGcct  | gctgctcctg  | caagcttagg  | gttggctgct | gggccaacga | ttcttgaaac  | 420  |
| tgtgaaggag  | aatgcgaaag  | cttctttaca  | agaccgagct | cagcctgtat | ctaccgccga  | 480  |
| tgtctcaag   | agccgtttgg  | aaaagctcac  | taattctcac | cctgtcatgt | tattcatgaa  | 540  |
| aggatttct   | gaagagccta  | ggtgtgggtt  | tagcagga   | gtagttgaca | ttttgaaaga  | 600  |
| ggttaacgtt  | gatttttgaa  | gttttgacat  | actatcggat | aacgaagtgc | gagagggttt  | 660  |
| gaagaaattc  | tctaactggc  | caacgttttc  | tcagctgtac | tgcaacggag | agctttcttg  | 720  |
| tggagctgat  | atgcgaatg   | cgatgcacga  | gagcgtgaa  | ctaaaagatg | ctttcaaga   | 780  |
| tcttgggata  | acgcagattg  | gttcaaaaga  | aagtcaggat | gaagctggaa | aaggaggagg  | 840  |
| ggttagttca  | ggaaacacag  | gcttaagtga  | gacctccga  | gctcggtcg  | aagggtctggt | 900  |
| caattccaaa  | ccagttatgc  | tgttcatgaa  | aggaagacca | gaagaaccaa | agtgtgggtt  | 960  |
| cagtgggaaa  | gtggttgaaa  | tcctcaacca  | agaaaaatc  | gagtttggga | gtttcgatat  | 1020 |
| cctcttagat  | gaogaaagttc | gccaaaggct  | taaagtgtat | tcaaaactgt | caagctatcc  | 1080 |
| tcagctttac  | gtgaaaggcg  | agcttatgg   | tggatcacag | attgtcttgg | agatgcaaaa  | 1140 |
| gagcggtag   | ctgaaaaagg  | tctaccgaga  | aagggtcac  | tggaacacag | agcttgaag   | 1200 |
| atagattgaa  | ggcactgata  | aattcctcgg  | aagtaatgct | attcatgaaa | ggttcaccag  | 1260 |
| atgaaccgaa  | atgcggattt  | agctccaaag  | ttgtgaaagc | attgagagga | gaaaacgtga  | 1320 |
| gtttcggata  | gtttgatata  | ttgactgatg  | aagaagtaag | gcaagggatt | aagaatttct  | 1380 |
| caaaactggc  | aacttttctt  | cagctatact  | acaaaggtga | gttaattgga | ggatgtgata  | 1440 |
| tcattatgga  | gctaagtgat  | agtggatgat  | tcaaagcaac | tctatccgag | taagtaatat  | 1500 |
| atacaagttc  | ctgtctgtcg  | gtttgccttg  | gtgagagata | acatttcagt | tatggtaata  | 1560 |
| ataatgttta  | ggtgtttaca  | acattgatata | tgttcttctt | caagctttgt | cttgttattt  | 1620 |
| ctatttgctga | gtctattaga  | ttcataacta  | tttttctctc | tttgt      |             |      |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1567214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Asp | Pro | Ser | Pro | Ser | Ser | Lys | Met | Ser | Gly | Thr | Val | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Ser | Lys | Ala | Glu | Leu | Asp | Asn | Leu | Arg | Gln | Ser | Gly | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Leu | His | Phe | Trp | Ala | Ser | Trp | Cys | Asp | Ala | Ser | Lys | Gln | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Val | Phe | Ser | His | Leu | Ala | Thr | Asp | Phe | Pro | Arg | Ala | His | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Arg | Val | Glu | Ala | Glu | Glu | His | Pro | Glu | Ile | Ser | Glu | Ala | Tyr | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Ala | Ala | Val | Pro | Tyr | Phe | Val | Phe | Phe | Lys | Asp | Gly | Lys | Thr | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Thr | Leu | Glu | Gly | Ala | Asp | Pro | Ser | Ser | Leu | Ala | Asn | Lys | Val | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Val | Ala | Gly | Ser | Ser | Thr | Ser | Ala | Glu | Pro | Ala | Ala | Pro | Ala | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Leu | Ala | Ala | Gly | Pro | Thr | Ile | Leu | Glu | Thr | Val | Lys | Glu | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Lys | Ala | Ser | Leu | Gln | Asp | Arg | Ala | Gln | Pro | Val | Ser | Thr | Ala | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Ala Leu Lys Ser Arg Leu Glu Lys Leu Thr Asn Ser His Pro Val Met  
165 170 175  
Leu Phe Met Lys Gly Ile Pro Glu Glu Pro Arg Cys Gly Phe Ser Arg  
180 185 190  
Lys Val Val Asp Ile Leu Lys Glu Val Asn Val Asp Phe Gly Ser Phe  
195 200 205  
Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu Lys Lys Phe Ser  
210 215 220  
Asn Trp Pro Thr Phe Pro Gln Leu Tyr Cys Asn Gly Glu Leu Leu Gly  
225 230 235 240  
Gly Ala Asp Ile Ala Ile Ala Met His Glu Ser Gly Glu Leu Lys Asp  
245 250 255  
Ala Phe Lys Asp Leu Gly Ile Thr Thr Val Gly Ser Lys Glu Ser Gln  
260 265 270  
Asp Glu Ala Gly Lys Gly Gly Gly Val Ser Ser Gly Asn Thr Gly Leu  
275 280 285  
Ser Glu Thr Leu Arg Ala Arg Leu Glu Gly Leu Val Asn Ser Lys Pro  
290 295 300  
Val Met Leu Phe Met Lys Gly Arg Pro Glu Glu Pro Lys Cys Gly Phe  
305 310 315 320  
Ser Gly Lys Val Val Glu Ile Leu Asn Gln Glu Lys Ile Glu Phe Gly  
325 330 335  
Ser Phe Asp Ile Leu Leu Asp Asp Glu Val Arg Gln Gly Leu Lys Val  
340 345 350  
Tyr Ser Asn Trp Ser Ser Tyr Pro Gln Leu Tyr Val Lys Gly Glu Leu  
355 360 365  
Met Gly Gly Ser Asp Ile Val Leu Glu Met Gln Lys Ser Gly Glu Leu  
370 375 380  
Lys Lys Val Tyr Arg Glu Arg Asp His Trp Arg Thr Glu Ser  
385 390 395

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Ala Glu Leu Asp Asn  
1 5 10 15  
Leu Arg Gln Ser Gly Ala Pro Val Val Leu His Phe Trp Ala Ser Trp  
20 25 30  
Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr  
35 40 45  
Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro  
50 55 60  
Glu Ile Ser Glu Ala Tyr Ser Val Ala Ala Val Pro Tyr Phe Val Phe  
65 70 75 80  
Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser  
85 90 95  
Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala  
100 105 110  
Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile  
115 120 125  
Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala  
130 135 140  
Gln Pro Val Ser Thr Ala Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu

145 150 155 160  
Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Ile Pro Glu Glu  
165 170 175  
Pro Arg Cys Gly Phe Ser Arg Lys Val Val Asp Ile Leu Lys Glu Val  
180 185 190  
Asn Val Asp Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg  
195 200 205  
Glu Gly Leu Lys Lys Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr  
210 215 220  
Cys Asn Gly Glu Leu Leu Gly Gly Ala Asp Ile Ala Ile Ala Met His  
225 230 235 240  
Glu Ser Gly Glu Leu Lys Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr  
245 250 255  
Val Gly Ser Lys Glu Ser Gln Asp Glu Ala Gly Lys Gly Gly Gly Val  
260 265 270  
Ser Ser Gly Asn Thr Gly Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu  
275 280 285  
Gly Leu Val Asn Ser Lys Pro Val Met Leu Phe Met Lys Gly Arg Pro  
290 295 300  
Glu Glu Pro Lys Cys Gly Phe Ser Gly Lys Val Val Glu Ile Leu Asn  
305 310 315 320  
Gln Glu Lys Ile Glu Phe Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu  
325 330 335  
Val Arg Gln Gly Leu Lys Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln  
340 345 350  
Leu Tyr Val Lys Gly Glu Leu Met Gly Gly Ser Asp Ile Val Leu Glu  
355 360 365  
Met Gln Lys Ser Gly Glu Leu Lys Lys Val Tyr Arg Glu Arg Asp His  
370 375 380  
Trp Arg Thr Glu Ser  
385

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1567216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Met Asp Gln Val Phe Ser His Leu Ala Thr Asp Phe Pro Arg Ala His  
1 5 10 15  
Phe Phe Arg Val Glu Ala Glu Glu His Pro Glu Ile Ser Glu Ala Tyr  
20 25 30  
Ser Val Ala Ala Val Pro Tyr Phe Val Phe Phe Lys Asp Gly Lys Thr  
35 40 45  
Val Asp Thr Leu Glu Gly Ala Asp Pro Ser Ser Leu Ala Asn Lys Val  
50 55 60  
Gly Lys Val Ala Gly Ser Ser Thr Ser Ala Glu Pro Ala Ala Pro Ala  
65 70 75 80  
Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile Leu Glu Thr Val Lys Glu  
85 90 95  
Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala Gln Pro Val Ser Thr Ala  
100 105 110  
Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu Thr Asn Ser His Pro Val  
115 120 125  
Met Leu Phe Met Lys Gly Ile Pro Glu Glu Pro Arg Cys Gly Phe Ser  
130 135 140



Arg Lys Val Val Asp Ile Leu Lys Glu Val Asn Val Asp Phe Gly Ser  
145 150 155 160  
Phe Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu Lys Lys Phe  
165 170 175  
Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Cys Asn Gly Glu Leu Leu  
180 185 190  
Gly Gly Ala Asp Ile Ala Ile Ala Met His Glu Ser Gly Glu Leu Lys  
195 200 205  
Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr Val Gly Ser Lys Glu Ser  
210 215 220  
Gln Asp Glu Ala Gly Lys Gly Gly Gly Val Ser Ser Gly Asn Thr Gly  
225 230 235 240  
Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu Gly Leu Val Asn Ser Lys  
245 250 255  
Pro Val Met Leu Phe Met Lys Gly Arg Pro Glu Glu Pro Lys Cys Gly  
260 265 270  
Phe Ser Gly Lys Val Val Glu Ile Leu Asn Gln Glu Lys Ile Glu Phe  
275 280 285  
Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu Val Arg Gln Gly Leu Lys  
290 295 300  
Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln Leu Tyr Val Lys Gly Glu  
305 310 315 320  
Leu Met Gly Gly Ser Asp Ile Val Leu Glu Met Gln Lys Ser Gly Glu  
325 330 335  
Leu Lys Lys Val Tyr Arg Glu Arg Asp His Trp Arg Thr Glu Ser  
340 345 350

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..788
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaacggtag aaacottgtt tttaaccgtc acggtcccta tataaaccta tgagctagcg  | 60  |
| acgacaagta ttcagtataa tcaatcagaa aacaagtaga aactttaaaa cgagagagag  | 120 |
| agaaagaaat ggcgacatcg ggaacgtacg tgacggaggt tccgttgaaa ggatcggcgg  | 180 |
| agaaacacta caagagctgg aagagcgaga accatgtctt cgctgacgcc attggccacc  | 240 |
| acatccaaaa tgtcgttggt cacgaaggcg aacatgactc tcacgggtct atcaggagtt  | 300 |
| gggactacac atatgatgga aagaaggaga tgttcaaaga gaagagagag atagatgatg  | 360 |
| agaataaaac attgacgaaa agaggactgg atggtcacgt gatggagcat ctcaaagtat  | 420 |
| ttgatatcat ctacgaattt attcccaaat ctgaggatag ctgcgtctgc aaaatcacta  | 480 |
| tgatatggga gaagcgcaac gatgactttc ccgaaccaag cggctacatg aaattcgtca  | 540 |
| agcaaattgt tgttgacatt gaaggccacg tcaacaaagc ttaaccacaa ccatcacctg  | 600 |
| catcactatc tcgatcgata ttgtattatt atggtgtctt ttcgataatc aatataataa  | 660 |
| agggggctct gtggagtttc tattctctgt aactgttttg ttttgggaata tgctgtgata | 720 |
| tgttgtCtat gtcctacata tatcggtttc gatataatga gtattaaata aagtacgttc  | 780 |
| agttatcc                                                           |     |

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1567241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser  
1 5 10 15  
Ala Glu Lys His Tyr Lys Ser Trp Lys Ser Glu Asn His Val Phe Ala  
20 25 30  
Asp Ala Ile Gly His His Ile Gln Asn Val Val Val His Glu Gly Glu  
35 40 45  
His Asp Ser His Gly Ser Ile Arg Ser Trp Asp Tyr Thr Tyr Asp Gly  
50 55 60  
Lys Lys Glu Met Phe Lys Glu Lys Arg Glu Ile Asp Asp Glu Asn Lys  
65 70 75 80  
Thr Leu Thr Lys Arg Gly Leu Asp Gly His Val Met Glu His Leu Lys  
85 90 95  
Val Phe Asp Ile Ile Tyr Glu Phe Ile Pro Lys Ser Glu Asp Ser Cys  
100 105 110  
Val Cys Lys Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro  
115 120 125  
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Gln Met Val Val Asp Ile  
130 135 140  
Glu Gly His Val Asn Lys Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1567242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Met Phe Lys Glu Lys Arg Glu Ile Asp Asp Glu Asn Lys Thr Leu Thr  
1 5 10 15  
Lys Arg Gly Leu Asp Gly His Val Met Glu His Leu Lys Val Phe Asp  
20 25 30  
Ile Ile Tyr Glu Phe Ile Pro Lys Ser Glu Asp Ser Cys Val Cys Lys  
35 40 45  
Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro Glu Pro Ser  
50 55 60  
Gly Tyr Met Lys Phe Val Lys Gln Met Val Val Asp Ile Glu Gly His  
65 70 75 80  
Val Asn Lys Ala

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1311

(D) OTHER INFORMATION: / Ceres Seq. ID 1567251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

aagtttcttt atcttttagt ttcccggttaa aaaatctctc tgatcatgtct atgttcttcc 60  
acgtcgttcc taatctccca agacagaatc tctaaacttc attttgctcc ttttccacac 120

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aaaactttTc tctccctcca aagaccacaa aaaatgttct tccttccttc aacttcaagt 180  
atctctcttt attcacacgt atagcatcca aaacaaaaaa tccataaccc ttctctctgt 240  
aaaagtttct tcttttctaa cttccccaga aaaaaaaaaa aaaaacattc tgttagaaaa 300  
ccatgagagg tctcgcggtg tgttacagtg aacacgccat taaagtatca gatacatatt 360  
gttcagggtc ttogaatcat tcctatatat ctccgacatt acctccttca atccccgaca 420  
cagtaaccac cacttataaa tcataatctcc cttcttccga caaacccgtc tctgtttcac 480  
tcacctgggc ggataatctc accgctcgta tctcaacgcc gccgaaatca tactctgttt 540  
cactcagaaa acctaaagga tcaagaaagt tgacttcttc ctccggttca ctcaacgccg 600  
agatcctatg ggatctatcg gaagagagta cgaaaacaac ggacctgaac caataagaag 660  
attcttcgtc gtcgtcgttg taaattccga gattaccctc ggagtcggcg acgttgacca 720  
cgagcgagac acgtcatcat cgtcgtcgtg gcgagtcctc aaaacggaga gattctctgg 780  
aacttggttg ctcacgacga aagctcaatt ctccgacgtc ggaaggaaac acgagataca 840  
gattcaatgc ggcggaggag gwggwggagg aggaggagag gaagggtatt tatggaaagt 900  
gaaaagtctt gaaacgatgt cggtttatgt tgataagagg aaagtgtttt cgggtgaagaa 960  
gcttaagtgg aacttttagag ggaatcaaac catgtttttc gatggaatgc ttatagacat 1020  
gatgtgggat ttacacgact ggttctacaa agaaacgttg tcgtctgttt cgactagttc 1080  
atcgtctaaa acggcgctcg cgtcatcgtc ttcttcaact tcatcgtcta ctctccgtg 1140  
tgctgtgttt atgttttaga ggaggagtgg ttttgatagt agattatgga ttgatgaaga 1200  
tgaacaagag agtaagatga agaagaatat tggttctaga gatgagaaac attcgttttc 1260  
acttatcatt tgtgcctcta aaaagtgacc aaataaacia ataaacattt t

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1567252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met Arg Gly Leu Ala Ala Cys Tyr Ser Glu His Ala Ile Lys Val Ser  
1 5 10 15  
Asp Thr Tyr Cys Ser Gly Pro Ser Asn His Ser Tyr Ile Ser Pro Thr  
20 25 30  
Leu Pro Pro Ser Ile Pro Asp Thr Val Thr Thr Thr Tyr Lys Ser Tyr  
35 40 45  
Leu Pro Ser Ser Asp Lys Pro Val Ser Val Ser Leu Thr Trp Ser Asp  
50 55 60  
Asn Leu Thr Val Val Ile Ser Thr Pro Pro Lys Ser Tyr Ser Val Ser  
65 70 75 80  
Leu Arg Lys Pro Lys Gly Ser Arg Lys Leu Thr Ser Ser Ser Gly Ser  
85 90 95  
Leu Asn Ala Glu Ile Leu Trp Asp Leu Ser Glu Glu Ser Thr Lys Thr  
100 105 110  
Thr Asp Leu Asn Gln  
115

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1567253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Met Gly Ser Ile Gly Arg Glu Tyr Glu Asn Asn Gly Pro Glu Pro Ile

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1590  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567261  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

```
ctcgcttcga tagctactga tttgattcta tgggttcgttc cagtcctccga aggtgtcact 60
cgcaacgcgt ggcaattact cgcgatcttc ctgcgccacca tcgtcgggat catcactcag 120
ccgcttcctc tcggtgctgt tgcctaatg ggattaggag cttccgttct caccaaaacc 180
ctaacgttcg ccgccgcgtt ctccgctttc ggagatccaa tcccgtggct catcgctctt 240
gccttcttct tcgctcgcgg tttcatcaaa accggtctcg gtaaccgtgt agcttaccag 300
ttcgttagac tcttcggtag ctccctccctt ggtctcgggt acagtctcgt cttcagtga 360
gctcttttag ctccggcgat tcttctgtc tcggctcgtg ccggtggaat ctttctcccg 420
ttggtgaaat ctctctgtgt tgcctgtggg agtaacgttg gggatggaac agagcaccgt 480
cttggtcgtt ggttgatgct tacttggttc cagacttctg tgatctcttc ttctatgttc 540
ttgacggcta tggctgcgaa tcttttgagt gctaatttgg cgtttaacac gattaagcag 600
acgattggat ggactgattg ggctaaagct gcgattgtac caggacttgt gtctttgatt 660
gttggtccgt ttcttttgta tctcatctat cctcctacgg tgaagagcag tcctgatgct 720
cctaagctgg ctcaggaaaa gcttgacaag atgggacctt tgcctaagaa cgaattgatt 780
atggctgcca ctttattcct cactgttggt ctctggatct ttggagctaa gttgggtgta 840
gatgctgtga ctgcagccat tcttggtatta tcagtccttc ttgtgacagg tgttgtgaca 900
tggaagagat gcttagctga gtgcgtcgca tgggacacac tcacctggtt cgctgctctc 960
attgcgatgg ctggttatct taacaaatat ggtctcattg agtgggttcag ccagaccgta 1020
gtcaagtttg tgggaggatt gggtttgta tggcagctat cttttggaat cctcgtcctc 1080
ttgtatttct aactcacta cttctttgct agtggagctg cccacattgg tgcGtatgtt 1140
cactgccttt ttatcggttt caaccgctct aggcactcca ccttactttg cagccttggt 1200
tcttgcttcc ctttccaacc tgatgggagg attgacccat tatggtatcg ggtctgcgcc 1260
tatcttctac ggagctaact acgtgcgcgt ggctaaatgg tggggctatg gattcctgat 1320
ttcaatagtc aacattctca tctggcttgg tgtaggtggg gcctgggtga agttcattgg 1380
cttggtgtga ggaccacat acaccaatct tccattctt ttccttactt atatatataa 1440
tctcttagaa cggctttgag attcagattt gagaaggatt gaaatcaggg ttataaggat 1500
tgagcagagt ttttctgcaa tttttattct cactcacaca cattttgaag tgtaagcaat 1560
cttaacttgc gtcaattttg tttgatttcc
```

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 425 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..425  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567262  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

```
Leu Ala Ser Ile Ala Thr Asp Leu Ile Leu Trp Phe Val Pro Val Pro
1 5 10 15
Glu Gly Val Thr Arg Asn Ala Trp Gln Leu Leu Ala Ile Phe Leu Ala
20 25 30
Thr Ile Val Gly Ile Ile Thr Gln Pro Leu Pro Leu Gly Ala Val Ala
35 40 45
Leu Met Gly Leu Gly Ala Ser Val Leu Thr Lys Thr Leu Thr Phe Ala
50 55 60
Ala Ala Phe Ser Ala Phe Gly Asp Pro Ile Pro Trp Leu Ile Ala Leu
65 70 75 80
Ala Phe Phe Phe Ala Arg Gly Phe Ile Lys Thr Gly Leu Gly Asn Arg
85 90 95
Val Ala Tyr Gln Phe Val Arg Leu Phe Gly Ser Ser Ser Leu Gly Leu
100 105 110
```

Gly Tyr Ser Leu Val Phe Ser Glu Ala Leu Leu Ala Pro Ala Ile Pro  
115 120 125  
Ser Val Ser Ala Arg Ala Gly Gly Ile Phe Leu Pro Leu Val Lys Ser  
130 135 140  
Leu Cys Val Ala Cys Gly Ser Asn Val Gly Asp Gly Thr Glu His Arg  
145 150 155 160  
Leu Gly Ser Trp Leu Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser  
165 170 175  
Ser Ser Met Phe Leu Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn  
180 185 190  
Leu Ala Phe Asn Thr Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala  
195 200 205  
Lys Ala Ala Ile Val Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe  
210 215 220  
Leu Leu Tyr Leu Ile Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala  
225 230 235 240  
Pro Lys Leu Ala Gln Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys  
245 250 255  
Asn Glu Leu Ile Met Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp  
260 265 270  
Ile Phe Gly Ala Lys Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu  
275 280 285  
Gly Leu Ser Val Leu Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys  
290 295 300  
Leu Ala Glu Ser Val Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu  
305 310 315 320  
Ile Ala Met Ala Gly Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe  
325 330 335  
Ser Gln Thr Val Val Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln  
340 345 350  
Leu Ser Phe Gly Ile Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe  
355 360 365  
Phe Ala Ser Gly Ala Ala His Ile Gly Ala Tyr Val His Cys Leu Phe  
370 375 380  
Ile Gly Phe Asn Arg Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly  
385 390 395 400  
Ser Cys Val Pro Phe Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr  
405 410 415  
Arg Val Cys Ala Tyr Leu Leu Arg Ser  
420 425

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1567263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Met Gly Leu Gly Ala Ser Val Leu Thr Lys Thr Leu Thr Phe Ala Ala  
1 5 10 15  
Ala Phe Ser Ala Phe Gly Asp Pro Ile Pro Trp Leu Ile Ala Leu Ala  
20 25 30  
Phe Phe Phe Ala Arg Gly Phe Ile Lys Thr Gly Leu Gly Asn Arg Val  
35 40 45  
Ala Tyr Gln Phe Val Arg Leu Phe Gly Ser Ser Ser Leu Gly Leu Gly  
50 55 60  
Tyr Ser Leu Val Phe Ser Glu Ala Leu Leu Ala Pro Ala Ile Pro Ser

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |
| Val | Ser | Ala | Arg | Ala | Gly | Gly |
|     |     | 85  |     | 90  |     | 95  |
| Cys | Val | Ala | Cys | Gly | Ser | Asn |
|     |     | 100 |     | 105 |     | 110 |
| Gly | Ser | Trp | Leu | Met | Leu | Thr |
|     |     | 115 |     | 120 |     | 125 |
| Ser | Met | Phe | Leu | Thr | Ala | Met |
|     |     | 130 |     | 135 |     | 140 |
| Ala | Phe | Asn | Thr | Ile | Lys | Gln |
|     |     | 145 |     | 150 |     | 155 |
| Ala | Ala | Ile | Val | Pro | Gly | Leu |
|     |     | 165 |     | 170 |     | 175 |
| Leu | Tyr | Leu | Ile | Tyr | Pro | Pro |
|     |     | 180 |     | 185 |     | 190 |
| Lys | Leu | Ala | Gln | Glu | Lys | Leu |
|     |     | 195 |     | 200 |     | 205 |
| Glu | Leu | Ile | Met | Ala | Ala | Thr |
|     |     | 210 |     | 215 |     | 220 |
| Phe | Gly | Ala | Lys | Leu | Gly | Val |
|     |     | 225 |     | 230 |     | 235 |
| Leu | Ser | Val | Leu | Leu | Val | Thr |
|     |     | 245 |     | 250 |     | 255 |
| Ala | Glu | Ser | Val | Ala | Trp | Asp |
|     |     | 260 |     | 265 |     | 270 |
| Ala | Met | Ala | Gly | Tyr | Leu | Asn |
|     |     | 275 |     | 280 |     | 285 |
| Gln | Thr | Val | Val | Lys | Phe | Val |
|     |     | 290 |     | 295 |     | 300 |
| Ser | Phe | Gly | Ile | Leu | Val | Leu |
|     |     | 305 |     | 310 |     | 315 |
| Ala | Ser | Gly | Ala | Ala | His | Ile |
|     |     | 325 |     | 330 |     | 335 |
| Gly | Phe | Asn | Arg | Ser | Arg | His |
|     |     | 340 |     | 345 |     | 350 |
| Cys | Val | Pro | Phe | Gln | Pro | Asp |
|     |     | 355 |     | 360 |     | 365 |
| Val | Cys | Ala | Tyr | Leu | Leu | Arg |
|     |     | 370 |     | 375 |     |     |

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..260

(D) OTHER INFORMATION: / Ceres Seq. ID 1567264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Cys | Phe | Gln | Thr | Ser | Val | Ile | Ser | Ser | Ser | Met | Phe | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Ala | Met | Ala | Ala | Asn | Pro | Leu | Ser | Ala | Asn | Leu | Ala | Phe | Asn | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Lys | Gln | Thr | Ile | Gly | Trp | Thr | Asp | Trp | Ala | Lys | Ala | Ala | Ile | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Gly | Leu | Val | Ser | Leu | Ile | Val | Val | Pro | Phe | Leu | Leu | Tyr | Leu | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Tyr | Pro | Pro | Thr | Val | Lys | Ser | Ser | Pro | Asp | Ala | Pro | Lys | Leu | Ala | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys Asn Glu Leu Ile Met  
85 90 95  
Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp Ile Phe Gly Ala Lys  
100 105 110  
Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu Gly Leu Ser Val Leu  
115 120 125  
Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys Leu Ala Glu Ser Val  
130 135 140  
Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu Ile Ala Met Ala Gly  
145 150 155 160  
Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe Ser Gln Thr Val Val  
165 170 175  
Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln Leu Ser Phe Gly Ile  
180 185 190  
Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe Phe Ala Ser Gly Ala  
195 200 205  
Ala His Ile Gly Ala Tyr Val His Cys Leu Phe Ile Gly Phe Asn Arg  
210 215 220  
Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly Ser Cys Val Pro Phe  
225 230 235 240  
Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr Arg Val Cys Ala Tyr  
245 250 255  
Leu Leu Arg Ser  
260

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| actgggtctt  | cttcagcttc | tgagtcttct | cctctctctc | tatctctcaa  | gtgggctttg  | 60   |
| ctttgctggt  | tttgtcttcc | ttcgacgact | cacttttgca | gattctcata  | aattcttcaa  | 120  |
| agctttgagt  | cttttttcag | attcgaaggt | cggttttata | tatgcttcaa  | atctcttacc  | 180  |
| caaatcaggt  | atggagactc | tgcatccatt | ctctcaccta | cctatctctg  | accaccgggt  | 240  |
| cgttggtcaa  | gagatggtga | gctttcacag | ctcgagtagc | ggtagctgga  | ctaaagaaga  | 300  |
| gaacaagatg  | ttcgaacgag | ctcttgcgat | atacgctgaa | gactcgcttg  | atcgctgggt  | 360  |
| taaagttgct  | tccatgatcc | ctggaagac  | tgtttttgat | gttatgaagc  | aatatagtaa  | 420  |
| gcttgaagaa  | gacgttttgc | atattgaagc | aggacgtggt | cccattctctg | gttatcctgc  | 480  |
| agcttcttct  | cccttggggg | ttgacacgga | catgtgtcgt | aaacggccta  | gtggagctag  | 540  |
| aggatctgat  | caagatcgaa | agaaaggagt | cccttgga   | gaggaagaac  | acaggagatt  | 600  |
| cttggttaggc | ctactcaagt | acggtaaagg | agattggaga | aacatatacg  | gaaacttcgt  | 660  |
| ggtgtcaaa   | acgccaacgc | aagtggcgag | ccacgcccac | aagtattacc  | agagacagct  | 720  |
| ctccggagcc  | aaggacaaac | gcaggccaag | tatccatgac | atcacaccgc  | gcaaAtcttc  | 780  |
| tcaatgccaa  | tctcaaccgt | tccttttccg | atcatagaga | tattctccct  | gatttaggggt | 840  |
| ttatcgataa  | ggatgatacg | gaggaggag  | taatatttat | gggtcagaat  | ctctcttcag  | 900  |
| aaaatctggt  | ttctccatca | ccaacttcat | tcgaagctgc | cattaacttc  | gcgggagaaa  | 960  |
| atgtcttcag  | tgccggagct | taaggcaaca | tagaatcccc | aaactcagcg  | ttcttaagaa  | 1020 |
| tctgagtttt  | gaaactgtaa | ttagagaaat | ataagcaaaa | ccaagtttat  | tatatatgta  | 1080 |
| ttgtgtgggt  | taaaagtaag | aacttgtttt | tactctgtat | ttttgtgttt  | ctgtctacta  | 1140 |
| aataacctgtt | atgttaaaaa | attctgtgct |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..271  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Leu Gly Leu Leu Gln Leu Leu Ser Leu Leu Leu Ser Leu Tyr Leu Ser  
1                  5                  10                  15  
Ser Gly Leu Cys Phe Ala Val Phe Val Phe Leu Arg Arg Leu Thr Phe  
          20                  25                  30  
Ala Asp Ser His Lys Phe Phe Lys Ala Leu Ser Leu Phe Ser Asp Ser  
          35                  40                  45  
Lys Val Gly Phe Ile Tyr Ala Ser Asn Leu Leu Pro Lys Ser Gly Met  
          50                  55                  60  
Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe  
65                  70                  75                  80  
Val Val Gln Glu Met Val Ser Phe His Ser Ser Ser Ser Gly Ser Trp  
          85                  90                  95  
Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala  
          100                  105                  110  
Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly  
          115                  120                  125  
Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp  
          130                  135                  140  
Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala  
145                  150                  155                  160  
Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro  
          165                  170                  175  
Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp  
          180                  185                  190  
Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly  
          195                  200                  205  
Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr  
          210                  215                  220  
Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu  
225                  230                  235                  240  
Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr  
          245                  250                  255  
Gly Lys Ser Ser Gln Cys Gln Ser Gln Pro Phe Leu Phe Arg Ser  
          260                  265                  270

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 208 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..208  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg  
1                  5                  10                  15  
Phe Val Val Gln Glu Met Val Ser Phe His Ser Ser Ser Ser Gly Ser  
          20                  25                  30  
Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr  
          35                  40                  45  
Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro  
50                  55                  60

(2) INFORMATION FOR SEO ID NO:540:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1567268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

(2) INFORMATION FOR SEO ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..480  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| ctaaagattg  | caaatccgtg | ttctatctct  | ctcaacaatt | atttcccctg | cttccaaagc | 60  |
| tttgacaaca  | tttctattca | aaaacttttag | ttttgagttt | tttttttctt | gtatacttct | 120 |
| ccccaaaata  | tgagcgatcc | caagtatgca  | tatccttacc | cggcaccggg | aaattaccgc | 180 |
| caagggtccgc | Caccgcgggt | ggGagtaccg  | ccacagtatt | atcctccacc | accgccaccg | 240 |
| cctcctcctc  | caccaccacc | acgaaaagtt  | ggttttcttg | aaggactatt | agcagctctg | 300 |
| tggtgtgtgct | gcttggtgga | tgaatgttgc  | tgtgaccgca | ccattatatg | ctttgattaa | 360 |
| gttttcagga  | aaaagtatgt | ctgttaattt  | cattatgctt | atgagggtta | tacaataatt | 420 |
| gttgtgatat  | catgtgacta | ctactttctt  | ttcttgctgc | tttaattagg | ttttagtctt | 480 |

(2) INFORMATION FOR SEQ ID NO:542:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asp | Pro | Lys | Tyr | Ala | Tyr | Pro | Tyr | Pro | Ala | Pro | Gly | Asn | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Gln | Gly | Pro | Pro | Pro | Pro | Val | Gly | Val | Pro | Pro | Gln | Tyr | Tyr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Arg | Lys | Val | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Glu | Gly | Leu | Leu | Ala | Ala | Leu | Cys | Cys | Cys | Cys | Leu | Val | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Cys | Cys | Cys | Asp | Pro | Thr | Ile | Ile | Cys | Phe | Asp |     |     |     |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 48 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..48  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ile | Leu | Thr | Arg | His | Arg | Glu | Ile | Thr | Arg | Lys | Val | Arg | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Arg | Trp | Glu | Tyr | Arg | His | Ser | Ile | Ile | Leu | His | His | Arg | His | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Leu | His | His | His | His | Glu | Lys | Leu | Val | Phe | Leu | Lys | Asp | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 949 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..949  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| aatctctcgt | cgtcatttct | tctgtctcacc | gttgaatctg | aaaatgatcg | ccggagtatt | 60  |
| gcgccgatct | tactcccgt  | cgaggcagac  | tctctccgcc | gcgttagcct | ccttcaattc | 120 |
| gtgtatttcg | cacaatctca | ctccagccac  | caccggagct | tccgtcagct | ctcgattcac | 180 |
| tctcgcgtcg | tctcctaact | cgtttggcat  | cagagcgagg | aacatccaca | ttagatctga | 240 |
| gccgtcgatg | attgttcccg | caGgaatcgc  | gtcacaaggt | tacgccactg | tcacaaagga | 300 |
| tcgcaaaaac | gagattaaga | aagctaagat  | taaaatttct | ccagacaatg | tcagaccatt | 360 |
| gagtaggaag | gagatcgctc | tccagaaaga  | gccagcagaa | gaaagcacat | caaagataaa | 420 |
| aggaacaaag | atttgtatag | cgattcggtc  | ttttgttaac | ccggaaaagc | aagcttggtg | 480 |
| tcttctctct | cacactcgta | aagtcgcaat  | gcccgataca | cgaactctgt | acacggtgct | 540 |
| gcggtcgctt | cacgtcgata | agaagtctag  | agaacagttt | gagatgaggt | tcaagaaacg | 600 |
| ttttcttgtc | atcaaagctc | agagtcatga  | gttgagcaag | aagctgtttt | ggttaaaacg | 660 |
| ttatcgtatt | cttgagctc  | aatatgaact  | ccagttccat | tgcaagacct | gtttggatat | 720 |
| gactcaagtg | ttaggcaaca | tcaatggctc  | caccaccaat | gcttactgag | atggctaaag | 780 |
| acatcatttt | gtagaagttt | caagacccaa  | ccgggtacta | tgcaataatt | tcgaacctta | 840 |
| cggatccatg | aaaccagctt | tgtttcacat  | cagatcaagt | agttattttc | ttgcttagta | 900 |
| taaacatgtg | tttttgaacg | attttgaaag  | atacaattga | gtttcagtt  |            |     |

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 255 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..255  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Arg | Arg | His | Phe | Phe | Val | Ser | Pro | Leu | Asn | Leu | Lys | Met | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gly | Val | Leu | Arg | Arg | Ser | Ser | Leu | Pro | Ser | Arg | Gln | Thr | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Leu | Ala | Ser | Phe | Asn | Ser | Cys | Ile | Ser | His | Asn | Leu | Thr | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Thr | Gly | Ala | Ser | Val | Ser | Ser | Arg | Phe | Thr | Leu | Ala | Ser | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Asn | Ser | Phe | Gly | Ile | Arg | Ala | Arg | Asn | Ile | His | Ile | Arg | Ser | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Ser | Met | Ile | Val | Pro | Ala | Gly | Ile | Ala | Ser | Gln | Gly | Tyr | Ala | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Thr | Lys | Asp | Arg | Lys | Asn | Glu | Ile | Lys | Lys | Ala | Lys | Ile | Lys | Ile |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Pro | Asp | Asn | Val | Arg | Pro | Leu | Ser | Arg | Lys | Glu | Ile | Ala | Leu | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Glu | Pro | Ala | Glu | Glu | Ser | Thr | Ser | Lys | Ile | Lys | Gly | Thr | Lys | Ile |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Cys | Ile | Ala | Ile | Arg | Ser | Phe | Val | Asn | Pro | Glu | Lys | Gln | Ala | Trp | Cys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Pro | Pro | His | Thr | Arg | Lys | Val | Ala | Met | Pro | Asp | Thr | Arg | Thr | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Thr | Val | Leu | Arg | Ser | Pro | His | Val | Asp | Lys | Lys | Ser | Arg | Glu | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |

Phe Glu Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala Gln Ser  
195 200 205  
His Glu Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg Ile Leu  
210 215 220  
Gly Ala Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu Asp Met  
225 230 235 240  
Thr Gln Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala Tyr  
245 250 255

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1567286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Met Ile Ala Gly Val Leu Arg Arg Ser Ser Leu Pro Ser Arg Gln Thr  
1 5 10 15  
Leu Ser Ala Ala Leu Ala Ser Phe Asn Ser Cys Ile Ser His Asn Leu  
20 25 30  
Thr Pro Ala Thr Thr Gly Ala Ser Val Ser Ser Arg Phe Thr Leu Ala  
35 40 45  
Ser Ser Pro Asn Ser Phe Gly Ile Arg Ala Arg Asn Ile His Ile Arg  
50 55 60  
Ser Glu Pro Ser Met Ile Val Pro Ala Gly Ile Ala Ser Gln Gly Tyr  
65 70 75 80  
Ala Thr Val Thr Lys Asp Arg Lys Asn Glu Ile Lys Lys Ala Lys Ile  
85 90 95  
Lys Ile Ser Pro Asp Asn Val Arg Pro Leu Ser Arg Lys Glu Ile Ala  
100 105 110  
Leu Gln Lys Glu Pro Ala Glu Glu Ser Thr Ser Lys Ile Lys Gly Thr  
115 120 125  
Lys Ile Cys Ile Ala Ile Arg Ser Phe Val Asn Pro Glu Lys Gln Ala  
130 135 140  
Trp Cys Leu Pro Pro His Thr Arg Lys Val Ala Met Pro Asp Thr Arg  
145 150 155 160  
Thr Leu Tyr Thr Val Leu Arg Ser Pro His Val Asp Lys Lys Ser Arg  
165 170 175  
Glu Gln Phe Glu Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala  
180 185 190  
Gln Ser His Glu Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg  
195 200 205  
Ile Leu Gly Ala Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu  
210 215 220  
Asp Met Thr Gln Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala  
225 230 235 240  
Tyr

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1567287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```
Met Ile Val Pro Ala Gly Ile Ala Ser Gln Gly Tyr Ala Thr Val Thr
1 5 10 15
Lys Asp Arg Lys Asn Glu Ile Lys Lys Ala Lys Ile Lys Ile Ser Pro
20 25 30
Asp Asn Val Arg Pro Leu Ser Arg Lys Glu Ile Ala Leu Gln Lys Glu
35 40 45
Pro Ala Glu Glu Ser Thr Ser Lys Ile Lys Gly Thr Lys Ile Cys Ile
50 55 60
Ala Ile Arg Ser Phe Val Asn Pro Glu Lys Gln Ala Trp Cys Leu Pro
65 70 75 80
Pro His Thr Arg Lys Val Ala Met Pro Asp Thr Arg Thr Leu Tyr Thr
85 90 95
Val Leu Arg Ser Pro His Val Asp Lys Lys Ser Arg Glu Gln Phe Glu
100 105 110
Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala Gln Ser His Glu
115 120 125
Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg Ile Leu Gly Ala
130 135 140
Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu Asp Met Thr Gln
145 150 155 160
Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala Tyr
165 170
```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1698

(D) OTHER INFORMATION: / Ceres Seq. ID 1567288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```
cywagamcat cctaatacaaa aaataacaatc gtcttcttca tcattttctc ttcttcttct 60
ccaagaaaaac actgaagaag aaatgggggt ccttaagcca accatggcga ttctttttct 120
agcgatggtc gccgtttcat cagccgtgga catgtcaatc atctoctacg acgagaaaca 180
tggcgtctcc accaccggtg gccgtagcga agccgaggtt atgagtatct acgaggcatg 240
gttggtgaaa cacggcaagg ctacagagcca gaactctctt gttgagaaag atcgacgggt 300
cgagatcttt aaagacaatc ttctgttctg cgatgaacat aacgagaaga atcttagtta 360
tagattgggt ttgactcgtt ttgcggatct tactaacgat gagtatagat ccaagtatct 420
tggagctaag atggagaaga aaggtgagag aaggactagc ctacggtagc aggcctcgtg 480
cggatgatgag ctaccggagt ctattgactg gaggaagaaa ggagccgtgg ctgaggtcaa 540
agatcagggg ggttgccgga gttgttgggc gttttcaacc attggagcag tggaggggat 600
aaaccagatc gtaaccggag acctaataac cttgtctgaa caagagttgg tcgattgtga 660
cacttcatac aacgaagggt gtaacggagg tcttatggac tatgcttttg agttcattat 720
caagaatggt ggaatcgata cagacaaaga ttatccttac aagggtgttg atggaacttg 780
tgaccagatc aggaaaaaacg cttaaagttg cactatcgat tcatatgagg atgttccaac 840
ttacagcgag gaatcgttga aAgaaagcag ttgctcatca acccattaAg catcgccatt 900
gasgctggtg gtcgtgcgtt ccagctctat gattcgggta tatttgatgg aagttgtgga 960
acacaactag accacggagt tgtggcgggt ggatacggaa ctgagaacgg caaagattac 1020
tggattgtga gaaactcatg gggtaaaagc tggggagaga gtggatacct aaggatggcg 1080
cgtaacattg cgtcttcatt aggaaaatgt ggaatcgaga ttgaaccttc ataccgata 1140
aagaatggcg aaaacccgcc aaacccggga ccttcacctc catctcccat caagcctcca 1200
acccaatgtg acagttacta cacttgtcct gagagcaaca cttgttgttg tctgtttgag 1260
tatggcaagt attgctttgc ttggggatgt tgcccactag aagcagccac ttgctgtgat 1320
gacaactata gttgctgccc tcacgagtac ccggtttgtg accttgatca aggaacctgt 1380
ttattgagca agaacagtcc atttagtggt aaggccttaa agcgtaaacc cgcaacgcca 1440
```

```
ttctggtcac aaggcagaaa gaacattgcc taaacattgc ttcttcaaga ggactctggc 1500
tcatgagaga agagatctct ctgaagggat ttatcagatg ctttttaatg ttgttggtta 1560
tgccataact agatacataa aaaatgcagc tgttggggtt cgtgtatata aaaaaaggac 1620
cctatgtttc attcagtttc atagtgggtt ttcattgata cagtacattt attgttaatt 1680
caagaaaatt gaatwttt
```

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```
Xaa Xaa His Pro Asn Gln Lys Ile Gln Ser Ser Ser Ser Ser Phe Ser
1 5 10 15
Leu Leu Leu Leu Gln Glu Asn Thr Glu Glu Met Gly Phe Leu Lys
20 25 30
Pro Thr Met Ala Ile Leu Phe Leu Ala Met Val Ala Val Ser Ser Ala
35 40 45
Val Asp Met Ser Ile Ile Ser Tyr Asp Glu Lys His Gly Val Ser Thr
50 55 60
Thr Gly Gly Arg Ser Glu Ala Glu Val Met Ser Ile Tyr Glu Ala Trp
65 70 75 80
Leu Val Lys His Gly Lys Ala Gln Ser Gln Asn Ser Leu Val Glu Lys
85 90 95
Asp Arg Arg Phe Glu Ile Phe Lys Asp Asn Leu Arg Phe Val Asp Glu
100 105 110
His Asn Glu Lys Asn Leu Ser Tyr Arg Leu Gly Leu Thr Arg Phe Ala
115 120 125
Asp Leu Thr Asn Asp Glu Tyr Arg Ser Lys Tyr Leu Gly Ala Lys Met
130 135 140
Glu Lys Lys Gly Glu Arg Arg Thr Ser Leu Arg Tyr Glu Ala Arg Val
145 150 155 160
Gly Asp Glu Leu Pro Glu Ser Ile Asp Trp Arg Lys Lys Gly Ala Val
165 170 175
Ala Glu Val Lys Asp Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser
180 185 190
Thr Ile Gly Ala Val Glu Gly Ile Asn Gln Ile Val Thr Gly Asp Leu
195 200 205
Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys Asp Thr Ser Tyr Asn
210 215 220
Glu Gly Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Glu Phe Ile Ile
225 230 235 240
Lys Asn Gly Gly Ile Asp Thr Asp Lys Asp Tyr Pro Tyr Lys Gly Val
245 250 255
Asp Gly Thr Cys Asp Gln Ile Arg Lys Asn Ala Lys Val Val Thr Ile
260 265 270
Asp Ser Tyr Glu Asp Val Pro Thr Tyr Ser Glu Glu Ser Leu Lys Glu
275 280 285
Ser Ser Cys Ser Ser Thr His
290 295
```

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..268  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567290  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Leu | Lys | Pro | Thr | Met | Ala | Ile | Leu | Phe | Leu | Ala | Met | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Ser | Ser | Ala | Val | Asp | Met | Ser | Ile | Ile | Ser | Tyr | Asp | Glu | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| His | Gly | Val | Ser | Thr | Thr | Gly | Gly | Arg | Ser | Glu | Ala | Glu | Val | Met | Ser |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ile | Tyr | Glu | Ala | Trp | Leu | Val | Lys | His | Gly | Lys | Ala | Gln | Ser | Gln | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Val | Glu | Lys | Asp | Arg | Arg | Phe | Glu | Ile | Phe | Lys | Asp | Asn | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Phe | Val | Asp | Glu | His | Asn | Glu | Lys | Asn | Leu | Ser | Tyr | Arg | Leu | Gly |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Leu | Thr | Arg | Phe | Ala | Asp | Leu | Thr | Asn | Asp | Glu | Tyr | Arg | Ser | Lys | Tyr |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Gly | Ala | Lys | Met | Glu | Lys | Lys | Gly | Glu | Arg | Arg | Thr | Ser | Leu | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Tyr | Glu | Ala | Arg | Val | Gly | Asp | Glu | Leu | Pro | Glu | Ser | Ile | Asp | Trp | Arg |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Lys | Lys | Gly | Ala | Val | Ala | Glu | Val | Lys | Asp | Gln | Gly | Gly | Cys | Gly | Ser |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Cys | Trp | Ala | Phe | Ser | Thr | Ile | Gly | Ala | Val | Glu | Gly | Ile | Asn | Gln | Ile |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Val | Thr | Gly | Asp | Leu | Ile | Thr | Leu | Ser | Glu | Gln | Glu | Leu | Val | Asp | Cys |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Thr | Ser | Tyr | Asn | Glu | Gly | Cys | Asn | Gly | Gly | Leu | Met | Asp | Tyr | Ala |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Phe | Glu | Phe | Ile | Ile | Lys | Asn | Gly | Gly | Ile | Asp | Thr | Asp | Lys | Asp | Tyr |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Pro | Tyr | Lys | Gly | Val | Asp | Gly | Thr | Cys | Asp | Gln | Ile | Arg | Lys | Asn | Ala |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Lys | Val | Val | Thr | Ile | Asp | Ser | Tyr | Glu | Asp | Val | Pro | Thr | Tyr | Ser | Glu |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Glu | Ser | Leu | Lys | Glu | Ser | Ser | Cys | Ser | Ser | Thr | His |     |     |     |     |
|     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 261 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..261  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Leu | Phe | Leu | Ala | Met | Val | Ala | Val | Ser | Ser | Ala | Val | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Ser | Ile | Ile | Ser | Tyr | Asp | Glu | Lys | His | Gly | Val | Ser | Thr | Thr | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gly | Arg | Ser | Glu | Ala | Glu | Val | Met | Ser | Ile | Tyr | Glu | Ala | Trp | Leu | Val |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | His | Gly | Lys | Ala | Gln | Ser | Gln | Asn | Ser | Leu | Val | Glu | Lys | Asp | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Phe | Glu | Ile | Phe | Lys | Asp | Asn | Leu | Arg | Phe | Val | Asp | Glu | His | Asn |



65 70 75 80  
Glu Lys Asn Leu Ser Tyr Arg Leu Gly Leu Thr Arg Phe Ala Asp Leu  
85 90 95  
Thr Asn Asp Glu Tyr Arg Ser Lys Tyr Leu Gly Ala Lys Met Glu Lys  
100 105 110  
Lys Gly Glu Arg Arg Thr Ser Leu Arg Tyr Glu Ala Arg Val Gly Asp  
115 120 125  
Glu Leu Pro Glu Ser Ile Asp Trp Arg Lys Lys Gly Ala Val Ala Glu  
130 135 140  
Val Lys Asp Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Thr Ile  
145 150 155  
Gly Ala Val Glu Gly Ile Asn Gln Ile Val Thr Gly Asp Leu Ile Thr  
165 170 175  
Leu Ser Glu Gln Glu Leu Val Asp Cys Asp Thr Ser Tyr Asn Glu Gly  
180 185 190  
Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Glu Phe Ile Ile Lys Asn  
195 200 205  
Gly Gly Ile Asp Thr Asp Lys Asp Tyr Pro Tyr Lys Gly Val Asp Gly  
210 215 220  
Thr Cys Asp Gln Ile Arg Lys Asn Ala Lys Val Val Thr Ile Asp Ser  
225 230 235  
Tyr Glu Asp Val Pro Thr Tyr Ser Glu Glu Ser Leu Lys Glu Ser Ser  
245 250 255  
Cys Ser Ser Thr His  
260

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| aactctcatc  | ttcttttctc | tttctttttc  | ctctttctcc  | attgcttggt | gattgatgat  | 60   |
| cttgaagcaa  | ggatcatgag | gttctctcac  | agattttctgt | tggaggatat | gcccagaagaa | 120  |
| accttttcgg  | actctctctg | taaaaataat  | tgcatccaag  | agttgaaaac | tctaggatac  | 180  |
| tggtcatcct  | attgtcttga | cgagtgtcct  | tccatctgcg  | agatcgtcgt | aatttcaggt  | 240  |
| ctttcaccac  | ctgcagagat | ccaccacgac  | gacaacttaa  | agaggatctt | gatcatctct  | 300  |
| gcttcatcta  | tcatcacaac | tctgtttctc  | cttactttac  | ttgttctctg | cttcaagttt  | 360  |
| tactatagga  | ggagaagatc | aataacaaca  | tcaagaagat  | ggagtatgga | agaagctagg  | 420  |
| aattgggatt  | ttgatggacc | agcacctggt  | attgttgatc  | atccgatttg | gcatatcaga  | 480  |
| accatagggg  | tgaatccaac | ggttataagt  | tccatcaaag  | tttgtcagta | tagtaaaaaa  | 540  |
| gatgggtgtg  | tggaaggaa  | tgattgctcc  | gtttgtttta  | gcgaattcga | agaagaagag  | 600  |
| acgcttagat  | tgttaccaaa | gtgtaaaacat | gcttttcatc  | tttattgtat | tgatacttgg  | 660  |
| cttagatcac  | acaccaattg | tccgcttagt  | cgtgctccta  | tcgttgaggc | caacacaatg  | 720  |
| attgatgatc  | atagtggagg | gctagaggag  | ataagtgtga  | tgattccaga | agaaaatgga  | 780  |
| gatgataccg  | atgaagaaat | cgaggaagaa  | agagatggct  | ttgttagtaa | tattagtaga  | 840  |
| gatcatgggtg | agtcacaaca | acagcgagtg  | agacgatcag  | tgctggttga | ttcgttatcg  | 900  |
| ggtttaaggg  | taagtgaagt | tggtgtgggt  | agagaaaagg  | agaagttgaa | gagaggcaat  | 960  |
| aatattggat  | ctgggaggtc | aagtttattg  | aagagatcta  | tctcttacag | tggaagtagt  | 1020 |
| tactagctag  | cttcagtgtc | aataataaaa  | acaagaagtc  | cataaagtaa | gtaagtttct  | 1080 |
| tgaagaagaa  | aatcaaatac | aacccaacaa  | catatagggt  | gtattcatat | gtatgaaggt  | 1140 |
| gatataagat  | tacgattatc | aaagctagtc  | actcttgtaa  | agttaaaaga | gagttttgac  | 1200 |
| aacttctact  | actctgtcta | gatactctgg  | atttgtggat  | taagtataaa | tatacaccaa  | 1260 |
| actTcgtttt  | gtatgttact | tatttattgt  | tcctcaagaa  | ataccatctg | gattttaatt  | 1320 |
| atTTTT      |            |             |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 339 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..339  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567306  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Asn Ser His Leu Leu Phe Ser Phe Phe Phe Leu Phe Leu His Cys Leu  
1                   5                   10                   15  
Leu Ile Asp Asp Leu Glu Ala Arg Ile Met Arg Phe Leu His Arg Phe  
                  20                   25                   30  
Leu Leu Glu Asp Met Pro Lys Glu Thr Phe Ser Asp Ser Leu Cys Lys  
                  35                   40                   45  
Asn Asn Cys Ile Gln Glu Leu Lys Thr Leu Gly Tyr Cys Ser Ser Tyr  
50                   55                   60  
Cys Leu Asp Glu Cys Pro Ser Ile Cys Glu Ile Val Val Ile Ser Gly  
65                   70                   75                   80  
Leu Ser Pro Pro Ala Glu Ile His His Asp Asp Asn Leu Lys Arg Ile  
                  85                   90                   95  
Leu Ile Ile Ser Ala Ser Ser Ile Ile Thr Thr Leu Phe Leu Leu Thr  
                  100                   105                   110  
Leu Leu Val Leu Cys Phe Lys Phe Tyr Tyr Arg Arg Arg Arg Ser Ile  
                  115                   120                   125  
Thr Thr Ser Arg Arg Trp Ser Met Glu Glu Ala Arg Asn Trp Asp Phe  
130                   135                   140  
Asp Gly Pro Ala Pro Val Ile Val Asp His Pro Ile Trp His Ile Arg  
145                   150                   155                   160  
Thr Ile Gly Leu Asn Pro Thr Val Ile Ser Ser Ile Lys Val Cys Gln  
                  165                   170                   175  
Tyr Ser Lys Lys Asp Gly Val Val Glu Gly Thr Asp Cys Ser Val Cys  
                  180                   185                   190  
Leu Ser Glu Phe Glu Glu Glu Glu Thr Leu Arg Leu Leu Pro Lys Cys  
195                   200                   205  
Lys His Ala Phe His Leu Tyr Cys Ile Asp Thr Trp Leu Arg Ser His  
210                   215                   220  
Thr Asn Cys Pro Leu Ser Arg Ala Pro Ile Val Glu Ala Asn Thr Met  
225                   230                   235                   240  
Ile Asp Asp His Ser Glu Gly Leu Glu Glu Ile Ser Val Met Ile Pro  
                  245                   250                   255  
Glu Glu Asn Gly Asp Asp Thr Asp Glu Glu Ile Glu Glu Glu Arg Asp  
                  260                   265                   270  
Gly Phe Val Ser Asn Ile Ser Arg Asp His Gly Glu Ser Gln Gln Gln  
275                   280                   285  
Arg Val Arg Arg Ser Val Ser Leu Asp Ser Leu Ser Gly Leu Arg Val  
290                   295                   300  
Ser Glu Val Val Val Gly Arg Glu Lys Glu Lys Leu Lys Arg Gly Asn  
305                   310                   315                   320  
Asn Ile Gly Ser Gly Arg Ser Ser Leu Leu Lys Arg Ser Ile Ser Tyr  
                  325                   330                   335  
Ser Gly Lys

- (2) INFORMATION FOR SEQ ID NO:554:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 314 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..314  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567307  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met Arg Phe Leu His Arg Phe Leu Leu Glu Asp Met Pro Lys Glu Thr  
1                   5                   10                   15  
Phe Ser Asp Ser Leu Cys Lys Asn Asn Cys Ile Gln Glu Leu Lys Thr  
          20                   25                   30  
Leu Gly Tyr Cys Ser Ser Tyr Cys Leu Asp Glu Cys Pro Ser Ile Cys  
          35                   40                   45  
Glu Ile Val Val Ile Ser Gly Leu Ser Pro Pro Ala Glu Ile His His  
          50                   55                   60  
Asp Asp Asn Leu Lys Arg Ile Leu Ile Ile Ser Ala Ser Ser Ile Ile  
65                   70                   75                   80  
Thr Thr Leu Phe Leu Leu Thr Leu Leu Val Leu Cys Phe Lys Phe Tyr  
          85                   90                   95  
Tyr Arg Arg Arg Arg Ser Ile Thr Thr Ser Arg Arg Trp Ser Met Glu  
          100                   105                   110  
Glu Ala Arg Asn Trp Asp Phe Asp Gly Pro Ala Pro Val Ile Val Asp  
          115                   120                   125  
His Pro Ile Trp His Ile Arg Thr Ile Gly Leu Asn Pro Thr Val Ile  
          130                   135                   140  
Ser Ser Ile Lys Val Cys Gln Tyr Ser Lys Lys Asp Gly Val Val Glu  
145                   150                   155                   160  
Gly Thr Asp Cys Ser Val Cys Leu Ser Glu Phe Glu Glu Glu Glu Thr  
          165                   170                   175  
Leu Arg Leu Leu Pro Lys Cys Lys His Ala Phe His Leu Tyr Cys Ile  
          180                   185                   190  
Asp Thr Trp Leu Arg Ser His Thr Asn Cys Pro Leu Ser Arg Ala Pro  
          195                   200                   205  
Ile Val Glu Ala Asn Thr Met Ile Asp Asp His Ser Glu Gly Leu Glu  
          210                   215                   220  
Glu Ile Ser Val Met Ile Pro Glu Glu Asn Gly Asp Asp Thr Asp Glu  
225                   230                   235                   240  
Glu Ile Glu Glu Glu Arg Asp Gly Phe Val Ser Asn Ile Ser Arg Asp  
          245                   250                   255  
His Gly Glu Ser Gln Gln Gln Arg Val Arg Arg Ser Val Ser Leu Asp  
          260                   265                   270  
Ser Leu Ser Gly Leu Arg Val Ser Glu Val Val Val Gly Arg Glu Lys  
          275                   280                   285  
Glu Lys Leu Lys Arg Gly Asn Asn Ile Gly Ser Gly Arg Ser Ser Leu  
          290                   295                   300  
Leu Lys Arg Ser Ile Ser Tyr Ser Gly Lys  
305                   310

(2) INFORMATION FOR SEQ ID NO:555:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 303 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..303  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567308  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Met Pro Lys Glu Thr Phe Ser Asp Ser Leu Cys Lys Asn Asn Cys Ile  
1                   5                   10                   15  
Gln Glu Leu Lys Thr Leu Gly Tyr Cys Ser Ser Tyr Cys Leu Asp Glu

20 25 30  
Cys Pro Ser Ile Cys Glu Ile Val Ile Ser Gly Leu Ser Pro Pro  
35 40 45  
Ala Glu Ile His His Asp Asp Asn Leu Lys Arg Ile Leu Ile Ile Ser  
50 55 60  
Ala Ser Ser Ile Ile Thr Thr Leu Phe Leu Leu Thr Leu Leu Val Leu  
65 70 75 80  
Cys Phe Lys Phe Tyr Tyr Arg Arg Arg Arg Ser Ile Thr Thr Ser Arg  
85 90 95  
Arg Trp Ser Met Glu Glu Ala Arg Asn Trp Asp Phe Asp Gly Pro Ala  
100 105 110  
Pro Val Ile Val Asp His Pro Ile Trp His Ile Arg Thr Ile Gly Leu  
115 120 125  
Asn Pro Thr Val Ile Ser Ser Ile Lys Val Cys Gln Tyr Ser Lys Lys  
130 135 140  
Asp Gly Val Val Glu Gly Thr Asp Cys Ser Val Cys Leu Ser Glu Phe  
145 150 155 160  
Glu Glu Glu Glu Thr Leu Arg Leu Leu Pro Lys Cys Lys His Ala Phe  
165 170 175  
His Leu Tyr Cys Ile Asp Thr Trp Leu Arg Ser His Thr Asn Cys Pro  
180 185 190  
Leu Ser Arg Ala Pro Ile Val Glu Ala Asn Thr Met Ile Asp Asp His  
195 200 205  
Ser Glu Gly Leu Glu Glu Ile Ser Val Met Ile Pro Glu Glu Asn Gly  
210 215 220  
Asp Asp Thr Asp Glu Glu Ile Glu Glu Glu Arg Asp Gly Phe Val Ser  
225 230 235 240  
Asn Ile Ser Arg Asp His Gly Glu Ser Gln Gln Gln Arg Val Arg Arg  
245 250 255  
Ser Val Ser Leu Asp Ser Leu Ser Gly Leu Arg Val Ser Glu Val Val  
260 265 270  
Val Gly Arg Glu Lys Glu Lys Leu Lys Arg Gly Asn Asn Ile Gly Ser  
275 280 285  
Gly Arg Ser Ser Leu Leu Lys Arg Ser Ile Ser Tyr Ser Gly Lys  
290 295 300

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1670
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaaaggatc aaacatagta tagcttggac tctttttgcc gtctatgata tctctcaatc | 60  |
| tctcatctta gctttctttc tctctctctt tgtgtcttca tttgtttatc tcatcaatgg | 120 |
| attcaaattt tcattactcg atagatctta acgaagatca aaaccatcac gaacaaccct | 180 |
| ttttctatcc tcttggatcc tcttctctgc ttcacatca tcatcatcat catcatcatc  | 240 |
| aagtcccttc taattcttca tcttctctct cgtccatttc atcgctctcc tcttacctcc | 300 |
| ctttcttgat caactctcaa gaagatcaac atgttgccca caacaacact tatcacgctg | 360 |
| atcatctcca tctttctcaa cccctcaagg ccaagatgtt tgtggctaac ggtggatcat | 420 |
| catcatgcga tcacatggtg ccaaagaagg agacaagact gaaactaacg ataaggaaaa | 480 |
| aagatcacga agaccaacc catcctcttc atcaaaaacc gacaaaacc gattcagact   | 540 |
| ccgacaagtg gttgatgtcc ccaaagatgc ggttgatcaa gaaaacaatc accaacaata | 600 |
| aacagctcac tgatcagact aataataata atcataaaga aagtgatcac taccctttga | 660 |
| atcataagac taatttcgac gaggatcacc atgaagatct taatttcaag aacgtcttga | 720 |
| ccaggaagac cacggccgag accaccgaga atcgctacaa tacaatcaac gagaacggtt | 780 |
| atagtaataa caatggcgtg attagggttt gttcggattg taacaccacc aagactcctc | 840 |

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tttggcgaag tggacctcga ggtcccaagt ctctttgtaa cgcattgtgt atacggcaaa 900
gaaaggcaag ggcagccgct atggccgcgg ccgctgcagc cggcgaccaa gaggtggcgg 960
tagcgccccg agtgcaacaa ttaccgctga aaaagaagtt gcaaaaataa aaaaaagaga 1020
tcaaacggag gggaaaaata caatcactct cctccaatgg tggccaaggc caaaaagtgc 1080
aagatcaaag aggaagagga gaaggMaatg gaagcggaaa cggttgccgg agattcagag 1140
atcagcaaat ctacaacttc ttctaattct tcgatttcgt caaacaatt ttgcttcgat 1200
gatttgacaa taatgttgag caaaagctca gcttatcaac aagtgttccc acaagatgag 1260
aaggaggctg ctgttttgct catggctctg tcgtatggaa tggttcacgg ttgatcagat 1320
catcacaata tcctcattac aaaaaggttt attttaatag taatatatag attatagtaa 1380
tcataataat gattgattgt taaatcttgg agtgattagt ttagtttttg cagttggtct 1440
aatatcagga gtcaaaacat tttataataa gagtgtgtga gagtttaata tgataattaa 1500
tagctctata tatgtttatg gagattttgg ttttgagttt gttgtgtttt tgttttccga 1560
tggaacgaac attagtcacc cgataatgtg ggtaattctt gttcatttac aagttttata 1620
gtactgtatt gtgtaacgag gttggagaaa taatataatc aattaagggt
```

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1567310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

```
Met Asp Ser Asn Phe His Tyr Ser Ile Asp Leu Asn Glu Asp Gln Asn
1 5 10 15
His His Glu Gln Pro Phe Phe Tyr Pro Leu Gly Ser Ser Ser Ser Leu
20 25 30
His His His His His His His His Gln Val Pro Ser Asn Ser Ser
35 40 45
Ser Ser Ser Ser Ser Ile Ser Ser Leu Ser Ser Tyr Leu Pro Phe Leu
50 55 60
Ile Asn Ser Gln Glu Asp Gln His Val Ala Tyr Asn Asn Thr Tyr His
65 70 75 80
Ala Asp His Leu His Leu Ser Gln Pro Leu Lys Ala Lys Met Phe Val
85 90 95
Ala Asn Gly Gly Ser Ser Ser Cys Asp His Met Val Pro Lys Lys Glu
100 105 110
Thr Arg Leu Lys Leu Thr Ile Arg Lys Lys Asp His Glu Asp Gln Pro
115 120 125
His Pro Leu His Gln Asn Pro Thr Lys Pro Asp Ser Asp Ser Asp Lys
130 135 140
Trp Leu Met Ser Pro Lys Met Arg Leu Ile Lys Lys Thr Ile Thr Asn
145 150 155 160
Asn Lys Gln Leu Thr Asp Gln Thr Asn Asn Asn His Lys Glu Ser
165 170 175
Asp His Tyr Pro Leu Asn His Lys Thr Asn Phe Asp Glu Asp His His
180 185 190
Glu Asp Leu Asn Phe Lys Asn Val Leu Thr Arg Lys Thr Thr Ala Ala
195 200 205
Thr Thr Glu Asn Arg Tyr Asn Thr Ile Asn Glu Asn Gly Tyr Ser Asn
210 215 220
Asn Asn Gly Val Ile Arg Val Cys Ser Asp Cys Asn Thr Thr Lys Thr
225 230 235 240
Pro Leu Trp Arg Ser Gly Pro Arg Gly Pro Lys Ser Leu Cys Asn Ala
245 250 255
Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Ala Met Ala Ala Ala
260 265 270
Ala Ala Ala Gly Asp Gln Glu Val Ala Val Ala Pro Arg Val Gln Gln
```

275 280 285  
Leu Pro Leu Lys Lys Lys Leu Gln Asn Lys Lys Lys Glu Ile Lys Arg  
290 295 300  
Arg Gly Lys Ile Gln Ser Leu Ser Ser Asn Gly Gly Gln Gly Gln Lys  
305 310 315 320  
Val Gln Asp Gln Arg Gly Arg Gly Glu Xaa Asn Gly Ser Gly Asn Gly  
325 330 335  
Cys Arg Arg Phe Arg Asp Gln Gln Ile Tyr Asn Phe Phe  
340 345

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1567311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

Met Phe Val Ala Asn Gly Gly Ser Ser Cys Asp His Met Val Pro  
1 5 10 15  
Lys Lys Glu Thr Arg Leu Lys Leu Thr Ile Arg Lys Lys Asp His Glu  
20 25 30  
Asp Gln Pro His Pro Leu His Gln Asn Pro Thr Lys Pro Asp Ser Asp  
35 40 45  
Ser Asp Lys Trp Leu Met Ser Pro Lys Met Arg Leu Ile Lys Lys Thr  
50 55 60  
Ile Thr Asn Asn Lys Gln Leu Thr Asp Gln Thr Asn Asn Asn Asn His  
65 70 75 80  
Lys Glu Ser Asp His Tyr Pro Leu Asn His Lys Thr Asn Phe Asp Glu  
85 90 95  
Asp His His Glu Asp Leu Asn Phe Lys Asn Val Leu Thr Arg Lys Thr  
100 105 110  
Thr Ala Ala Thr Thr Glu Asn Arg Tyr Asn Thr Ile Asn Glu Asn Gly  
115 120 125  
Tyr Ser Asn Asn Asn Gly Val Ile Arg Val Cys Ser Asp Cys Asn Thr  
130 135 140  
Thr Lys Thr Pro Leu Trp Arg Ser Gly Pro Arg Gly Pro Lys Ser Leu  
145 150 155 160  
Cys Asn Ala Cys Gly Ile Arg Gln Arg Lys Ala Arg Arg Ala Ala Met  
165 170 175  
Ala Ala Ala Ala Ala Ala Gly Asp Gln Glu Val Ala Val Ala Pro Arg  
180 185 190  
Val Gln Gln Leu Pro Leu Lys Lys Leu Gln Asn Lys Lys Lys Glu  
195 200 205  
Ile Lys Arg Arg Gly Lys Ile Gln Ser Leu Ser Ser Asn Gly Gly Gln  
210 215 220  
Gly Gln Lys Val Gln Asp Gln Arg Gly Arg Gly Glu Xaa Asn Gly Ser  
225 230 235 240  
Gly Asn Gly Cys Arg Arg Phe Arg Asp Gln Gln Ile Tyr Asn Phe Phe  
245 250 255

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..243  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567312  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Lys | Lys | Glu | Thr | Arg | Leu | Lys | Leu | Thr | Ile | Arg | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | His | Glu | Asp | Gln | Pro | His | Pro | Leu | His | Gln | Asn | Pro | Thr | Lys | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ser | Asp | Ser | Asp | Lys | Trp | Leu | Met | Ser | Pro | Lys | Met | Arg | Leu | Ile |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Lys | Thr | Ile | Thr | Asn | Asn | Lys | Gln | Leu | Thr | Asp | Gln | Thr | Asn | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asn | Asn | His | Lys | Glu | Ser | Asp | His | Tyr | Pro | Leu | Asn | His | Lys | Thr | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Asp | Glu | Asp | His | His | Glu | Asp | Leu | Asn | Phe | Lys | Asn | Val | Leu | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Lys | Thr | Thr | Ala | Ala | Thr | Thr | Glu | Asn | Arg | Tyr | Asn | Thr | Ile | Asn |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asn | Gly | Tyr | Ser | Asn | Asn | Asn | Gly | Val | Ile | Arg | Val | Cys | Ser | Asp |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Cys | Asn | Thr | Thr | Lys | Thr | Pro | Leu | Trp | Arg | Ser | Gly | Pro | Arg | Gly | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ser | Leu | Cys | Asn | Ala | Cys | Gly | Ile | Arg | Gln | Arg | Lys | Ala | Arg | Arg |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Ala | Met | Ala | Ala | Ala | Ala | Ala | Gly | Asp | Gln | Glu | Val | Ala | Val |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Pro | Arg | Val | Gln | Gln | Leu | Pro | Leu | Lys | Lys | Lys | Leu | Gln | Asn | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Lys | Glu | Ile | Lys | Arg | Arg | Gly | Lys | Ile | Gln | Ser | Leu | Ser | Ser | Asn |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Gln | Gly | Gln | Lys | Val | Gln | Asp | Gln | Arg | Gly | Arg | Gly | Glu | Xaa |
|     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |     |
| Asn | Gly | Ser | Gly | Asn | Gly | Cys | Arg | Arg | Phe | Arg | Asp | Gln | Gln | Ile | Tyr |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Asn | Phe | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1018 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..1018  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| acttttacaa  | ctaactcata | agtaaaacac  | agacagtttt | tagatggcta  | agatatattc | 60  |
| cccttctttt  | cccggtactc | tctgtctttg  | catttttact | ctcttgacgc  | taatgttcac | 120 |
| tccgggtttcc | gctcgaccgc | cgacattcgt  | cgaggatttc | aaagccgcct  | ggtcggaatc | 180 |
| tcacatccgt  | caaatggaag | acggaaaaagc | tatccagctc | gtccttgatc  | agagcactgg | 240 |
| atgtggattt  | gcttccaaaa | gaaaatatct  | attcggacga | gtgagcatga  | ggatcaaact | 300 |
| cattcccggga | gactctgccg | gtacgGtcac  | cgctttctac | atgaactccg  | atacgccac  | 360 |
| ggtgagagac  | gagctagatt | ttgagttctt  | gggaaacaga | agtgggtcaac | cttactcagt | 420 |
| gcaaacaaac  | atatttgctc | atggc aaagg | agatagagaa | caaagagtta  | atctttggtt | 480 |
| cgacccatct  | atggattacc | acacttacac  | tatcttatgg | tcacacaaac  | acattgtttt | 540 |
| ttacgtagac  | gatgtgccaa | taagagaata  | caaaaacaac | gaagccaaga  | acatagctta | 600 |
| ccaacatca   | caacctatgg | gagtatactc  | aacattatgg | gaagcagatg  | actgggcaac | 660 |

acgtggtgga ttagagaaaa ttgattggag caaagctcca ttttatgctt attacaaaga 720  
tttcgacatc gaaggttgtc ctgttcctgg accaaccttt tTgtccatcg aaccctcata 780  
attggtggga aggttatgcc tatcagtctc ttaacgccgt tgaagctcga cgttaccggt 840  
gggttagagt aaaccatatg gtttatgatt attgtactga ccggtctagg tttcctgtcc 900  
caccacccga gtgtcgtgct tgaaaataat tgcatacgta cgttgcaatg atcatgtttc 960  
gtcttgtacg agattttata tataaattgt gggaaaatgt ggattgtatt gtcctctt

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1567318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

Met Ala Lys Ile Tyr Ser Pro Ser Phe Pro Gly Thr Leu Cys Leu Cys  
1 5 10 15  
Ile Phe Thr Leu Thr Leu Met Phe Ile Arg Val Ser Ala Arg Pro  
20 25 30  
Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile  
35 40 45  
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser  
50 55 60  
Thr Gly Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val  
65 70 75 80  
Ser Met Arg Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr  
85 90 95  
Ala Phe Tyr Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp  
100 105 110  
Phe Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr  
115 120 125  
Asn Ile Phe Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu  
130 135 140  
Trp Phe Asp Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser  
145 150 155 160  
His Lys His Ile Val Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr  
165 170 175  
Lys Asn Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met  
180 185 190  
Gly Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly  
195 200 205  
Gly Leu Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr  
210 215 220  
Lys Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Leu  
225 230 235 240  
Ser Ile Glu Pro Ser  
245

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1567319



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ile | Arg | Val | Ser | Ala | Arg | Pro | Ala | Thr | Phe | Val | Glu | Asp | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Ala | Trp | Ser | Glu | Ser | His | Ile | Arg | Gln | Met | Glu | Asp | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Gln | Leu | Val | Leu | Asp | Gln | Ser | Thr | Gly | Cys | Gly | Phe | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Arg | Lys | Tyr | Leu | Phe | Gly | Arg | Val | Ser | Met | Arg | Ile | Lys | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Gly | Asp | Ser | Ala | Gly | Thr | Val | Thr | Ala | Phe | Tyr | Met | Asn | Ser | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ala | Thr | Val | Arg | Asp | Glu | Leu | Asp | Phe | Glu | Phe | Leu | Gly | Asn | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Gln | Pro | Tyr | Ser | Val | Gln | Thr | Asn | Ile | Phe | Ala | His | Gly | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Asp | Arg | Glu | Gln | Arg | Val | Asn | Leu | Trp | Phe | Asp | Pro | Ser | Met | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | His | Thr | Tyr | Thr | Ile | Leu | Trp | Ser | His | Lys | His | Ile | Val | Phe | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asp | Asp | Val | Pro | Ile | Arg | Glu | Tyr | Lys | Asn | Asn | Glu | Ala | Lys | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Ala | Tyr | Pro | Thr | Ser | Gln | Pro | Met | Gly | Val | Tyr | Ser | Thr | Leu | Trp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ala | Asp | Asp | Trp | Ala | Thr | Arg | Gly | Gly | Leu | Glu | Lys | Ile | Asp | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Lys | Ala | Pro | Phe | Tyr | Ala | Tyr | Tyr | Lys | Asp | Phe | Asp | Ile | Glu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Pro | Val | Pro | Gly | Pro | Thr | Phe | Leu | Ser | Ile | Glu | Pro | Ser |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asp | Gly | Lys | Ala | Ile | Gln | Leu | Val | Leu | Asp | Gln | Ser | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Gly | Phe | Ala | Ser | Lys | Arg | Lys | Tyr | Leu | Phe | Gly | Arg | Val | Ser | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Lys | Leu | Ile | Pro | Gly | Asp | Ser | Ala | Gly | Thr | Val | Thr | Ala | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Tyr | Met | Asn | Ser | Asp | Thr | Ala | Thr | Val | Arg | Asp | Glu | Leu | Asp | Phe | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Leu | Gly | Asn | Arg | Ser | Gly | Gln | Pro | Tyr | Ser | Val | Gln | Thr | Asn | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Ala | His | Gly | Lys | Gly | Asp | Arg | Glu | Gln | Arg | Val | Asn | Leu | Trp | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Pro | Ser | Met | Asp | Tyr | His | Thr | Tyr | Thr | Ile | Leu | Trp | Ser | His | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| His | Ile | Val | Phe | Tyr | Val | Asp | Asp | Val | Pro | Ile | Arg | Glu | Tyr | Lys | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Glu | Ala | Lys | Asn | Ile | Ala | Tyr | Pro | Thr | Ser | Gln | Pro | Met | Gly | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Ser | Thr | Leu | Trp | Glu | Ala | Asp | Asp | Trp | Ala | Thr | Arg | Gly | Gly | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp  
165 170 175  
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Leu Ser Ile  
180 185 190  
Glu Pro Ser  
195

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| agaaagcgag agcgaNtgat tcagaagatt ctgagaatga agaggatgag gatgaagaag | 60  |
| tagtagtaga agaagaagag gaggaagaag acgagggagg tagtgaagat ggcggagagg | 120 |
| gaagtcaaaa cgaaggagaa ctaaaaactg aggatggtgg tgaagaggaa agcgaataat | 180 |
| tgtaagatcg ttggttggtt gtaatgtagc ctagtttcac tatgtactgt tgtagagtgg | 240 |
| tgatattttg taccttttta atgtgctaata catatttatg                      |     |

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Ala Arg Ala Xaa Asp Ser Glu Asp Ser Glu Asn Glu Glu Asp Glu |  |
| 1 5 10 15                                                       |  |
| Asp Glu Glu Val Val Val Glu Glu Glu Glu Glu Glu Asp Glu Gly     |  |
| 20 25 30                                                        |  |
| Gly Ser Glu Asp Gly Gly Glu Gly Ser Gln Asn Glu Gly Glu Leu Lys |  |
| 35 40 45                                                        |  |
| Thr Glu Asp Gly Gly Glu Glu Glu Ser Glu                         |  |
| 50 55                                                           |  |

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ctgccaaaca tatacatcaa agcttgactc tctttttctc tcccatggaa tcgacaaaga  | 60  |
| agcaagtctc gctggagcta cttccatggt tagttgtcca caccgatgga acggtagaga  | 120 |
| gactagcggg aaccgaggtt tgtcctcccg gtttgatcc aataaccggg gttttctcta   | 180 |
| aagatatcat tatcgaaccg aaaaccggtt tatctgccg aatctatcga cccttctcga   | 240 |
| ttcaaccggg tcagaagatt cctctcatgc tctattttca tggcgggtgca tttctcatct | 300 |
| cctccacttc cttcccctct taccacacca gtcttaacaa aattgtcaat caggctaacg  | 360 |

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| tcatagccgt  | ctctgtcaat  | tacagactag  | caccagaaca | tccacttcct  | acagcgtacg  | 420  |
| aagactcatg  | gactgcgcta  | aatactatcc  | aagccataaa | cgagccgtgg  | atcaacgact  | 480  |
| acgcgcgactt | ggacagtata  | ttcctagtgg  | gagatagcgc | cggagctaata | atctcgcacc  | 540  |
| acctcgcaatt | tcgagccaaa  | caatctgacc  | Aaaaccgtga | aaataaaaagg | catttggaatg | 600  |
| atccaccccat | atTTTTTgggg | aacacaacct  | atcggagcag | agatcaaaga  | cgaagcgatg  | 660  |
| aaacaaatgg  | tggacggatg  | gtgggaattt  | gtgtgcccct | ccaagaaagg  | atctgatgac  | 720  |
| ccgtggatta  | atccgtttgc  | ggacgggtca  | ccggatcttg | gagggttagg  | gtgtgagaga  | 780  |
| gtgatgatta  | ctgtggcgga  | gaaagatata  | ttgaatgaga | gaggggaagat | gtatTTTtgaa | 840  |
| agattgggtga | agagtgaagt  | gaaaggaaag  | gttgagatta | tggagacgaa  | agagaaagat  | 900  |
| catgtTTTTc  | atatTTTTga  | gcccgaattgt | gatgaagcta | tggagatggt  | acgatgcttg  | 960  |
| gctctcttta  | taaaccaagt  | tgaagcttga  | tattatTTgt | tttgccataa  | tttgatggct  | 1020 |
| TTTTtaagt   | ttgtataatt  | tttacaTgtt  | tgttaatggt | gttgTtattg  | tctTTTcttt  | 1080 |
| taaattTgtg  | tattacattt  | atatgtggtt  | aaattTgtgt | TTTTcc      |             |      |

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Lys | His | Ile | His | Gln | Ser | Leu | Thr | Leu | Phe | Phe | Ser | Pro | Met | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Thr | Lys | Lys | Gln | Val | Ser | Leu | Glu | Leu | Leu | Pro | Trp | Leu | Val | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Thr | Asp | Gly | Thr | Val | Glu | Arg | Leu | Ala | Gly | Thr | Glu | Val | Cys | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Gly | Leu | Asp | Pro | Ile | Thr | Gly | Val | Phe | Ser | Lys | Asp | Ile | Ile | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Pro | Lys | Thr | Gly | Leu | Ser | Ala | Arg | Ile | Tyr | Arg | Pro | Phe | Ser | Ile |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gln | Pro | Gly | Gln | Lys | Ile | Pro | Leu | Met | Leu | Tyr | Phe | His | Gly | Gly | Ala |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Phe | Leu | Ile | Ser | Ser | Thr | Ser | Phe | Pro | Ser | Tyr | His | Thr | Ser | Leu | Asn |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Ile | Val | Asn | Gln | Ala | Asn | Val | Ile | Ala | Val | Ser | Val | Asn | Tyr | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Ala | Pro | Glu | His | Pro | Leu | Pro | Thr | Ala | Tyr | Glu | Asp | Ser | Trp | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Leu | Asn | Thr | Ile | Gln | Ala | Ile | Asn | Glu | Pro | Trp | Ile | Asn | Asp | Tyr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Asp | Leu | Asp | Ser | Ile | Phe | Leu | Val | Gly | Asp | Ser | Ala | Gly | Ala | Asn |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ile | Ser | His | His | Leu | Ala | Phe | Arg | Ala | Lys | Gln | Ser | Asp | Gln | Asn | Arg |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Glu | Asn | Lys | Arg | His | Trp | Asn | Asp | Pro | Pro | Ile | Phe | Leu | Gly | Asn | Thr |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Thr | Tyr | Arg | Ser | Arg | Asp | Gln | Arg | Arg | Ser | Asp | Glu | Thr | Asn | Gly | Gly |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Arg | Met | Val | Gly | Ile | Cys | Val | Pro | Leu | Gln | Glu | Arg | Ile |     |     |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1567333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met Glu Ser Thr Lys Lys Gln Val Ser Leu Glu Leu Leu Pro Trp Leu  
1 5 10 15  
Val Val His Thr Asp Gly Thr Val Glu Arg Leu Ala Gly Thr Glu Val  
20 25 30  
Cys Pro Pro Gly Leu Asp Pro Ile Thr Gly Val Phe Ser Lys Asp Ile  
35 40 45  
Ile Ile Glu Pro Lys Thr Gly Leu Ser Ala Arg Ile Tyr Arg Pro Phe  
50 55 60  
Ser Ile Gln Pro Gly Gln Lys Ile Pro Leu Met Leu Tyr Phe His Gly  
65 70 75 80  
Gly Ala Phe Leu Ile Ser Ser Thr Ser Phe Pro Ser Tyr His Thr Ser  
85 90 95  
Leu Asn Lys Ile Val Asn Gln Ala Asn Val Ile Ala Val Ser Val Asn  
100 105 110  
Tyr Arg Leu Ala Pro Glu His Pro Leu Pro Thr Ala Tyr Glu Asp Ser  
115 120 125  
Trp Thr Ala Leu Asn Thr Ile Gln Ala Ile Asn Glu Pro Trp Ile Asn  
130 135 140  
Asp Tyr Ala Asp Leu Asp Ser Ile Phe Leu Val Gly Asp Ser Ala Gly  
145 150 155 160  
Ala Asn Ile Ser His His Leu Ala Phe Arg Ala Lys Gln Ser Asp Gln  
165 170 175  
Asn Arg Glu Asn Lys Arg His Trp Asn Asp Pro Pro Ile Phe Leu Gly  
180 185 190  
Asn Thr Thr Tyr Arg Ser Arg Asp Gln Arg Arg Ser Asp Glu Thr Asn  
195 200 205  
Gly Gly Arg Met Val Gly Ile Cys Val Pro Leu Gln Glu Arg Ile  
210 215 220

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1567334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

Met Leu Tyr Phe His Gly Gly Ala Phe Leu Ile Ser Ser Thr Ser Phe  
1 5 10 15  
Pro Ser Tyr His Thr Ser Leu Asn Lys Ile Val Asn Gln Ala Asn Val  
20 25 30  
Ile Ala Val Ser Val Asn Tyr Arg Leu Ala Pro Glu His Pro Leu Pro  
35 40 45  
Thr Ala Tyr Glu Asp Ser Trp Thr Ala Leu Asn Thr Ile Gln Ala Ile  
50 55 60  
Asn Glu Pro Trp Ile Asn Asp Tyr Ala Asp Leu Asp Ser Ile Phe Leu  
65 70 75 80  
Val Gly Asp Ser Ala Gly Ala Asn Ile Ser His His Leu Ala Phe Arg  
85 90 95  
Ala Lys Gln Ser Asp Gln Asn Arg Glu Asn Lys Arg His Trp Asn Asp  
100 105 110  
Pro Pro Ile Phe Leu Gly Asn Thr Thr Tyr Arg Ser Arg Asp Gln Arg

115 120 125  
Arg Ser Asp Glu Thr Asn Gly Gly Arg Met Val Gly Ile Cys Val Pro  
130 135 140  
Leu Gln Glu Arg Ile  
145

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1877  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

aaacaaaaac aMcaattaag ctaaaaaaaa aaccaaagga tgtctcagaa actcatgttc 60  
ttgttcacccc ttgcctgcct ctccctcgta ccatctcctt ttatctccgc ccaaataccg 120  
gccattggaa atgccacttc accgtcaaat atatgtagat tcgcgcgga tccatcttat 180  
tgtagatcgg ttcttccaaa ccagcccgga gatatatatt cctacggacg ttgtctcta 240  
cgaagatccc tctccagccc gccggttcac ttcgatgatc gacgctgaac ttgaccggaa 300  
aggcaaaagt gctgctaaat ccacagtagg ggctctcgaa gactgcaaat tcctagccag 360  
cctgactatg gactacctcc ttagtagctc acagacggct gattccacca aaacactgtc 420  
gttatctagg gccgaggatg ttcatacatt tctgagtgtc gccatcacca atgagcagac 480  
ttgtcttgaa ggacttaaat caacggcgctc cgaaaatggg ctttccgggtg atcttttcaa 540  
cgatacaaaa ctctatgggg tgtctcttgc ctttttctcc aaagggttggg tgccaagaag 600  
gcaaaagatcg agaccgattt ggcaaccaca agccagggtt aaaaagtttt ttggtttccg 660  
taacggtaaa ttaccgttaa agatgacgga aagggcacgt gccgtttaca acaccgtgac 720  
tagaagaaaag cttctccaat cggatgcaga cgccgttcag gtgagcgaca ttgtgacggt 780  
gatccagaac gggacgggaa acttcaogac cataaacgcc gccattgcag ctgcacaaa 840  
taaaactgac ggtagtaacg gttacttctt gatctacgta acggcgggat tgtacgagga 900  
atacgtggaa gttcccaaga acaagagata tgtgatgatg atcggtgacg gcatcaacca 960  
gaccgttatc accggaaaca ggagtgtcgt tgatggatgg acaactttca attcagccac 1020  
atttattcta tcagggtccca actttatttg tgtaaacata acaatccgca atacggcagg 1080  
accaacaaaa ggccaagctg tggcattgag gagtgggtggg gacttgtctg ttttctacag 1140  
ttgtagtitt gaagcctatc aagacacgtt atacacacat tctctcagac agttttatcg 1200  
tgaatgtgat gtctatggta ctgttgattt tatatttggg aacgctgcag tggattaca 1260  
aaactgtaat ttgtatccac gtcaacctcg caaagggtcaa tcgaacgagg ttacggctca 1320  
aggctcgact gatccgaacc aaaacactgg gacggcaatt catggttgta ctataagacc 1380  
ggcagatgat ttggctacga gcaactatac agtgaagact tatcttggtc gaccatggaa 1440  
ggaatattct agaaccgttg tcatgcaaac ttacatagac ggggttctag aaccgagtgg 1500  
ttggaatgca tggctctggtg attttgcatt gagcacactt tactacgcgg aatataataa 1560  
taccggacct ggttctgaca cgacaaaacc agtcacttgg cctggttatc acgtcatcaa 1620  
cgcaactgat gcttccaatt tcacggtcac caatttccct gttgggtgaag gttggattgg 1680  
acaaaccgga gtgcctttcg tgggtggact gatcgcataa tcaaccaacc ttatactata 1740  
tatgatatgt taattagtta aattatttaa tcattcatgt gttgtttttt taatcaaata 1800  
attatttagt ggtgcctgat tcaatacgat ttgtaataac ttttaacttac tattgtacaa 1860  
ccgaatggtt ttcttcg

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..529  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |
| Asn | Ala | Thr | Asp | Ala | Ser | Asn | Phe | Thr | Val | Thr | Asn | Phe | Leu | Val | Gly |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |
| Glu | Gly | Trp | Ile | Gly | Gln | Thr | Gly | Val | Pro | Phe | Val | Gly | Gly | Leu | Ile |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |

Ala

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1567337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ile | Asp | Ala | Glu | Leu | Asp | Arg | Lys | Gly | Lys | Val | Ala | Ala | Lys | Ser |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Thr | Val | Gly | Ala | Leu | Glu | Asp | Cys | Lys | Phe | Leu | Ala | Ser | Leu | Thr | Met |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Asp | Tyr | Leu | Leu | Ser | Ser | Ser | Gln | Thr | Ala | Asp | Ser | Thr | Lys | Thr | Leu |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Ser | Leu | Ser | Arg | Ala | Glu | Asp | Val | His | Thr | Phe | Leu | Ser | Ala | Ala | Ile |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Thr | Asn | Glu | Gln | Thr | Cys | Leu | Glu | Gly | Leu | Lys | Ser | Thr | Ala | Ser | Glu |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Asn | Gly | Leu | Ser | Gly | Asp | Leu | Phe | Asn | Asp | Thr | Lys | Leu | Tyr | Gly | Val |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Ser | Leu | Ala | Leu | Phe | Ser | Lys | Gly | Trp | Val | Pro | Arg | Arg | Gln | Arg | Ser |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Arg | Pro | Ile | Trp | Gln | Pro | Gln | Ala | Arg | Phe | Lys | Lys | Phe | Phe | Gly | Phe |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Arg | Asn | Gly | Lys | Leu | Pro | Leu | Lys | Met | Thr | Glu | Arg | Ala | Arg | Ala | Val |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Tyr | Asn | Thr | Val | Thr | Arg | Arg | Lys | Leu | Leu | Gln | Ser | Asp | Ala | Asp | Ala |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Val | Gln | Val | Ser | Asp | Ile | Val | Thr | Val | Ile | Gln | Asn | Gly | Thr | Gly | Asn |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Phe | Thr | Thr | Ile | Asn | Ala | Ala | Ile | Ala | Ala | Ala | Pro | Asn | Lys | Thr | Asp |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Gly | Ser | Asn | Gly | Tyr | Phe | Leu | Ile | Tyr | Val | Thr | Ala | Gly | Leu | Tyr | Glu |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Glu | Tyr | Val | Glu | Val | Pro | Lys | Asn | Lys | Arg | Tyr | Val | Met | Met | Ile | Gly |  |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Asp | Gly | Ile | Asn | Gln | Thr | Val | Ile | Thr | Gly | Asn | Arg | Ser | Val | Val | Asp |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Gly | Trp | Thr | Thr | Phe | Asn | Ser | Ala | Thr | Phe | Ile | Leu | Ser | Gly | Pro | Asn |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Phe | Ile | Gly | Val | Asn | Ile | Thr | Ile | Arg | Asn | Thr | Ala | Gly | Pro | Thr | Lys |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Gly | Gln | Ala | Val | Ala | Leu | Arg | Ser | Gly | Gly | Asp | Leu | Ser | Val | Phe | Tyr |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Ser | Cys | Ser | Phe | Glu | Ala | Tyr | Gln | Asp | Thr | Leu | Tyr | Thr | His | Ser | Leu |  |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Arg | Gln | Phe | Tyr | Arg | Glu | Cys | Asp | Val | Tyr | Gly | Thr | Val | Asp | Phe | Ile |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Phe | Gly | Asn | Ala | Ala | Val | Val | Leu | Gln | Asn | Cys | Asn | Leu | Tyr | Pro | Arg |  |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |

Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr  
340 345 350  
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg  
355 360 365  
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu  
370 375 380  
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr  
385 390 395 400  
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp  
405 410 415  
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro  
420 425 430  
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile  
435 440 445  
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly  
450 455 460  
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile  
465 470 475 480  
Ala

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1567338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

Met Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr  
1 5 10 15  
Leu Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala  
20 25 30  
Ile Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser  
35 40 45  
Glu Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly  
50 55 60  
Val Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg  
65 70 75 80  
Ser Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly  
85 90 95  
Phe Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala  
100 105 110  
Val Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp  
115 120 125  
Ala Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly  
130 135 140  
Asn Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Ala Pro Asn Lys Thr  
145 150 155 160  
Asp Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr  
165 170 175  
Glu Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile  
180 185 190  
Gly Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val  
195 200 205  
Asp Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro  
210 215 220  
Asn Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr



225 230 235 240  
Lys Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe  
245 250 255  
Tyr Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser  
260 265 270  
Leu Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe  
275 280 285  
Ile Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro  
290 295 300  
Arg Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg  
305 310 315 320  
Thr Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile  
325 330 335  
Arg Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr  
340 345 350  
Leu Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr  
355 360 365  
Tyr Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly  
370 375 380  
Asp Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly  
385 390 395 400  
Pro Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val  
405 410 415  
Ile Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val  
420 425 430  
Gly Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu  
435 440 445  
Ile Ala  
450

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| aaaatctctc  | ttttcacgcc  | aatgaaagt   | ttaaaacctt  | tgaattgttt | attgaaagtt  | 60   |
| tacatttttc  | tgttgaatcc  | aactatgttt  | agattgagaa  | gtctcttgtc | gctgaagagt  | 120  |
| tottcgattg  | tagaattgtc  | atcacaaaac  | gtcacagaag  | caattcgttt | cgctccattt  | 180  |
| cattcgacaa  | gtgttctgtc  | tgaaaaatcg  | aggagtagat  | ttggttctgc | tagagattcc  | 240  |
| gaaGgcgaac  | gatcttcaaa  | gaactcctcc  | ataagattta  | catgtaccgt | aaaggagaag  | 300  |
| ggtcgtacca  | gtgctaagaa  | gactgtggat  | aaactccttt  | tccacagggg | aattaatgat  | 360  |
| ccgcttcaga  | atgagtggca  | tttcggggcca | agtcgcgtta  | tccgggatag | gcatatgaag  | 420  |
| aaaaaatctc  | cgcctggcag  | gggaaagaag  | cctcgagata  | agaaaacaaa | acgatggcac  | 480  |
| agagaaggta  | atccggacga  | tgattttggc  | actgatgcta  | ataatacatt | cgagaacaaa  | 540  |
| tggagagaac  | gctggacagc  | tcaatctcag  | aaggcttcat  | attcgaaaga | ctcgacagcg  | 600  |
| ggatttgaat  | ggagagaagg  | ctggagctgg  | accactcaat  | ctcagaggag | caaaagttgg  | 660  |
| aataaagagt  | cttttgatga  | acctttgaac  | gttgagttaa  | ggtctgagag | gaTtgttcta  | 720  |
| ggattgcctc  | ttgaagggtcc | catcaagggt  | gatgatgtta  | agaatgcctt | ccgatcttct  | 780  |
| gcgttgaagt  | ggcatccaga  | taagcaccag  | gggccttctc  | aggtggcagc | gcaagagaaa  | 840  |
| ttcaaaactc  | gtgttgatgc  | atacaagtcc  | ctctgtttctg | cactcgcttg | acgttacaca  | 900  |
| taggcattga  | tgcaccattt  | tagcattagt  | tgataaggct  | gcttctgaaa | cgtttttcgag | 960  |
| agatacacccg | gttttttagat | gatgggtttg  | atttggttca  | tgagaatcca | ccagctacaa  | 1020 |
| gattgcacac  | ggcacaccaa  | tgtgtctctc  | gtccttttcc  | aacatttgat | aacaaaaaca  | 1080 |
| tgtatgtgaa  | agatttatgc  | tagtgcccaa  | cttttagctg  | actgcttctt | tttttaaaac  | 1140 |
| acactgatgt  | gaaagacaat  | aacttgagaa  | tacatcgtgt  | atacaaaaca | ctattaaagc  | 1200 |

aattttatttt gt

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Ser | Leu | Phe | Thr | Pro | Asn | Glu | Ser | Leu | Lys | Pro | Leu | Asn | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Lys | Val | Tyr | Ile | Phe | Leu | Leu | Asn | Pro | Thr | Met | Phe | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | Leu | Leu | Ser | Leu | Lys | Ser | Ser | Ser | Ile | Val | Glu | Leu | Ser | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gln | Asn | Val | Thr | Glu | Ala | Ile | Arg | Phe | Ala | Pro | Phe | His | Ser | Thr | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Ser | Glu | Lys | Ser | Arg | Ser | Arg | Phe | Gly | Ser | Ala | Arg | Asp | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Gly | Glu | Arg | Ser | Ser | Lys | Asn | Ser | Ser | Ile | Arg | Phe | Thr | Cys | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Lys | Glu | Lys | Gly | Arg | Thr | Ser | Ala | Lys | Lys | Thr | Val | Asp | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Phe | His | Arg | Gly | Ile | Asn | Asp | Pro | Leu | Gln | Asn | Glu | Trp | His | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Pro | Ser | Pro | Leu | Ile | Arg | Asp | Arg | His | Met | Lys | Lys | Lys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gly | Arg | Gly | Lys | Lys | Pro | Arg | Asp | Lys | Lys | Thr | Lys | Arg | Trp | His |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Glu | Gly | Asn | Pro | Asp | Asp | Asp | Phe | Gly | Thr | Asp | Ala | Asn | Asn | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Glu | Asn | Lys | Trp | Arg | Glu | Arg | Trp | Thr | Ala | Gln | Ser | Gln | Lys | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Tyr | Ser | Lys | Asp | Ser | Thr | Ala | Gly | Phe | Glu | Trp | Arg | Glu | Gly | Trp |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Trp | Thr | Thr | Gln | Ser | Gln | Arg | Ser | Lys | Ser | Trp | Asn | Lys | Glu | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Phe | Asp | Glu | Pro | Leu | Asn | Val | Glu | Phe | Arg | Ser | Glu | Arg | Ile | Val | Leu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Leu | Pro | Leu | Glu | Gly | Pro | Ile | Lys | Val | Asp | Asp | Val | Lys | Asn | Ala |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Phe | Arg | Ser | Ser | Ala | Leu | Lys | Trp | His | Pro | Asp | Lys | His | Gln | Gly | Pro |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Gln | Val | Ala | Ala | Gln | Glu | Lys | Phe | Lys | Leu | Cys | Val | Asp | Ala | Tyr |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Leu | Cys | Ser | Ala | Leu | Ala |     |     |     |     |     |     |     |     |
| 290 |     |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..268

SEQUENCE 1-296

(D) OTHER INFORMATION: / Ceres Seq. ID 1567345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Phe Arg Leu Arg Ser Leu Leu Ser Leu Lys Ser Ser Ser Ile Val  
1 5 10 15  
Glu Leu Ser Ser Gln Asn Val Thr Glu Ala Ile Arg Phe Ala Pro Phe  
20 25 30  
His Ser Thr Ser Val Leu Ser Glu Lys Ser Arg Ser Arg Phe Gly Ser  
35 40 45  
Ala Arg Asp Ser Glu Gly Glu Arg Ser Ser Lys Asn Ser Ser Ile Arg  
50 55 60  
Phe Thr Cys Thr Val Lys Glu Lys Gly Arg Thr Ser Ala Lys Lys Thr  
65 70 75 80  
Val Asp Lys Leu Leu Phe His Arg Gly Ile Asn Asp Pro Leu Gln Asn  
85 90 95  
Glu Trp His Phe Gly Pro Ser Pro Leu Ile Arg Asp Arg His Met Lys  
100 105 110  
Lys Lys Ser Pro Pro Gly Arg Gly Lys Lys Pro Arg Asp Lys Lys Thr  
115 120 125  
Lys Arg Trp His Arg Glu Gly Asn Pro Asp Asp Asp Phe Gly Thr Asp  
130 135 140  
Ala Asn Asn Thr Phe Glu Asn Lys Trp Arg Glu Arg Trp Thr Ala Gln  
145 150 155 160  
Ser Gln Lys Ala Ser Tyr Ser Lys Asp Ser Thr Ala Gly Phe Glu Trp  
165 170 175  
Arg Glu Gly Trp Ser Trp Thr Thr Gln Ser Gln Arg Ser Lys Ser Trp  
180 185 190  
Asn Lys Glu Ser Phe Asp Glu Pro Leu Asn Val Glu Phe Arg Ser Glu  
195 200 205  
Arg Ile Val Leu Gly Leu Pro Leu Glu Gly Pro Ile Lys Val Asp Asp  
210 215 220  
Val Lys Asn Ala Phe Arg Ser Ser Ala Leu Lys Trp His Pro Asp Lys  
225 230 235 240  
His Gln Gly Pro Ser Gln Val Ala Ala Gln Glu Lys Phe Lys Leu Cys  
245 250 255  
Val Asp Ala Tyr Lys Ser Leu Cys Ser Ala Leu Ala  
260 265

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1567346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Met Lys Lys Lys Ser Pro Pro Gly Arg Gly Lys Lys Pro Arg Asp Lys  
1 5 10 15  
Lys Thr Lys Arg Trp His Arg Glu Gly Asn Pro Asp Asp Asp Phe Gly  
20 25 30  
Thr Asp Ala Asn Asn Thr Phe Glu Asn Lys Trp Arg Glu Arg Trp Thr  
35 40 45  
Ala Gln Ser Gln Lys Ala Ser Tyr Ser Lys Asp Ser Thr Ala Gly Phe  
50 55 60  
Glu Trp Arg Glu Gly Trp Ser Trp Thr Thr Gln Ser Gln Arg Ser Lys  
65 70 75 80  
Ser Trp Asn Lys Glu Ser Phe Asp Glu Pro Leu Asn Val Glu Phe Arg  
85 90 95  
Ser Glu Arg Ile Val Leu Gly Leu Pro Leu Glu Gly Pro Ile Lys Val

100 105 110  
Asp Asp Val Lys Asn Ala Phe Arg Ser Ser Ala Leu Lys Trp His Pro  
115 120 125  
Asp Lys His Gln Gly Pro Ser Gln Val Ala Ala Gln Glu Lys Phe Lys  
130 135 140  
Leu Cys Val Asp Ala Tyr Lys Ser Leu Cys Ser Ala Leu Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1077
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

aactcacacat ccacaaaaag agagtttagag attccaagga ggagagtgcg tgagCgtgac 60  
aatggaaact gacaaaagat ggtctctcgc cgggaaaaca gctctggtaa ccggcgggac 120  
tcgtggaatc gggagagcag ttgttagagga actagcaaaa tttttgcaaa agttcatact 180  
tgttcaagga accaggaaga gctaaatgca tgcttgaatg attggaaagc gaatggttta 240  
gtcgtgtctg gttcggtttg tgatgcttcg gttagggatc agagggagaa gttgattcag 300  
gaagcttctt ctgccttcag tggcaagctc aacatcctta taaacaatgt tggaaactaat 360  
gtcaggaac caacagttga atactcaagc gaggaatatg ccaaaatcat gtcgaccaac 420  
ttagaatccg ctttccatct atctcaaatt gctcatcctc ttctaaaagc atctggtgtc 480  
ggaagcattg tgttcatctc ctctgtagct ggcctgggtg atcttagcag tggatctatc 540  
tatggtgcaa cttaaaggagc acttaaatcag cttaacaaga atctagcttg cgagtgggca 600  
agcgacaaca tcagaaccaa ttgctgtggc ccattggtaca tcaagacctc acttgtggaa 660  
acgtactctg agaagaaaga atttgtggag gctgtagttt caaggacccc acttgggcgc 720  
gttgagaaac cagaggaagt ctcatcgttg gttgcctttc tctgccttcc cgcacatctc 780  
tatattaccg gacaggtcat atccgtcgat ggaggattca ctgtcaacgg ttttagctat 840  
gctatgaagc cttaatctcg aatcgcaaca ttactaataa agcaagaatc ctcgtgatgt 900  
gttggtcttg tttgtctttg tttagttttt gtgacttctt taaacatata gtaatatcaa 960  
aacgtttgaa tttctaattg agccgttaaa taaatcaagg cacagttgtg caccagttta 1020  
tgtagacctt caacatttgt cattgattta ggtatatgga tgagagtatt ttgatcgc

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met Val Ser Arg Arg Glu Asn Ser Ser Gly Asn Arg Arg Asp Ser Trp  
1 5 10 15  
Asn Arg Glu Ser Ser Cys Arg Gly Thr Ser Lys Ile Phe Ala Lys Val  
20 25 30  
His Thr Cys Ser Arg Asn Gln Glu Leu Asn Ala Cys Leu Asn Asp  
35 40 45  
Trp Lys Ala Asn Gly Leu Val Val Ser Gly Ser Val Cys Asp Ala Ser  
50 55 60  
Val Arg Asp Gln Arg Glu Lys Leu Ile Gln Glu Ala Ser Ser Ala Phe  
65 70 75 80  
Ser Gly Lys Leu Asn Ile Leu Ile Asn Asn Val Gly Thr Asn Val Arg  
85 90 95

Lys Pro

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..148
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567349

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1438

(D) OTHER INFORMATION: / Ceres Seq. ID 1567371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

atcaaattaa	aaccctccag	cctccaacaa	caaaatttac	caacactctc	tctttctctt	60
tctctctgaa	aacttaaaac	gatggctata	accgccactc	aaaacgacgg	cgtttcacta	120
aacgccaata	agatttcgta	tgatcttggt	gaaactgatg	ttgagatcat	cacctccggg	180
cgtcgtagta	ttccggcaca	ctccggcatc	ctcgtctcgg	tctcaccggg	actgacgaac	240
atcatcgaga	agccgaggaa	gattcacggc	ggatcatcga	agaaagttat	taagattctc	300
gggtgttccat	gcgacgccgt	ttcagtcctc	gtcagattcc	tctattctcc	gagtgtcacg	360
gagaatgaga	tggaaaaata	cggaatccat	ctactggctt	tatcacacgt	gtatatgggtg	420
actcagttaa	agcaacgggtg	cactaaaggc	gtcggtgaga	gagtaaccgc	cgaaaaacgtt	480
gtcgatatcc	tccagctggc	tcgtctctgc	gacgcacctg	acctctgtct	caagtgtatg	540
cgattcattc	actacaagtt	caagaccggt	gaacagacag	aaggatggaa	gtttcttcaa	600
gaacacgatc	cttttcttga	acttgacatt	ctccaattca	tgcacgatgc	agaatcgagg	660
aagaaaagaa	gaaggagaca	cagacgagaa	cagaatctgt	atttgcagct	gagtgaagcc	720
atggaatgta	tagaacacat	atgcaccgaa	ggttgcacac	tggtcggacc	atcgtctaac	780
ttagacaaca	agtcaacatg	tcaagcaaaa	cccgggtccat	gcagtgcggt	ttcgacttgt	840
taaggacttc	aacttcttat	acgtcacttt	gcagtatgca	agaaaagagt	cgatggcaaa	900
ggttgtgtcc	gatgcaagag	aatgattcaa	ctccttagac	tccattcttc	gatttgtgac	960
caatctgaat	cttgccgtgt	ccctctttgc	aggcaatata	agaatagagg	tgaaaaggac	1020
aagMaaaatg	gttgaggaca	cgaagtggaa	ggttctggtg	agaagagtag	cgtctgctaa	1080
agccatgtct	tcgttgtctc	aatcaaagaW	gaWaaaaagt	gaagtgttat	ttaaagaaga	1140
agcagaagat	ttgatcagaa	tccggaacaa	gttaatgtga	atatacaata	tatgtgtttt	1200
tattagatta	tatagtgagc	gattgttaga	agccattaat	tacttgagtc	ggaaggttta	1260
tttgtttgtt	atgtgtctct	cggactgggt	gattgggtta	aacttgtcaa	tgagtaaccc	1320
tttgaatctg	tcgttttgtt	tggtcggtcg	aattatatag	aatgtatta	ttggttataa	1380
aatggtatta	gggtttttgg	agactttgtg	gcaaaaagta	tacagattga	tccggttt	

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1567372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met	Ala	Ile	Thr	Ala	Thr	Gln	Asn	Asp	Gly	Val	Ser	Leu	Asn	Ala	Asn
1				5					10					15	
Lys	Ile	Ser	Tyr	Asp	Leu	Val	Glu	Thr	Asp	Val	Glu	Ile	Ile	Thr	Ser
			20						25					30	
Gly	Arg	Arg	Ser	Ile	Pro	Ala	His	Ser	Gly	Ile	Leu	Ala	Ser	Val	Ser
			35						40					45	
Pro	Val	Leu	Thr	Asn	Ile	Ile	Glu	Lys	Pro	Arg	Lys	Ile	His	Gly	Gly
			50				55				60				
Ser	Ser	Lys	Lys	Val	Ile	Lys	Ile	Leu	Gly	Val	Pro	Cys	Asp	Ala	Val
				70					75					80	
Ser	Val	Phe	Val	Arg	Phe	Leu	Tyr	Ser	Pro	Ser	Val	Thr	Glu	Asn	Glu
				85					90					95	
Met	Glu	Lys	Tyr	Gly	Ile	His	Leu	Leu	Ala	Leu	Ser	His	Val	Tyr	Met
			100						105					110	
Val	Thr	Gln	Leu	Lys	Gln	Arg	Cys	Thr	Lys	Gly	Val	Gly	Glu	Arg	Val
			115				120						125		
Thr	Ala	Glu	Asn	Val	Val	Asp	Ile	Leu	Gln	Leu	Ala	Arg	Leu	Cys	Asp
			130				135					140			
Ala	Pro	Asp	Leu	Cys	Leu	Lys	Cys	Met	Arg	Phe	Ile	His	Tyr	Lys	Phe
					150					155					160

Lys Thr Val Glu Gln Thr Glu Gly Trp Lys Phe Leu Gln Glu His Asp
165 170 175
Pro Phe Leu Glu Leu Asp Ile Leu Gln Phe Ile Asp Asp Ala Glu Ser
180 185 190
Arg Lys Lys Arg Arg Arg Arg His Arg Arg Glu Gln Asn Leu Tyr Leu
195 200 205
Gln Leu Ser Glu Ala Met Glu Cys Ile Glu His Ile Cys Thr Glu Gly
210 215 220
Cys Thr Leu Val Gly Pro Ser Ser Asn Leu Asp Asn Lys Ser Thr Cys
225 230 235 240
Gln Ala Lys Pro Gly Pro Cys Ser Ala Phe Ser Thr Cys
245 250

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met Glu Lys Tyr Gly Ile His Leu Leu Ala Leu Ser His Val Tyr Met
1 5 10 15
Val Thr Gln Leu Lys Gln Arg Cys Thr Lys Gly Val Gly Glu Arg Val
20 25 30
Thr Ala Glu Asn Val Val Asp Ile Leu Gln Leu Ala Arg Leu Cys Asp
35 40 45
Ala Pro Asp Leu Cys Leu Lys Cys Met Arg Phe Ile His Tyr Lys Phe
50 55 60
Lys Thr Val Glu Gln Thr Glu Gly Trp Lys Phe Leu Gln Glu His Asp
65 70 75 80
Pro Phe Leu Glu Leu Asp Ile Leu Gln Phe Ile Asp Asp Ala Glu Ser
85 90 95
Arg Lys Lys Arg Arg Arg Arg His Arg Arg Glu Gln Asn Leu Tyr Leu
100 105 110
Gln Leu Ser Glu Ala Met Glu Cys Ile Glu His Ile Cys Thr Glu Gly
115 120 125
Cys Thr Leu Val Gly Pro Ser Ser Asn Leu Asp Asn Lys Ser Thr Cys
130 135 140
Gln Ala Lys Pro Gly Pro Cys Ser Ala Phe Ser Thr Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

Met Val Thr Gln Leu Lys Gln Arg Cys Thr Lys Gly Val Gly Glu Arg
1 5 10 15
Val Thr Ala Glu Asn Val Val Asp Ile Leu Gln Leu Ala Arg Leu Cys
20 25 30
Asp Ala Pro Asp Leu Cys Leu Lys Cys Met Arg Phe Ile His Tyr Lys

(D) OTHER INFORMATION: / Ceres Seq. ID 1567384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met	Ala	Arg	Lys	Lys	His	Arg	Lys	Leu	Phe	Pro	Thr	Leu	Ala	Ser	Glu
1				5					10					15	
Thr	Asn	Lys	Thr	Leu	Asp	Cys	Ser	Asn	Gly	Val	Cys	Asp	Pro	Ile	Cys
			20					25					30		
Pro	Tyr	Asn	Cys	Tyr	Pro	Glu	Pro	Asp	Tyr	Tyr	Thr	Ile	Ser	Pro	Gln
		35				40						45			
Leu	Pro	Pro	Trp	Ser	Ser	Ser	Pro	Gln	Pro	Ser	Pro	Cys	Pro	Ser	Pro
	50					55					60				
Ser	Ile	Ser	Ala	Val	Tyr	Leu	Pro	Ser	Gln	Asp	Ser	Ser	Ser	Ser	Leu
65					70				75						80
Asp	Ala	Ile	Ser	Ile	Ile	Thr	Ile	Thr	Gly	Ala	Val	Leu	Ala	Ile	Leu
				85					90					95	
Leu	Thr	Gly	Phe	Phe	Leu	Val	Ala	Lys	Phe	Phe	Ser	Asp	Ser	Val	Asn
			100					105					110		
Arg	Val	Asn	Gln	Gly	Thr	Tyr	Gln	Ser	Asp	Asn	Glu	Asp	Asn	Asp	Thr
		115					120					125			
Val	Met	Glu	Glu	Glu	Phe	Gln	Asp	Arg	Glu	Gln	Val	Asp	His	Pro	Ile
	130					135					140				
Trp	Leu	Ile	Arg	Thr	Thr	Gly	Leu	Gln	Gln	Ser	Ile	Ile	Asn	Ser	Ile
145					150					155					160
Thr	Ile	Cys	Asn	Tyr	Xaa	Arg	Gly	Asp	Gly	Leu	Ile	Glu	Arg	Thr	Asp
			165					170						175	
Cys	Pro	Val	Cys	Leu	Asn	Glu	Phe	Glu	Glu	Asp	Glu	Ser	Leu	Arg	Leu
			180					185					190		
Leu	Pro	Lys	Cys	Asn	His	Ala	Phe	His	Ile	Ser	Cys	Ile	Asp	Thr	Trp
		195				200						205			
Leu	Ser	Ser	His	Thr	Asn	Cys	Pro	Leu	Cys	Arg	Ala	Gly	Ile	Ala	Met
	210				215						220				
Ile	Ser	Val	Thr	Thr	Pro	Arg	Tyr	Ser	Gly	Pro	Val	Glu	Val	Thr	Pro
225					230					235					240
Gly	Gly	Ser	Gly	Ser	His	Leu	Glu	Asn	Asp	Gly	Val	Asp	Glu	Glu	Asp
			245						250					255	
His	Gly	Glu	Ile	Glu	Asn	Arg	Val	Asp	Ser	Asp	Phe	Lys	Glu	Ser	Asp
			260					265					270		
Asp	Ser	Asp	Ile	Arg	Ile	Glu	Ile	Tyr	Arg	Phe	Asp	Ser	Asp	Gly	Asp
		275				280					285				
Gly	Ser	Glu	Thr	Glu	Thr	Lys	Glu	Arg	Val	Arg	Val	Leu	Lys	Glu	Cys
		290				295					300				
Met	Asp	Pro	Asn	Gly	Gly	Asp	Ser	Val	Asn	Ser	Leu	Ser	His	Thr	Lys
305				310						315					320
Thr	His	Val	Glu	Ser	Val	Asp	Phe	Pro	Gly	Lys	Ser	Cys	Glu	Asn	Gln
			325						330					335	
Ser	Glu	Glu	Phe	Thr	Arg	His	Asn	Gly	Glu	Asp	Glu	Ala	Ser	Cys	Ser
			340					345					350		
Glu	Glu	Asn	Gly	Gly	Gly	Ser	Asn	Gln	Leu	Arg	Arg	Ser	Cys	Asp	Ser
		355					360					365			
Gly	Glu	Leu	Asn	Gly	Glu	Thr	Thr	Gly	Asp	Glu	Gly	Lys	Ser	Gln	Ser
		370				375					380				
Asp	Ile	Ser	Ser	Ser	Thr	Leu	Lys	Thr	Asn	Gly	Ser	Ser	Ser	Ser	Val
385					390					395					400
Ser	Cys	Phe	Asn	Lys	Asn	Lys	Ser	Ser	Val	Phe	Pro	Leu			
			405						410						

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

U.S. PAT. & TRADEMARK OFFICE

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1567385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met	Glu	Glu	Glu	Phe	Gln	Asp	Arg	Glu	Gln	Val	Asp	His	Pro	Ile	Trp
1				5					10					15	
Leu	Ile	Arg	Thr	Thr	Gly	Leu	Gln	Gln	Ser	Ile	Ile	Asn	Ser	Ile	Thr
			20					25					30		
Ile	Cys	Asn	Tyr	Xaa	Arg	Gly	Asp	Gly	Leu	Ile	Glu	Arg	Thr	Asp	Cys
		35					40					45			
Pro	Val	Cys	Leu	Asn	Glu	Phe	Glu	Glu	Asp	Glu	Ser	Leu	Arg	Leu	Leu
	50					55					60				
Pro	Lys	Cys	Asn	His	Ala	Phe	His	Ile	Ser	Cys	Ile	Asp	Thr	Trp	Leu
65					70					75				80	
Ser	Ser	His	Thr	Asn	Cys	Pro	Leu	Cys	Arg	Ala	Gly	Ile	Ala	Met	Ile
				85					90					95	
Ser	Val	Thr	Thr	Pro	Arg	Tyr	Ser	Gly	Pro	Val	Glu	Val	Thr	Pro	Gly
			100					105					110		
Gly	Ser	Gly	Ser	His	Leu	Glu	Asn	Asp	Gly	Val	Asp	Glu	Glu	Asp	His
		115					120					125			
Gly	Glu	Ile	Glu	Asn	Arg	Val	Asp	Ser	Asp	Phe	Lys	Glu	Ser	Asp	Asp
	130					135					140				
Ser	Asp	Ile	Arg	Ile	Glu	Ile	Tyr	Arg	Phe	Asp	Ser	Asp	Gly	Asp	Gly
145					150					155				160	
Ser	Glu	Thr	Glu	Thr	Lys	Glu	Arg	Val	Arg	Val	Leu	Lys	Glu	Cys	Met
				165					170					175	
Asp	Pro	Asn	Gly	Gly	Asp	Ser	Val	Asn	Ser	Leu	Ser	His	Thr	Lys	Thr
		180						185					190		
His	Val	Glu	Ser	Val	Asp	Phe	Pro	Gly	Lys	Ser	Cys	Glu	Asn	Gln	Ser
	195						200					205			
Glu	Glu	Phe	Thr	Arg	His	Asn	Gly	Glu	Asp	Glu	Ala	Ser	Cys	Ser	Glu
	210					215					220				
Glu	Asn	Gly	Gly	Gly	Ser	Asn	Gln	Leu	Arg	Arg	Ser	Cys	Asp	Ser	Gly
225					230					235				240	
Glu	Leu	Asn	Gly	Glu	Thr	Thr	Gly	Asp	Glu	Gly	Lys	Ser	Gln	Ser	Asp
			245						250					255	
Ile	Ser	Ser	Ser	Thr	Leu	Lys	Thr	Asn	Gly	Ser	Ser	Ser	Ser	Val	Ser
			260					265						270	
Cys	Phe	Asn	Lys	Asn	Lys	Ser	Ser	Val	Phe	Pro	Leu				
	275						280								

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2184

(D) OTHER INFORMATION: / Ceres Seq. ID 1567390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

accagcccca	ttaataaacc	accgggctct	gtttcaataa	aaaaaatccc	ctccctctca	60
tatttacctc	ccgaataaaa	ccggagggag	agaaaaaaca	taaaaagcaa	aaaaaaaggt	120
aaaatcaaaa	agggaaaaaa	tatataacaa	caaaaaaaaa	aagttagaaa	aaatggcagt	180
aggaaaggtt	gtggtatctg	tggcatcact	cctcctagtg	gtgggtgttg	ccataggagt	240
tatcacgttc	gttaataaaag	gaggcggcgc	caatggcgac	agtaatggtc	ccataaaactc	300
tcatcagaaa	gcggttcaga	caatttgcca	gtcaaccaca	gaccaaggtt	cgtgcgcgaa	360
aacactcgac	ccagtcaaaa	gtgatgatcc	aagcaagctt	gtcaaagcct	tcctgatggc	420
tactaaagac	gcgatcacaa	aatcctcaaa	cttcacggct	tcgaccgaag	Gaggtatggg	480
tactaacatg	aacgcgacca	gcaaagccgt	tcttgattac	tgcaagagag	tattgatgta	540

cgctcttgag gatcttgaga ccattgttga agagatgggt gaggatcttc agcagagtgg 600
aactaagctt gaccagctca aacaatgggt aactggagtt ttcaactacc aaaccgattg 660
tcttgacgac atcgaggaag ttgagctaaa gaagatcatg ggtgaaggaa tctctaactc 720
caagggttttg accagtaacg ctatcgatat cttccattcc gttgttaccg cgatggccca 780
aatgggtgtc aaagtgcagc atatgaagaa cataaccatg ggagccggag ccggtggagc 840
tgcacgtcgc cttcttgaag acaacgactc taagggactc cccaaatggg tttctggtaa 900
agacaggaag cttatggcta aggcgggacg tggcgctcca gctggcgggt atgatggat 960
cgggtgaaggc ggtgggtggtg gcggtaagat caaggcgact catgtagtgg ctaaggatgg 1020
aagtggacag ttttaagacca tttctgaggg gggttatggct tgcccggata aaaaccctgg 1080
aaggtgcatt atccatatca aggctggtat ctacaatgaa caagtcagaa tccctaagaa 1140
gaagaacaac attttcatgt tcggtgatgg tgctacacaa accatcatta cctttgacag 1200
aagtgtttaa cttagcccag gaaccactac ttcactcagt ggcaccgttc aggtcgaatc 1260
tgaggggattc atggcgaaat ggattgggtt taagaacact gctggtccat tgggacacca 1320
agcggtcgca ctccgtgtga acggagaccg tgcggtcata ttcaactgta gattcgacgg 1380
ttaccaagac acactctacg tcaacaacgg acgtcaattc tacaggaaca ttgttgtatc 1440
cggtagacgtg gatttcatct tcggaaaatc cgcaactgtg atccaaaact ctctcatcct 1500
cgtccgaaaag ggaagccccg gacaatccaa ctacgttacg gctgacggta atgaaaaggg 1560
tgcagcgatg aagatcggtg tcgtcctcca taactgccgt atcataccgg acaaggagct 1620
cgaagctgac aagctaacca tcaaatcgta cctaggaagg ccgtggaaga agtttgccac 1680
gactgtgatt attggaactg agattgggtg tttgattaaa ccagaaggat ggaccgaatg 1740
gcaaggagaa caaaaccaca agactgctaa atacattgag ttcaataacc gtggaccggg 1800
agctgccact actcagaggc ctccctgggt taaggtggct aagtctgcgg ctgaggttga 1860
aacttacacc gtggctaact ggggttggtcc agctaactgg atccaagaag ccaacgtgcc 1920
cgtccaacta ggattgtaag aggacaacac aaaaaagtta agaataaaac agtatgtgat 1980
aatgttaagg taacgatacg acgtogtctc tggggatcag aactcttttt tggatactat 2040
atacaaagat agggttctag acgtgttgag atgatgtttg tataagattg ctttcgttca 2100
cgtgcaaaaag aggaaaaaaa attgttttgt ttttttttt gtagtacaaa taattaattt 2160
ttttttatca catgttgtat cctt

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1567391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Met Ala Val Gly Lys Val Val Val Ser Val Ala Ser Leu Leu Leu Val
1 5 10 15
Val Gly Val Ala Ile Gly Val Ile Thr Phe Val Asn Lys Gly Gly Gly
20 25 30
Ala Asn Gly Asp Ser Asn Gly Pro Ile Asn Ser His Gln Lys Ala Val
35 40 45
Gln Thr Ile Cys Gln Ser Thr Thr Asp Gln Gly Ser Cys Ala Lys Thr
50 55 60
Leu Asp Pro Val Lys Ser Asp Asp Pro Ser Lys Leu Val Lys Ala Phe
65 70 75 80
Leu Met Ala Thr Lys Asp Ala Ile Thr Lys Ser Ser Asn Phe Thr Ala
85 90 95
Ser Thr Glu Gly Gly Met Gly Thr Asn Met Asn Ala Thr Ser Lys Ala
100 105 110
Val Leu Asp Tyr Cys Lys Arg Val Leu Met Tyr Ala Leu Glu Asp Leu
115 120 125
Glu Thr Ile Val Glu Glu Met Gly Glu Asp Leu Gln Gln Ser Gly Thr
130 135 140
Lys Leu Asp Gln Leu Lys Gln Trp Leu Thr Gly Val Phe Asn Tyr Gln
145 150 155 160
Thr Asp Cys Leu Asp Asp Ile Glu Glu Val Glu Leu Lys Lys Ile Met

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1567392

Met 1	Ala	Thr	Lys	Asp 5	Ala	Ile	Thr	Lys	Ser 10	Ser	Asn	Phe	Thr	Ala 15	Ser
Thr	Glu	Gly	Gly 20	Met	Gly	Thr	Asn	Met 25	Asn	Ala	Thr	Ser 30	Lys	Ala	Val
Leu	Asp	Tyr 35	Cys	Lys	Arg	Val	Leu 40	Met	Tyr	Ala	Leu 45	Glu	Asp	Leu	Glu
Thr	Ile 50	Val	Glu	Glu	Met	Gly 55	Glu	Asp	Leu	Gln 60	Gln	Ser	Gly	Thr	Lys
Leu 65	Asp	Gln	Leu	Lys	Gln 70	Trp	Leu	Thr	Gly	Val 75	Phe	Asn	Tyr	Gln	Thr 80
Asp	Cys	Leu	Asp	Asp 85	Ile	Glu	Glu	Val	Glu 90	Leu	Lys	Lys	Ile	Met 95	Gly
Glu	Gly	Ile	Ser 100	Asn	Ser	Lys	Val	Leu 105	Thr	Ser	Asn	Ala 110	Ile	Asp	Ile
Phe	His	Ser 115	Val	Val	Thr	Ala	Met 120	Ala	Gln	Met	Gly 125	Val	Lys	Val	Asp
Asp	Met 130	Lys	Asn	Ile	Thr	Met 135	Gly	Ala	Gly	Ala	Gly 140	Gly	Ala	Ala	Arg
Arg 145	Leu	Leu	Glu	Asp	Asn 150	Asp	Ser	Lys	Gly	Leu 155	Pro	Lys	Trp	Phe	Ser 160
Gly	Lys	Asp	Arg	Lys 165	Leu	Met	Ala	Lys	Ala 170	Gly	Arg	Gly	Ala	Pro 175	Ala
Gly	Gly	Asp	Asp 180	Gly	Ile	Gly	Glu 185	Gly	Gly	Gly	Gly	Gly 190	Gly	Lys	Ile
Lys	Ala 195	Thr	His	Val	Val	Ala	Lys 200	Asp	Gly	Ser	Gly	Gln 205	Phe	Lys	Thr
Ile	Ser 210	Glu	Ala	Val	Met	Ala 215	Cys	Pro	Asp	Lys	Asn 220	Pro	Gly	Arg	Cys
Ile 225	Ile	His	Ile	Lys	Ala 230	Gly	Ile	Tyr	Asn	Glu 235	Gln	Val	Arg	Ile	Pro 240
Lys	Lys	Lys	Asn	Asn 245	Ile	Phe	Met	Phe	Gly 250	Asp	Gly	Ala	Thr	Gln 255	Thr
Ile	Ile	Thr	Phe 260	Asp	Arg	Ser	Val	Lys 265	Leu	Ser	Pro	Gly	Thr 270	Thr	Thr
Ser	Leu 275	Ser	Gly	Thr	Val	Gln 280	Val	Glu	Ser	Glu	Gly 285	Phe	Met	Ala	Lys
Trp	Ile 290	Gly	Phe	Lys	Asn	Thr 295	Ala	Gly	Pro	Leu	Gly 300	His	Gln	Ala	Val
Ala 305	Leu	Arg	Val	Asn	Gly 310	Asp	Arg	Ala	Val	Ile 315	Phe	Asn	Cys	Arg	Phe 320
Asp	Gly	Tyr	Gln	Asp 325	Thr	Leu	Tyr	Val	Asn 330	Asn	Gly	Arg	Gln	Phe 335	Tyr
Arg	Asn	Ile	Val	Val 340	Ser	Gly	Thr	Val 345	Asp	Phe	Ile	Phe	Gly 350	Lys	Ser
Ala	Thr 355	Val	Ile	Gln	Asn	Ser	Leu 360	Ile	Leu	Val	Arg	Lys 365	Gly	Ser	Pro
Gly	Gln 370	Ser	Asn	Tyr	Val	Thr 375	Ala	Asp	Gly	Asn	Glu 380	Lys	Gly	Ala	Ala
Met 385	Lys	Ile	Gly	Ile	Val 390	Leu	His	Asn	Cys	Arg 395	Ile	Ile	Pro	Asp	Lys 400
Glu	Leu	Glu	Ala	Asp 405	Lys	Leu	Thr	Ile	Lys 410	Ser	Tyr	Leu	Gly	Arg 415	Pro
Trp	Lys	Lys	Phe 420	Ala	Thr	Thr	Val	Ile 425	Ile	Gly	Thr	Glu	Ile 430	Gly	Asp
Leu	Ile 435	Lys	Pro	Glu	Gly	Trp	Thr 440	Glu	Trp	Gln	Gly	Glu 445	Gln	Asn	His
Lys	Thr	Ala	Lys	Tyr	Ile	Glu	Phe	Asn	Asn	Arg	Gly	Pro	Gly	Ala	Ala

(2) INFORMATION FOR SEQ ID NO:591:

(A) LENGTH: 487 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1567393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

[illegible]

(2) INFORMATION FOR SEQ ID NO:592:

(A) LENGTH: 1090 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1090

(D) OTHER INFORMATION: / Ceres Seq. ID 1567394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

ctacaacaaa	cccagtggtg	cacttcattt	tactgcgtca	aataatgact	gtggagttag	60
agactttgac	atggagagat	accagcttgt	taagcatttc	cgttttcctt	ggccagtgaa	120
tcacgcatct	ttgagtcctg	atggtaaatt	actggctatt	gttgagaca	acccggaggG	180
ccttattgta	gacccaaca	caggaaagac	gttggaaca	ctatcaggac	acttggaactt	240
ttcctttgcc	tctgcgtggc	atccggatgg	agtcactttc	tctacaggaa	accaagataa	300
gacttgtcgt	gtatgggaca	tccgtaacct	atctcagctc	gttactgtct	tgaagggtaa	360
cctggggagca	atccggtc aa	tccgtatcac	atcagatgga	aaatacatgg	ccatggctga	420
acccgctgac	tttgccatct	tctatgatgt	ctcaaacggg	tatgaacagc	agcaggaaat	480
cgacttcttt	ggggaaatct	ctggaatatc	tttcagccct	gacacagagg	cgctatttat	540
tggggtatgg	gaccgcactt	atggtagcct	ccttgagttt	ggtcggcgca	ggaactattc	600
ctaccttgac	tcgtatcttt	aagctagaag	agaagtatac	acaaccctgt	ccaatgaaga	660
aaagagagct	cattcagcaa	ccagtgaaca	tgacagaagc	aaagcataga	tatatggata	720
tctcaaagat	gtaaatgatg	tgttgtgcaa	atgctagtta	gttagtgtct	tttgtttctt	780
tctccggctg	gtgtgttatt	ttccttatgt	ctggttatgt	ctggtctcaa	aaggttcaag	840
atgtgtacag	aaagggctgg	ttcagtggtg	gcacagactg	gattaggact	tgaggggtggC	900
tccgcagcgg	gttctggatt	caaagtcggg	aggatcattg	ttgttgtgtt	tggtggcttg	960
tgatcttttc	tttttgttcc	ttgtacttgt	ggttggtgta	ggaactcgag	tgttttagatc	1020
ctgttctgag	tttagaattt	ggagatactt	aactaaatta	aaataaatta	ataatagtc	1080
tttgttcgtt						

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1567395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Tyr	Asn	Lys	Pro	Ser	Gly	Ala	Leu	His	Phe	Thr	Ala	Ser	Asn	Asn	Asp
1				5					10					15	
Cys	Gly	Val	Arg	Asp	Phe	Asp	Met	Glu	Arg	Tyr	Gln	Leu	Val	Lys	His
			20					25					30		
Phe	Arg	Phe	Pro	Trp	Pro	Val	Asn	His	Ala	Ser	Leu	Ser	Pro	Asp	Gly
		35					40					45			
Lys	Leu	Leu	Ala	Ile	Val	Gly	Asp	Asn	Pro	Glu	Gly	Leu	Ile	Val	Asp
	50					55					60				
Pro	Asn	Thr	Gly	Lys	Thr	Leu	Glu	Thr	Leu	Ser	Gly	His	Leu	Asp	Phe
65					70				75						80
Ser	Phe	Ala	Ser	Ala	Trp	His	Pro	Asp	Gly	Val	Thr	Phe	Ser	Thr	Gly
			85						90					95	
Asn	Gln	Asp	Lys	Thr	Cys	Arg	Val	Trp	Asp	Ile	Arg	Asn	Leu	Ser	Gln
			100					105					110		
Ser	Val	Thr	Val	Leu	Lys	Gly	Asn	Leu	Gly	Ala	Ile	Arg	Ser	Ile	Arg
		115					120					125			
Tyr	Thr	Ser	Asp	Gly	Lys	Tyr	Met	Ala	Met	Ala	Glu	Pro	Ala	Asp	Phe
	130					135						140			
Val	His	Val	Tyr	Asp	Val	Ser	Asn	Gly	Tyr	Glu	Thr	Glu	Gln	Glu	Ile
145					150					155					160
Asp	Phe	Phe	Gly	Glu	Ile	Ser	Gly	Ile	Ser	Phe	Ser	Pro	Asp	Thr	Glu
			165						170					175	
Ala	Leu	Phe	Ile	Gly	Val	Trp	Asp	Arg	Thr	Tyr	Gly	Ser	Leu	Leu	Glu
			180					185					190		
Phe	Gly	Arg	Arg	Arg	Asn	Tyr	Ser	Tyr	Leu	Asp	Ser	Tyr	Leu		
	195					200						205			

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1567396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Met	Glu	Arg	Tyr	Gln	Leu	Val	Lys	His	Phe	Arg	Phe	Pro	Trp	Pro	Val
1					5				10					15	
Asn	His	Ala	Ser	Leu	Ser	Pro	Asp	Gly	Lys	Leu	Leu	Ala	Ile	Val	Gly
			20					25					30		
Asp	Asn	Pro	Glu	Gly	Leu	Ile	Val	Asp	Pro	Asn	Thr	Gly	Lys	Thr	Leu
		35					40					45			
Glu	Thr	Leu	Ser	Gly	His	Leu	Asp	Phe	Ser	Phe	Ala	Ser	Ala	Trp	His
	50					55					60				
Pro	Asp	Gly	Val	Thr	Phe	Ser	Thr	Gly	Asn	Gln	Asp	Lys	Thr	Cys	Arg
65					70					75					80
Val	Trp	Asp	Ile	Arg	Asn	Leu	Ser	Gln	Ser	Val	Thr	Val	Leu	Lys	Gly
			85						90					95	
Asn	Leu	Gly	Ala	Ile	Arg	Ser	Ile	Arg	Tyr	Thr	Ser	Asp	Gly	Lys	Tyr
		100						105					110		
Met	Ala	Met	Ala	Glu	Pro	Ala	Asp	Phe	Val	His	Val	Tyr	Asp	Val	Ser
		115					120					125			
Asn	Gly	Tyr	Glu	Thr	Glu	Gln	Glu	Ile	Asp	Phe	Phe	Gly	Glu	Ile	Ser
	130					135					140				
Gly	Ile	Ser	Phe	Ser	Pro	Asp	Thr	Glu	Ala	Leu	Phe	Ile	Gly	Val	Trp
145					150					155					160
Asp	Arg	Thr	Tyr	Gly	Ser	Leu	Leu	Glu	Phe	Gly	Arg	Arg	Arg	Asn	Tyr

165 170 175
Ser Tyr Leu Asp Ser Tyr Leu
180

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

Met	Glu	Asn	Thr	Trp	Pro	Trp	Leu	Asn	Arg	Leu	Thr	Leu	Ser	Met	Ser
1				5				10					15		
Met	Met	Ser	Gln	Thr	Gly	Met	Lys	Gln	Ser	Arg	Lys	Ser	Thr	Ser	Leu
			20					25					30		
Gly	Lys	Ser	Leu	Glu	Tyr	Leu	Ser	Ala	Leu	Thr	Gln	Arg	Arg	Tyr	Leu
			35				40					45			
Leu	Gly	Tyr	Gly	Thr	Ala	Leu	Met	Val	Ala	Ser	Leu	Ser	Leu	Val	Gly
			50				55				60				
Ala	Gly	Thr	Ile	Pro	Thr	Leu	Thr	Arg	Ile	Phe	Lys	Leu	Glu	Glu	Lys
65						70				75				80	
Tyr	Thr	Gln	Pro	Cys	Pro	Met	Lys	Lys	Arg	Glu	Leu	Ile	Gln	Gln	Pro
				85					90					95	
Val	Asn	Met	Thr	Glu	Ala	Lys	His	Arg	Tyr	Met	Asp	Ile	Ser	Lys	Met
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1449
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

aaccactcat	ctcaatttct	cccacggtct	agattctctc	cgcttctatg	tctttcccg	60
gaaaattcgg	gacagcgatt	cacgcgcgtc	tatcttttat	cgtcttcttc	ttcttcgacc	120
tcattgacgc	gattctctgt	gtcgtttaacg	agttcgtcga	tgagattttg	gaagaaaact	180
caacaggctg	ttactgcaacg	gcggcggctc	ctcaaagtct	aaccacgcac	gaaaatgagt	240
tgctgctcga	gactttatct	gggaggagaa	acagtttccg	ggaaatgtgg	tttctgggat	300
tcgcgagaga	attcaaatcc	aagctttccc	ggaaactgag	aaaatctaag	attcatcaag	360
agtcagtga	tcgatggcca	gattgtggat	gcaaactctg	caagtcAtgg	actaagaacg	420
aagatgggaa	tcttcacgtc	gtgggtcaaa	attctacttc	tcgagaaaaca	gagtactctg	480
ttcaagaacc	gtccgagaat	gtaatatcca	tacacgggtt	tatgggggtca	tcacattttt	540
ggacagaaac	tgtatttgaa	cacattcaaa	aagatgatta	taggctcctc	gcgatcgatc	600
ttttgggatt	cggggagagt	cctaagccaa	gggatagtct	ctatacattg	aaagatcatg	660
tggatacgat	agagagatct	gtcattaagc	cataccaatt	agattctttt	catgtggttg	720
cacattcaat	gggttgctta	attgctcttg	ctttggtctg	taaacattcc	aacattgtta	780
aatccgttac	tcttggtgca	ccgccttatt	ttccttcata	ggtagatgga	tcggtcttga	840
accgaatcgc	tagaaagcgg	ttgtggccac	cgcttgcggt	tgggacagcg	gtgatgtctt	900
ggtatgaaca	tattggtaga	tgcgatggtt	tcataatctg	caagcatcat	aagatatggg	960
agtggcta	caagctatgt	ataggtaaaa	gggagattca	ttggaagatc	aaggacataa	1020
caaggcacac	acatcactct	gcattggcata	gtatgcacaa	tgtgatatgt	ggtgggtcca	1080

```
aagtcgctga tgaacatctt gaaaccctaa taaagtctgg cgtaaagatt cacttgatgc 1140
aaggcgactg tgaccaaata gttccttcac attgctctgg caacatgaag aggacttttc 1200
cggcggtgga agttgatata attactgggtg ctgatcatga tagtatgata agcgaagag 1260
gagaagagtt tgctgagaaa ttggagagca tttggtgttc atttaaagag tctgggttagt 1320
tttttcaaac tttataggta ggaggcactg tagtcgatgt cgactgacta caagtttgag 1380
tccgattgta agatcaagtc tattgttaat gagccatcta atggacgcct atatggagtc 1440
caattatcg
```

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1567406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

```
Met Ser Phe Pro Arg Lys Phe Gly Thr Ala Ile His Ala Ala Leu Ser
1      5      10      15
Phe Ile Val Phe Phe Phe Asp Leu Ile Asp Ala Ile Leu Cys Val
20      25      30
Val Tyr Glu Phe Val Asp Glu Ile Leu Glu Glu Asn Ser Thr Gly Cys
35      40      45
Tyr Cys Thr Ala Ala Ala Pro Gln Ser Leu Thr Thr Asp Glu Asn Glu
50      55      60
Leu Ser Ser Glu Thr Leu Phe Gly Arg Arg Asn Ser Phe Arg Glu Met
65      70      75      80
Trp Phe Leu Gly Phe Ala Arg Glu Phe Lys Ser Lys Leu Ser Arg Lys
85      90      95
Leu Arg Lys Ser Lys Ile His Gln Glu Ser Val Asn Arg Trp Ser Asp
100     105     110
Cys Gly Cys Lys Ser Cys Lys Ser Trp Thr Lys Asn Glu Asp Gly Asn
115     120     125
Leu His Val Val Val Lys Asp Ser Thr Ser Arg Glu Thr Glu Tyr Ser
130     135     140
Val Gln Glu Pro Ser Glu Asn Val Ile Phe Ile His Gly Phe Met Gly
145     150     155     160
Ser Ser His Phe Trp Thr Glu Thr Val Phe Glu His Ile Gln Lys Asp
165     170     175
Asp Tyr Arg Leu Leu Ala Ile Asp Leu Leu Gly Phe Gly Glu Ser Pro
180     185     190
Lys Pro Arg Asp Ser Leu Tyr Thr Leu Lys Asp His Val Asp Thr Ile
195     200     205
Glu Arg Ser Val Ile Lys Pro Tyr Gln Leu Asp Ser Phe His Val Val
210     215     220
Ala His Ser Met Gly Cys Leu Ile Ala Leu Ala Leu Ala Ala Lys His
225     230     235     240
Ser Asn Ile Val Lys Ser Val Thr Leu Val Ala Pro Pro Tyr Phe Pro
245     250     255
Ser Ser Val Asp Gly Ser Val Leu Asn Arg Ile Ala Arg Lys Arg Leu
260     265     270
Trp Pro Pro Leu Ala Phe Gly Thr Ala Val Met Ser Trp Tyr Glu His
275     280     285
Ile Gly Arg Cys Val Cys Phe Ile Ile Cys Lys His His Lys Ile Trp
290     295     300
Glu Trp Leu Ile Lys Leu Cys Ile Gly Lys Arg Glu Ile His Trp Lys
305     310     315     320
Ile Lys Asp Ile Thr Arg His Thr His His Ser Ala Trp His Ser Met
325     330     335
```

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(2) INFORMATION FOR SEO ID NO:598:

(A) LENGTH: 344 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1567407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

[illegible]

290 295 300
Phe Pro Ala Val Glu Val Asp Ile Ile Thr Gly Ala Asp His Asp Ser
305 310 315 320
Met Ile Ser Gly Arg Gly Glu Glu Phe Ala Glu Lys Leu Glu Ser Ile
325 330 335
Trp Cys Ser Phe Lys Glu Ser Gly
340

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1567408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

Met Gly Ser Ser His Phe Trp Thr Glu Thr Val Phe Glu His Ile Gln
1 5 10 15
Lys Asp Asp Tyr Arg Leu Leu Ala Ile Asp Leu Leu Gly Phe Gly Glu
20 25 30
Ser Pro Lys Pro Arg Asp Ser Leu Tyr Thr Leu Lys Asp His Val Asp
35 40 45
Thr Ile Glu Arg Ser Val Ile Lys Pro Tyr Gln Leu Asp Ser Phe His
50 55 60
Val Val Ala His Ser Met Gly Cys Leu Ile Ala Leu Ala Leu Ala Ala
65 70 75 80
Lys His Ser Asn Ile Val Lys Ser Val Thr Leu Val Ala Pro Pro Tyr
85 90 95
Phe Pro Ser Ser Val Asp Gly Ser Val Leu Asn Arg Ile Ala Arg Lys
100 105 110
Arg Leu Trp Pro Pro Leu Ala Phe Gly Thr Ala Val Met Ser Trp Tyr
115 120 125
Glu His Ile Gly Arg Cys Val Cys Phe Ile Ile Cys Lys His His Lys
130 135 140
Ile Trp Glu Trp Leu Ile Lys Leu Cys Ile Gly Lys Arg Glu Ile His
145 150 155 160
Trp Lys Ile Lys Asp Ile Thr Arg His Thr His His Ser Ala Trp His
165 170 175
Ser Met His Asn Val Ile Cys Gly Gly Ser Lys Val Ala Asp Glu His
180 185 190
Leu Glu Thr Leu Ile Lys Ser Gly Val Lys Ile His Leu Met Gln Gly
195 200 205
Asp Cys Asp Gln Ile Val Pro Ser His Cys Ser Gly Asn Met Lys Arg
210 215 220
Thr Phe Pro Ala Val Glu Val Asp Ile Ile Thr Gly Ala Asp His Asp
225 230 235 240
Ser Met Ile Ser Gly Arg Gly Glu Glu Phe Ala Glu Lys Leu Glu Ser
245 250 255
Ile Trp Cys Ser Phe Lys Glu Ser Gly
260 265

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1054 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1054

(D) OTHER INFORMATION: / Ceres Seq. ID 1567417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

gaggtcgttt	gtctcggtga	tttctcttct	ccttcttctc	tcattttctt	catctgttct	60
ctcaacaaaa	aagtcacat	ttcaaaaact	tccggtgcca	ggaaacagaa	caggccctga	120
agctttcgct	tttgattcca	cggaaaaagg	attctacacc	ggagtcaccg	gcggtaaaat	180
cctcaaatat	cttccaaaaga	aagggttatgt	cgactttgcc	cagatcacaa	actcttcgaa	240
gtcttcgttg	tgcgacggag	cacttggaac	cactaacgtc	gaaaaatgtg	gtcgaccagc	300
cggaaatagcc	ttcaacacga	aaacagggtga	tctttacgtc	gtagatgctg	cattgggtct	360
ccacgtcatc	cctcgcctgt	ggggtttggc	taagaagatc	gccgacagtg	tcggCggcaa	420
gccctttttg	tttcttgacg	ggcTtgacGt	agatcccact	accggcgctc	tctatttcac	480
ttccttcagc	tcaacatttg	gccctagggg	tgtgttgaaa	gcagtggcaa	caaaagactc	540
gaccggtaag	ttcttcaa	acgatccatc	aaaaaaggtc	gtgactgtat	tgatggaagg	600
tcttagcggc	tcagccggat	gtgccgttag	ctcagatggt	tcattcgtgc	tggttggtca	660
gttcacaaaa	agtaacatca	agagggtattg	gatcaaagga	tccaaagctg	gtacttctga	720
agacttcacc	aactcgggtc	cgaacctga	caacatcaag	aggatcggtt	ctactggaaa	780
cttttggtt	gcttcgggtc	tgaactcagc	caccggaccg	acaaaCcctt	cggcggttaa	840
agtcagttct	gccggtaaa	tgcttcagac	cattccccta	aaagacaagt	ttggggatac	900
tttggttagt	gaagttaacg	aatacaaagg	acagctttat	atcggagctc	tttttggtcc	960
tttcgccgR	aattcttaag	ctttaaagtg	aacatgttat	tagtatgggt	tagaattaaa	1020
gtgattgaat	cgaaataaat	atggttacaa	aggc			

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1567418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Arg	Ser	Phe	Val	Ser	Leu	Ile	Ser	Leu	Leu	Leu	Leu	Ser	Phe	Ser
1			5						10				15	
Ser	Ser	Val	Leu	Ser	Thr	Lys	Lys	Ser	Ser	Phe	Gln	Lys	Leu	Pro
			20					25				30		Val
Pro	Gly	Asn	Arg	Thr	Gly	Pro	Glu	Ala	Phe	Ala	Phe	Asp	Ser	Thr
		35					40					45		Gly
Lys	Gly	Phe	Tyr	Thr	Gly	Val	Thr	Gly	Gly	Lys	Ile	Leu	Lys	Tyr
	50					55					60			Leu
Pro	Lys	Lys	Gly	Tyr	Val	Asp	Phe	Ala	Gln	Ile	Thr	Asn	Ser	Ser
65					70				75					80
Ser	Ser	Leu	Cys	Asp	Gly	Ala	Leu	Gly	Thr	Asn	Val	Glu	Lys	Cys
			85					90				95		
Gly	Arg	Pro	Ala	Gly	Ile	Ala	Phe	Asn	Thr	Lys	Thr	Gly	Asp	Leu
		100						105				110		Tyr
Val	Val	Asp	Ala	Ala	Leu	Gly	Leu	His	Val	Ile	Pro	Arg	Arg	Gly
		115					120				125			Gly
Leu	Ala	Lys	Lys	Ile	Ala	Asp	Ser	Val	Gly	Gly	Lys	Pro	Phe	Leu
	130				135						140			Phe
Leu	Asp	Gly	Leu	Asp	Val	Asp	Pro	Thr	Thr	Gly	Val	Val	Tyr	Phe
145					150				155					Thr
Ser	Phe	Ser	Ser	Thr	Phe	Gly	Pro	Arg	Asp	Val	Leu	Lys	Ala	Val
			165					170					175	Ala
Thr	Lys	Asp	Ser	Thr	Gly	Lys	Phe	Phe	Lys	Tyr	Asp	Pro	Ser	Lys
		180					185					190		Lys
Val	Val	Thr	Val	Leu	Met	Glu	Gly	Leu	Ser	Gly	Ser	Ala	Gly	Cys
		195				200					205			Ala
Val	Ser	Ser	Asp	Gly	Ser	Phe	Val	Leu	Val	Gly	Gln	Phe	Thr	Lys

210	215	220
Asn Ile Lys Arg Tyr Trp	Ile Lys Gly Ser Lys	Ala Gly Thr Ser Glu
225	230	235
Asp Phe Thr Asn Ser Val	Ser Asn Pro Asp Asn	Ile Lys Arg Ile Gly
245	250	255
Ser Thr Gly Asn Phe Trp	Val Ala Ser Val Val	Asn Ser Ala Thr Gly
260	265	270
Pro Thr Asn Pro Ser Ala	Val Lys Val Ser Ser	Ala Gly Lys Val Leu
275	280	285
Gln Thr Ile Pro Leu Lys	Asp Lys Phe Gly Asp	Thr Leu Val Ser Glu
290	295	300
Val Asn Glu Tyr Lys Gly	Gln Leu Tyr Ile Gly	Ala Leu Phe Gly Pro
305	310	315
Phe Ala Xaa Asn Ser		320
325		

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

atcaatagtt	caatactaag	aaaccggcct	atatatatat	ttgtggtcac	taattttctcc	60
aaaaaccagt	tgccttccgt	aaaaagatgg	aacctcagag	aaaacactcg	acagccctcc	120
acacgtgtca	tccctgccgg	cgaaccattc	catacagaat	ctacgccgta	tttcaacttgt	180
gtggcatcat	agctctcatg	tatcaccatg	tacactcact	tgtcaacgca	aacaacactc	240
taataacatg	tcttcttctc	ctctccgata	ttgttctcgc	cttcatgtgg	gcaaccacaa	300
cttccctccg	cttaaacccg	gttcatcgga	ccgagtaccc	tgaaaaatat	gctgctaaac	360
cggagGactt	tccaaagctg	gacgttttta	tatgcacggc	tgatccgtac	aaggagcctc	420
cgatgatggt	ggttaacacc	gctttatcgg	tgatggctta	cgagtatccg	tctcataaga	480
tctcagtgtg	cgtatcggac	gatggaggat	cttccttgac	tttgtttgct	cttatggagg	540
ctgccaaagt	ctctaagcat	tggttgccct	tttgcaagaa	taacaatggt	caagatcgct	600
ctcctgaagt	ttatttttct	tcaaagtcac	attcttgag	tgatgaagct	gaaaatctta	660
agatgatgta	cgaagacatg	aagagtagag	tccaacatgt	ggttgagagt	ggaaaagtgt	720
agBactgcgt	ttattgcatg	cgatcaattt	agttgtgtgt	tcgatctgtg	gacagataaa	780
ttcactcgtc	atgaccatcc	taccattatt	aagggtgctac	aacataacga	aacagagatg	840
atgccaaacc	ttatatatgt	ttcaagagaa	aagagtaaag	tttcaccaca	tcatttcaaa	900
gccggtgctc	ttataacttt	gttacgagta	tctgccgtga	tgacaaaactc	accaatcatt	960
ctaacactag	actgtgacat	gtactcaaac	aatcctacag	caccacttca	tgctctgtgc	1020
tatttttttag	accctaaaaat	caatttttgg	ttaggatttg	tgcaatttcc	tcaaaaaattt	1080
caaggaataa	acaaaaatga	tatttatgca	tccgagctca	aacgcccatt	tgacatcaac	1140
acggttggtg	ttgatggact	tatgggacca	gttcatatgg	gaactgggtg	tttcttcaat	1200
cgacggggcgt	tttatggggc	tccgactagt	ttgactttgc	ctgaCgatag	aaaaacttgg	1260
gccaaatcgg	attgccgata	aaccatttaa	aaccccaaat	attttggcgt	tggcacacga	1320
tgtagcagga	tgtaactacg	agtgaacac	caattgggga	tccaaggtaa	gattaaaaatg	1380
aacttttagct	ttatttttatg	tatgttgatt	ttttggttat	gtttacagat	tttgtttctt	1440
ttacatcaac	tagtcttctc	aaaatccat				

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

00000000-00000000

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1567420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met	Glu	Pro	Gln	Arg	Lys	His	Ser	Thr	Ala	Leu	His	Thr	Cys	His	Pro
1				5					10					15	
Cys	Arg	Arg	Thr	Ile	Pro	Tyr	Arg	Ile	Tyr	Ala	Val	Phe	His	Leu	Cys
			20					25					30		
Gly	Ile	Ile	Ala	Leu	Met	Tyr	His	His	Val	His	Ser	Leu	Val	Asn	Ala
			35				40					45			
Asn	Asn	Thr	Leu	Ile	Thr	Cys	Leu	Leu	Leu	Leu	Ser	Asp	Ile	Val	Leu
	50					55					60				
Ala	Phe	Met	Trp	Ala	Thr	Thr	Ser	Leu	Arg	Leu	Asn	Pro	Val	His	
65					70				75					80	
Arg	Thr	Glu	Tyr	Pro	Glu	Lys	Tyr	Ala	Ala	Lys	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Lys	Leu	Asp	Val	Phe	Ile	Cys	Thr	Ala	Asp	Pro	Tyr	Lys	Glu	Pro	Pro
			100					105					110		
Met	Met	Val	Val	Asn	Thr	Ala	Leu	Ser	Val	Met	Ala	Tyr	Glu	Tyr	Pro
		115					120					125			
Ser	His	Lys	Ile	Ser	Val	Tyr	Val	Ser	Asp	Asp	Gly	Gly	Ser	Ser	Leu
	130					135					140				
Thr	Leu	Phe	Ala	Leu	Met	Glu	Ala	Ala	Lys	Phe	Ser	Lys	His	Trp	Leu
145					150					155					160
Pro	Phe	Cys	Lys	Asn	Asn	Asn	Val	Gln	Asp	Arg	Ser	Pro	Glu	Val	Tyr
				165					170					175	
Phe	Ser	Ser	Lys	Ser	His	Ser	Trp	Ser	Asp	Glu	Ala	Glu	Asn	Leu	Lys
			180					185					190		
Met	Met	Tyr	Glu	Asp	Met	Lys	Ser	Arg	Val	Glu	His	Val	Val	Glu	Ser
		195				200						205			
Gly	Lys	Val	Glu	Xaa	Cys	Val	Tyr	Cys	Met	Arg	Ser	Ile			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1567421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met	Tyr	His	His	Val	His	Ser	Leu	Val	Asn	Ala	Asn	Asn	Thr	Leu	Ile
1				5					10					15	
Thr	Cys	Leu	Leu	Leu	Leu	Ser	Asp	Ile	Val	Leu	Ala	Phe	Met	Trp	Ala
			20					25					30		
Thr	Thr	Thr	Ser	Leu	Arg	Leu	Asn	Pro	Val	His	Arg	Thr	Glu	Tyr	Pro
			35				40					45			
Glu	Lys	Tyr	Ala	Ala	Lys	Pro	Glu	Asp	Phe	Pro	Lys	Leu	Asp	Val	Phe
	50					55					60				
Ile	Cys	Thr	Ala	Asp	Pro	Tyr	Lys	Glu	Pro	Pro	Met	Met	Val	Val	Asn
65					70					75					80
Thr	Ala	Leu	Ser	Val	Met	Ala	Tyr	Glu	Tyr	Pro	Ser	His	Lys	Ile	Ser
			85					90					95		
Val	Tyr	Val	Ser	Asp	Asp	Gly	Gly	Ser	Ser	Leu	Thr	Leu	Phe	Ala	Leu
			100					105					110		
Met	Glu	Ala	Ala	Lys	Phe	Ser	Lys	His	Trp	Leu	Pro	Phe	Cys	Lys	Asn
		115					120					125			
Asn	Asn	Val	Gln	Asp	Arg	Ser	Pro	Glu	Val	Tyr	Phe	Ser	Ser	Lys	Ser
	130					135						140			

His Ser Trp Ser Asp Glu Ala Glu Asn Leu Lys Met Met Tyr Glu Asp
145 150 155 160
Met Lys Ser Arg Val Glu His Val Val Glu Ser Gly Lys Val Glu Xaa
165 170 175
Cys Val Tyr Cys Met Arg Ser Ile
180

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1567422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met Trp Leu Arg Val Glu Lys Leu Xaa Thr Ala Phe Ile Ala Cys Asp
1 5 10 15
Gln Phe Ser Cys Val Phe Asp Leu Trp Thr Asp Lys Phe Thr Arg His
20 25 30
Asp His Pro Thr Ile Ile Lys Val Leu Gln His Asn Glu Thr Glu Met
35 40 45
Met Pro Asn Leu Ile Tyr Val Ser Arg Glu Lys Ser Lys Val Ser Pro
50 55 60
His His Phe Lys Ala Gly Ala Leu Asn Thr Leu Leu Arg Val Ser Ala
65 70 75 80
Val Met Thr Asn Ser Pro Ile Ile Leu Thr Leu Asp Cys Asp Met Tyr
85 90 95
Ser Asn Asn Pro Thr Ala Pro Leu His Ala Leu Cys Tyr Phe Leu Asp
100 105 110
Pro Lys Ile Asn Phe Gly Leu Gly Phe Val Gln Phe Pro Gln Lys Phe
115 120 125
Gln Gly Ile Asn Lys Asn Asp Ile Tyr Ala Ser Glu Leu Lys Arg Pro
130 135 140
Phe Asp Ile Asn Thr Val Gly Phe Asp Gly Leu Met Gly Pro Val His
145 150 155 160
Met Gly Thr Gly Cys Phe Phe Asn Arg Arg Ala Phe Tyr Gly Pro Pro
165 170 175
Thr Ser Leu Thr Leu Pro Asp Asp Arg Lys Thr Trp Ala Lys Ser Asp
180 185 190
Cys Arg

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1865

(D) OTHER INFORMATION: / Ceres Seq. ID 1567445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

ctgattat	ttt ccaatgactt	tcttctctgt	ctgattcg	ttt tgtttcggcg	attcaactct	60
tcttcaacgc	cctgagagtc	acgcacgaga	attggattga	tggtttttca	cacgcaggag	120
aggcgattcg	ttgtcttctt	cttgtcccgt	tgacctgttt	cgatctcaga	tggtgattat	180
gcagcagctg	attctaaatt	agggcattta	aatccgcctt	ccagggtgaat	ttttgaaaag	240
taattaaagg	gtgttcttga	atggacttga	aaatggataa	tgttattggg	ggaaagttaa	300


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aacttggtcg gaagatcggt ggtggctctt ttggagaact ttttcttgcc gtaagtttgc 360
aaaccggaga ggaagcagct gttaagctgg agcctgcgaa aactaagcat cccaacttc 420
attatgagtc gaagatatac atgctttctac aaggaggaag tggcatcccc agccttaagt 480
ggtttggggg tcagggagac tacaatgcga tggtcattga tctgcttggg ccgagtttgg 540
aagacttggt caactactgc aataggaggc ttactttgaa ggcagttttg atgcttgcag 600
atcaactgat tagcagagtt gaatatatgc attcaagggg gtttcttcac cgtgacatca 660
aacctgacaa tttcttgatg ggacttgggt gcaaagcaaa ccaggtgtat atcattgatt 720
ttgggcttgc aaagaagtat agggatctcc aaacacatag gcatatcccc tatagagaaa 780
acaagaacct tacgggcaca gctcgggatg ctagtgtcaa cactcaccta ggagttgagc 840
aaagtaggag ggatgatctg gagtctcttg gttacgtact catgtatttc ctgagaggaa 900
gcttaccgtg gcaggggacta aaagctggca caaagaagca aaagtatgac agaattagcg 960
agaagaaagt atcaactcct atagaggtct tgtgcaagtc atatccacc gaattcgtat 1020
catactttca atactgcaga tctctgcgat tcgaagacAa accagactac tcatatctaa 1080
agagactttt ccgagacttg tttatccgtg aaggttatca gtttgattat gtattcgact 1140
ggactgcatt gaaacaccct cagagtagtg ccaggtccca ttccagtaca catgaaaggc 1200
atcgtaccgg taaaccaggg atgggtgcgg gaccgtctgc tgaaaaacct gaaaggattt 1260
cagtagggaa catccgcgat aaattctcag gtgcggtcga agcatttgcg agaaggaaacg 1320
ttagaggacc cagtcccat caaaaccata ccagacatcg aactcttgac gaaattcctt 1380
caatgaaacc tgotgtgaat atggtatctg agaaaggaag aaacacttcc agatacggca 1440
gtgcttcgag gagagcagta gcctcaggaa gtagaccaag ctcatcaggt gaacaaaggg 1500
agagccggga ctcgagccgc gtagcctcaa gcggtggcgg tgtccgacca tcagtcttcc 1560
aaagaaccca agcagcagct gctgtgagtg gatacagatc aaagacagca tctgccttta 1620
accgcgaccg agtagccgct tcaagaacag cacgagacga ggctctcaga agcttcgagc 1680
ttctttogat ccgcaaatag agccttcac aattggctct ttgctgtaaa ttggattcct 1740
ctttacatat gttgtttggt cttttgttcc cacgaaactc ccaatttttc atgtattatc 1800
aaattctctg gattttgtat caatttttac acactttatt gtaatcatga caatttggtg 1860
agttt

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```

Met Asp Leu Lys Met Asp Asn Val Ile Gly Gly Lys Phe Lys Leu Gly
1      5      10      15
Arg Lys Ile Gly Gly Gly Ser Phe Gly Glu Leu Phe Leu Ala Val Ser
20      25      30
Leu Gln Thr Gly Glu Glu Ala Ala Val Lys Leu Glu Pro Ala Lys Thr
35      40      45
Lys His Pro Gln Leu His Tyr Glu Ser Lys Ile Tyr Met Leu Leu Gln
50      55      60
Gly Gly Ser Gly Ile Pro Ser Leu Lys Trp Phe Gly Val Gln Gly Asp
65      70      75      80
Tyr Asn Ala Met Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu
85      90      95
Phe Asn Tyr Cys Asn Arg Arg Leu Thr Leu Lys Ala Val Leu Met Leu
100     105     110
Ala Asp Gln Leu Ile Ser Arg Val Glu Tyr Met His Ser Arg Gly Phe
115     120     125
Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Arg
130     135     140
Lys Ala Asn Gln Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr
145     150     155     160
Arg Asp Leu Gln Thr His Arg His Ile Pro Tyr Arg Glu Asn Lys Asn
165     170     175

```

```

Leu Thr Gly Thr Ala Arg Tyr Ala Ser Val Asn Thr His Leu Gly Val
      180                      185                      190
Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met
      195                      200                      205
Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Gly Thr
      210                      215                      220
Lys Lys Gln Lys Tyr Asp Arg Ile Ser Glu Lys Lys Val Ser Thr Pro
225                      230                      235                      240
Ile Glu Val Leu Cys Lys Ser Tyr Pro Pro Glu Phe Val Ser Tyr Phe
      245                      250                      255
Gln Tyr Cys Arg Ser Leu Arg Phe Glu Asp Lys Pro Asp Tyr Ser Tyr
      260                      265                      270
Leu Lys Arg Leu Phe Arg Asp Leu Phe Ile Arg Glu Gly Tyr Gln Phe
      275                      280                      285
Asp Tyr Val Phe Asp Trp Thr Ala Leu Lys His Pro Gln Ser Ser Ala
      290                      295                      300
Arg Ser His Ser Ser Thr His Glu Arg His Arg Thr Gly Lys Pro Gly
305                      310                      315                      320
Met Gly Ala Gly Pro Ser Ala Glu Lys Pro Glu Arg Ile Ser Val Gly
      325                      330                      335
Asn Ile Arg Asp Lys Phe Ser Gly Ala Val Glu Ala Phe Ala Arg Arg
      340                      345                      350
Asn Val Arg Gly Pro Ser Pro His Gln Asn His Thr Arg His Arg Thr
      355                      360                      365
Leu Asp Glu Ile Pro Ser Met Lys Pro Ala Val Asn Met Val Ser Glu
      370                      375                      380
Lys Gly Arg Asn Thr Ser Arg Tyr Gly Ser Ala Ser Arg Arg Ala Val
385                      390                      395                      400
Ala Ser Gly Ser Arg Pro Ser Ser Ser Gly Glu Gln Arg Glu Ser Arg
      405                      410                      415
Asp Ser Ser Arg Val Ala Ser Ser Gly Gly Gly Val Arg Pro Ser Val
      420                      425                      430
Phe Gln Arg Thr Gln Ala Ala Ala Val Ser Gly Tyr Glu Ser Lys
      435                      440                      445
Thr Ala Ser Ala Phe Asn Arg Asp Arg Val Ala Ala Ser Arg Thr Ala
      450                      455                      460
Arg Asp Glu Ala Leu Arg Ser Phe Glu Leu Leu Ser Ile Arg Lys
465                      470                      475

```

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```

Met Asp Asn Val Ile Gly Gly Lys Phe Lys Leu Gly Arg Lys Ile Gly
1      5      10      15
Gly Gly Ser Phe Gly Glu Leu Phe Leu Ala Val Ser Leu Gln Thr Gly
      20      25      30
Glu Glu Ala Ala Val Lys Leu Glu Pro Ala Lys Thr Lys His Pro Gln
      35      40      45
Leu His Tyr Glu Ser Lys Ile Tyr Met Leu Leu Gln Gly Gly Ser Gly
      50      55      60
Ile Pro Ser Leu Lys Trp Phe Gly Val Gln Gly Asp Tyr Asn Ala Met
      65      70      75      80
Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Tyr Cys

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

Met Leu Leu Gln Gly Gly Ser Gly Ile Pro Ser Leu Lys Trp Phe Gly
1      5      10
Val Gln Gly Asp Tyr Asn Ala Met Val Ile Asp Leu Leu Gly Pro Ser
20      25      30
Leu Glu Asp Leu Phe Asn Tyr Cys Asn Arg Arg Leu Thr Leu Lys Ala
35      40      45
Val Leu Met Leu Ala Asp Gln Leu Ile Ser Arg Val Glu Tyr Met His
50      55      60
Ser Arg Gly Phe Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met
65      70      75
Gly Leu Gly Arg Lys Ala Asn Gln Val Tyr Ile Ile Asp Phe Gly Leu
85      90      95
Ala Lys Lys Tyr Arg Asp Leu Gln Thr His Arg His Ile Pro Tyr Arg
100     105     110
Glu Asn Lys Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Val Asn Thr
115     120     125
His Leu Gly Val Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly
130     135     140
Tyr Val Leu Met Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu
145     150     155
Lys Ala Gly Thr Lys Lys Gln Lys Tyr Asp Arg Ile Ser Glu Lys Lys
165     170     175
Val Ser Thr Pro Ile Glu Val Leu Cys Lys Ser Tyr Pro Pro Glu Phe
180     185     190
Val Ser Tyr Phe Gln Tyr Cys Arg Ser Leu Arg Phe Glu Asp Lys Pro
195     200     205
Asp Tyr Ser Tyr Leu Lys Arg Leu Phe Arg Asp Leu Phe Ile Arg Glu
210     215     220
Gly Tyr Gln Phe Asp Tyr Val Phe Asp Trp Thr Ala Leu Lys His Pro
225     230     235
Gln Ser Ser Ala Arg Ser His Ser Ser Thr His Glu Arg His Arg Thr
245     250     255
Gly Lys Pro Gly Met Gly Ala Gly Pro Ser Ala Glu Lys Pro Glu Arg
260     265     270
Ile Ser Val Gly Asn Ile Arg Asp Lys Phe Ser Gly Ala Val Glu Ala
275     280     285
Phe Ala Arg Arg Asn Val Arg Gly Pro Ser Pro His Gln Asn His Thr
290     295     300
Arg His Arg Thr Leu Asp Glu Ile Pro Ser Met Lys Pro Ala Val Asn
305     310     315
Met Val Ser Glu Lys Gly Arg Asn Thr Ser Arg Tyr Gly Ser Ala Ser
325     330     335
Arg Arg Ala Val Ala Ser Gly Ser Arg Pro Ser Ser Ser Gly Glu Gln
340     345     350
Arg Glu Ser Arg Asp Ser Ser Arg Val Ala Ser Ser Gly Gly Gly Val
355     360     365
Arg Pro Ser Val Phe Gln Arg Thr Gln Ala Ala Ala Val Ser Gly
370     375     380
Tyr Glu Ser Lys Thr Ala Ser Ala Phe Asn Arg Asp Arg Val Ala Ala
385     390     395
Ser Arg Thr Ala Arg Asp Glu Ala Leu Arg Ser Phe Glu Leu Leu Ser
405     410     415
Ile Arg Lys

```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..697

(D) OTHER INFORMATION: / Ceres Seq. ID 1567449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

aacgaatctt	gttttagtaaa	aagcgcaGct	gcaaaaaaaaa	tcgagtagag	aagaagtagg	60
cagacaaaga	agaagaagaa	gaagttctcg	gcgtgcttca	atggcgatat	cagtagcagc	120
ttcgtcctct	atggccgtga	tggttcacag	tgttcccgcc	gtatccaccc	gttgctccgc	180
cgtcccttat	cttcctcctc	gctcctttgg	ccgatcctct	ttcaccgttc	cgttgaagct	240
tgtttcaggg	aatggattgc	aaaaagtga	attgtagaag	acaagagctt	cttcagaaga	300
gacctcgtcc	attgatacca	acgaactcat	cacagatttg	aaggaaaagt	gggatgggtct	360
tgagaacaaa	tctactgtac	ttatatatgg	aggaggagcc	attggtgctg	tttggttctc	420
ttccattgtt	ggttggtgcc	tcaactctgt	tcctctgctt	ccgaaagtta	tggaacttgt	480
cggctctcggg	tacactggat	ggtttgctta	cagatacctt	ctcttcaagt	caagcagaaa	540
ggaattggct	gaggatattg	aatccttgaa	gaagaagatc	gcaggaagcg	aatagattca	600
ttttcaaata	aaaccagctt	tctctctgta	tgttttcctg	taatatcgtg	ttatattata	660
caatgtctct	gtttcaacat	tgtatctgtt	gcattctc			

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1567450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met	Ala	Ile	Ser	Val	Ala	Ala	Ser	Ser	Ser	Met	Ala	Val	Met	Val	Pro
1				5					10					15	
Arg	Val	Pro	Ala	Val	Ser	Thr	Arg	Cys	Ser	Ala	Val	Pro	Tyr	Leu	Pro
				20				25					30		
Pro	Arg	Ser	Phe	Gly	Arg	Ser	Ser	Phe	Thr	Val	Pro	Leu	Lys	Leu	Val
				35				40					45		
Ser	Gly	Asn	Gly	Leu	Gln	Lys	Val	Glu	Leu						
				50				55							

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1567451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met	Val	Leu	Arg	Thr	Asn	Leu	Leu	Tyr	Leu	Tyr	Met	Glu	Glu	Glu	Pro
1					5				10					15	
Leu	Leu	Leu	Phe	Gly	Tyr	Leu	Pro	Leu	Leu	Leu	Val	Pro	Ser	Thr	Leu
				20				25					30		
Phe	Leu	Cys	Phe	Arg	Lys	Leu	Trp	Asn	Leu	Ser	Val	Ser	Gly	Thr	Leu
				35				40					45		
Asp	Gly	Leu	Ser	Thr	Asp	Thr	Phe	Ser	Ser	Ser	Gln	Ala	Glu	Arg	Asn
				50				55					60		
Trp	Leu	Arg	Ile	Leu	Asn	Pro									
				65				70							

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
(D) OTHER INFORMATION: / Ceres Seq. ID 1567452
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:
Met Glu Glu Glu Pro Leu Leu Leu Phe Gly Tyr Leu Pro Leu Leu Leu
1 5 10 15
Val Pro Ser Thr Leu Phe Leu Cys Phe Arg Lys Leu Trp Asn Leu Ser
20 25 30
Val Ser Gly Thr Leu Asp Gly Leu Ser Thr Asp Thr Phe Ser Ser Ser
35 40 45
Gln Ala Glu Arg Asn Trp Leu Arg Ile Leu Asn Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1122

(D) OTHER INFORMATION: / Ceres Seq. ID 1567453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```
atTTTTtGat atGtaaaatt tatcgaaaac gttccatttc aatatgtaga caaagcggag      60
aagtatatTg tggaggcgGc aagcaaggga gcagagctag tgttgttccc ggagggggtt      120
atcgggtgtct atcctcgagg ttttaggttc ggtttagcgg ttggcgttca taacgaagaa      180
gggcgtgatg agtttcggaa gtaccatgct tctgctattc atgttctctg ccctgaagta      240
gcaagattgg ctgacgtggc taggaaaaac catgtgtact tggtaatggg agccatagag      300
aaggaagggt ataccctcta ttgcacagtt cttttcttta gtccacaggg tcagttcttg      360
ggcaagcacc gtaaacatcat gccacaagt ttggaacggt gcatttgggg ccaagggggac      420
ggatcaacca tccccgttta cgacactccc attggaaaac tcggtgctgc tatttgctgg      480
gagaatagga tgccccctcta cagaactgca ttgtacgcca aaggcattga gctttattgt      540
gcacctactg ctgatggttc gaaagaatgg caatcgtcga tgcttcacat tgcgatcgaa      600
ggtggatgtt tcgtcttgtc ggcttgccaa ttctgccagc gtaaacattt ccctgatcat      660
cctgactact tgtttaccga ttggtacgac gacaaagaac atgattctat tgtctcccaa      720
ggtggaagtg tcattatttc accttgggga caagttctcg ccggaccaaa ctttgaatca      780
gagggctctg tcacagctga tattgatctt ggtgatatag caagagccaa gttatacttc      840
gattcggttg gacattactc gagaccagat gttttacact tgaccgtaaa tgagcaccgc      900
aggaaatcgg ttacattcgt gacgaagggt gagaaagctg aggatgactc aaacaaatag      960
taagagactt gaagttcgta tctgctggag ttatgtcaat cgtatggagt caagtccaaa     1020
atgttctgtt gcgttttcat tttatgttca agtttatTTa tctttTctct tcaatggtaa     1080
gatctatgga gtcaagtaat aatggtaaga cttatgttgt tg
```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1567454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

2025 RELEASE UNDER E.O. 14176

```

Met Gly Ala Ile Glu Lys Glu Gly Tyr Thr Leu Tyr Cys Thr Val Leu
1      5      10      15
Phe Phe Ser Pro Gln Gly Gln Phe Leu Gly Lys His Arg Lys Leu Met
20      25      30
Pro Thr Ser Leu Glu Arg Cys Ile Trp Gly Gln Gly Asp Gly Ser Thr
35      40      45
Ile Pro Val Tyr Asp Thr Pro Ile Gly Lys Leu Gly Ala Ala Ile Cys
50      55      60
Trp Glu Asn Arg Met Pro Leu Tyr Arg Thr Ala Leu Tyr Ala Lys Gly
65      70      75      80
Ile Glu Leu Tyr Cys Ala Pro Thr Ala Asp Gly Ser Lys Glu Trp Gln
85      90      95
Ser Ser Met Leu His Ile Ala Ile Glu Gly Gly Cys Phe Val Leu Ser
100      105      110
Ala Cys Gln Phe Cys Gln Arg Lys His Phe Pro Asp His Pro Asp Tyr
115      120      125
Leu Phe Thr Asp Trp Tyr Asp Asp Lys Glu His Asp Ser Ile Val Ser
130      135      140
Gln Gly Gly Ser Val Ile Ile Ser Pro Leu Gly Gln Val Leu Ala Gly
145      150      155      160
Pro Asn Phe Glu Ser Glu Gly Leu Val Thr Ala Asp Ile Asp Leu Gly
165      170      175
Asp Ile Ala Arg Ala Lys Leu Tyr Phe Asp Ser Val Gly His Tyr Ser
180      185      190
Arg Pro Asp Val Leu His Leu Thr Val Asn Glu His Pro Arg Lys Ser
195      200      205
Val Thr Phe Val Thr Lys Val Glu Lys Ala Glu Asp Asp Ser Asn Lys
210      215      220

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

Met Pro Thr Ser Leu Glu Arg Cys Ile Trp Gly Gln Gly Asp Gly Ser
1      5      10      15
Thr Ile Pro Val Tyr Asp Thr Pro Ile Gly Lys Leu Gly Ala Ala Ile
20      25      30
Cys Trp Glu Asn Arg Met Pro Leu Tyr Arg Thr Ala Leu Tyr Ala Lys
35      40      45
Gly Ile Glu Leu Tyr Cys Ala Pro Thr Ala Asp Gly Ser Lys Glu Trp
50      55      60
Gln Ser Ser Met Leu His Ile Ala Ile Glu Gly Gly Cys Phe Val Leu
65      70      75      80
Ser Ala Cys Gln Phe Cys Gln Arg Lys His Phe Pro Asp His Pro Asp
85      90      95
Tyr Leu Phe Thr Asp Trp Tyr Asp Asp Lys Glu His Asp Ser Ile Val
100      105      110
Ser Gln Gly Gly Ser Val Ile Ile Ser Pro Leu Gly Gln Val Leu Ala
115      120      125
Gly Pro Asn Phe Glu Ser Glu Gly Leu Val Thr Ala Asp Ile Asp Leu
130      135      140
Gly Asp Ile Ala Arg Ala Lys Leu Tyr Phe Asp Ser Val Gly His Tyr

```

agctatcaat	ttacttgaga	agagatggtg	ggatcagagg	ttttggagga	atgtggagaa	60
aaaataagca	agaaagagtc	aaagaagcga	gccgctaaac	tggagaagtt	gctccgtaaa	120
cagtaacgag	aagaagccac	atcatcatct	ctttctctgg	aggaggagga	tgaatcgtgt	180
tccagcaact	acggtgacgt	gactactaac	gagttgcagt	cggctgttga	gggaaaagag	240
ctcactgatg	tgagcaactt	ggttgaagag	attgtggggt	cagaggtttc	gatcagaggt	300
cgactgcaca	agaatcgctt	agtcggtacc	aaattgtttg	tgatcttgag	ggaaagtggg	360
ttcacggttc	aatgcggtgt	ggaggagacc	agagttgggt	caaacatgat	taaatttgtc	420
aagcagctga	gtcggtgaat	tgttgttgac	cttatcggtg	tcgtctctca	cctaagaag	480
cctctcacag	gaaccacca	gcaggttgaa	atacatgtca	gaaaaatgta	ctgcctcagc	540
agatccttgc	caaattttacc	acttgttgtg	gaggatgctg	ctcgtagtga	atcagatatt	600

gaaaaatctg gcaaggatgg caaacaagct gctcgtgtcc ttcaggacac acgtttgaat 660
aatagggttc ttgacatcag aacaccggct aatcaagcca tcttccgtat tcagtgccaa 720
gtccaaattg cgttcagaga atacttacaa tccaaggggt ttcttgaaat ccacacaccg 780
aaattgatcg ctggcagtag tgaaggagggt tctgctgtgt ttaggttgga ctacaaaggg 840
cagcctgctt gtctggctca gtctcctcag cttcataagc agatggcgat atgtggtgac 900
atgcgacgcg tctttgaggt tggctcctgtt ttcagagctg aagactcctt cactcataga 960
cacctgtgtg aattcgttgg tcttgatgtg gagatggaga ttcgaatgca ctactctgag 1020
ataatggatc ttgtggggga gttgtttccg ttcataattca caaaaataga agaaagggtg 1080
ccaaaggaac ttgaatctgt cagaaagcaa tacccttttc aatctttgaa gtttcttccg 1140
caaacattga ggctaacctt tgcagaaggg attcaaagtc ttaaggaagc tggcgaggag 1200
gttgatcctc ttggtgatct aaatacagaa tctgagagga aacttggcca gcttgttctg 1260
gaaaagtaca agacggagtt ctacatgctg catcgctatc catcggtgtg cagaccgttc 1320
tacctatgc cctatgaaaa tgattctaac tacagcaact ctttcgatgt cttcatcaga 1380
ggagaggaga tcatgtcagg agctcaacgt atccatgacc cagaactctt ggagaagcgc 1440
gcaagagaat gcggcattga tgtcaagaca atatccacgt acattgatgc attcaggtac 1500
ggtgcNaccA cctcacggtg gattcggagt ggggctggag cgtgtggtaa tgctcttatg 1560
tgccctcaat aacatccgca aaacttgcgt attccctcgt gactctcaaa ggctcactcc 1620
ctaatatcat tgctcttccc tggcgactct caaaggctcg ctcccttaat atctatcttt 1680
gataattgtc cccgctcccg atttctaagt tatttttttg gtgcagttcg ttaggtgttt 1740
agttatcttt aaactatgta tgtgttgtaa cctttaaatt attaaggagc agtactattt 1800
gggcttttc g

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1567464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

Met Ile Lys Phe Val Lys Gln Leu Ser Arg Glu Ser Val Val Glu Leu
1 5 10 15
Ile Gly Val Val Ser His Pro Lys Lys Pro Leu Thr Gly Thr Thr Gln
20 25 30
Gln Val Glu Ile His Val Arg Lys Met Tyr Cys Leu Ser Arg Ser Leu
35 40 45
Pro Asn Leu Pro Leu Val Val Glu Asp Ala Ala Arg Ser Glu Ser Asp
50 55 60
Ile Glu Lys Ser Gly Lys Asp Gly Lys Gln Ala Ala Arg Val Leu Gln
65 70 75 80
Asp Thr Arg Leu Asn Asn Arg Val Leu Asp Ile Arg Thr Pro Ala Asn
85 90 95
Gln Ala Ile Phe Arg Ile Gln Cys Gln Val Gln Ile Ala Phe Arg Glu
100 105 110
Tyr Leu Gln Ser Lys Gly Phe Leu Glu Ile His Thr Pro Lys Leu Ile
115 120 125
Ala Gly Ser Ser Glu Gly Gly Ser Ala Val Phe Arg Leu Asp Tyr Lys
130 135 140
Gly Gln Pro Ala Cys Leu Ala Gln Ser Pro Gln Leu His Lys Gln Met
145 150 155 160
Ala Ile Cys Gly Asp Met Arg Arg Val Phe Glu Val Gly Pro Val Phe
165 170 175
Arg Ala Glu Asp Ser Phe Thr His Arg His Leu Cys Glu Phe Val Gly
180 185 190
Leu Asp Val Glu Met Glu Ile Arg Met His Tyr Ser Glu Ile Met Asp
195 200 205
Leu Val Gly Glu Leu Phe Pro Phe Ile Phe Thr Lys Ile Glu Glu Arg
210 215 220

Cys Pro Lys Glu Leu Glu Ser Val Arg Lys Gln Tyr Pro Phe Gln Ser
225 230 235 240
Leu Lys Phe Leu Pro Gln Thr Leu Arg Leu Thr Phe Ala Glu Gly Ile
245 250 255
Gln Met Leu Lys Glu Ala Gly Glu Glu Val Asp Pro Leu Gly Asp Leu
260 265 270
Asn Thr Glu Ser Glu Arg Lys Leu Gly Gln Leu Val Leu Glu Lys Tyr
275 280 285
Lys Thr Glu Phe Tyr Met Leu His Arg Tyr Pro Ser Ala Val Arg Pro
290 295 300
Phe Tyr Thr Met Pro Tyr Glu Asn Asp Ser Asn Tyr Ser Asn Ser Phe
305 310 315 320
Asp Val Phe Ile Arg Gly Glu Glu Ile Met Ser Gly Ala Gln Arg Ile
325 330 335
His Asp Pro Glu Leu Leu Glu Lys Arg Ala Arg Glu Cys Gly Ile Asp
340 345 350
Val Lys Thr Ile Ser Thr Tyr Ile Asp Ala Phe Arg Tyr Gly Xaa Thr
355 360 365
Thr Ser Arg Trp Ile Arg Ser Gly Ala Gly Ala Cys Gly Asn Ala Leu
370 375 380
Met Cys Pro Gln
385

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1567465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Tyr Cys Leu Ser Arg Ser Leu Pro Asn Leu Pro Leu Val Val Glu
1 5 10 15
Asp Ala Ala Arg Ser Glu Ser Asp Ile Glu Lys Ser Gly Lys Asp Gly
20 25 30
Lys Gln Ala Ala Arg Val Leu Gln Asp Thr Arg Leu Asn Asn Arg Val
35 40 45
Leu Asp Ile Arg Thr Pro Ala Asn Gln Ala Ile Phe Arg Ile Gln Cys
50 55 60
Gln Val Gln Ile Ala Phe Arg Glu Tyr Leu Gln Ser Lys Gly Phe Leu
65 70 75 80
Glu Ile His Thr Pro Lys Leu Ile Ala Gly Ser Ser Glu Gly Gly Ser
85 90 95
Ala Val Phe Arg Leu Asp Tyr Lys Gly Gln Pro Ala Cys Leu Ala Gln
100 105 110
Ser Pro Gln Leu His Lys Gln Met Ala Ile Cys Gly Asp Met Arg Arg
115 120 125
Val Phe Glu Val Gly Pro Val Phe Arg Ala Glu Asp Ser Phe Thr His
130 135 140
Arg His Leu Cys Glu Phe Val Gly Leu Asp Val Glu Met Glu Ile Arg
145 150 155 160
Met His Tyr Ser Glu Ile Met Asp Leu Val Gly Glu Leu Phe Pro Phe
165 170 175
Ile Phe Thr Lys Ile Glu Glu Arg Cys Pro Lys Glu Leu Glu Ser Val
180 185 190
Arg Lys Gln Tyr Pro Phe Gln Ser Leu Lys Phe Leu Pro Gln Thr Leu
195 200 205
Arg Leu Thr Phe Ala Glu Gly Ile Gln Met Leu Lys Glu Ala Gly Glu

210	215	220
Glu Val Asp Pro Leu Gly	Asp Leu Asn Thr	Glu Ser Glu Arg Lys Leu
225	230	235
Gly Gln Leu Val Leu	Glu Lys Tyr Lys Thr	Glu Phe Tyr Met Leu His
	245	250
Arg Tyr Pro Ser Ala	Val Arg Pro Phe Tyr Thr	Met Pro Tyr Glu Asn
	260	265
Asp Ser Asn Tyr Ser	Asn Ser Phe Asp Val Phe	Ile Arg Gly Glu Glu
	275	280
Ile Met Ser Gly Ala	Gln Arg Ile His Asp Pro	Glu Leu Leu Glu Lys
	290	295
Arg Ala Arg Glu Cys	Gly Ile Asp Val Lys Thr	Ile Ser Thr Tyr Ile
305	310	315
Asp Ala Phe Arg Tyr	Gly Xaa Thr Thr Ser Arg	Trp Ile Arg Ser Gly
	325	330
Ala Gly Ala Cys Gly	Asn Ala Leu Met Cys	Pro Gln
	340	345

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1567466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

Met Ala Ile Cys Gly Asp Met Arg Arg Val Phe Glu Val Gly Pro Val	
1	5 10 15
Phe Arg Ala Glu Asp Ser Phe Thr His Arg His Leu Cys Glu Phe Val	
	20 25 30
Gly Leu Asp Val Glu Met Glu Ile Arg Met His Tyr Ser Glu Ile Met	
	35 40 45
Asp Leu Val Gly Glu Leu Phe Pro Phe Ile Phe Thr Lys Ile Glu Glu	
	50 55 60
Arg Cys Pro Lys Glu Leu Glu Ser Val Arg Lys Gln Tyr Pro Phe Gln	
65	70 75 80
Ser Leu Lys Phe Leu Pro Gln Thr Leu Arg Leu Thr Phe Ala Glu Gly	
	85 90 95
Ile Gln Met Leu Lys Glu Ala Gly Glu Glu Val Asp Pro Leu Gly Asp	
	100 105 110
Leu Asn Thr Glu Ser Glu Arg Lys Leu Gly Gln Leu Val Leu Glu Lys	
	115 120 125
Tyr Lys Thr Glu Phe Tyr Met Leu His Arg Tyr Pro Ser Ala Val Arg	
	130 135 140
Pro Phe Tyr Thr Met Pro Tyr Glu Asn Asp Ser Asn Tyr Ser Asn Ser	
145	150 155 160
Phe Asp Val Phe Ile Arg Gly Glu Glu Ile Met Ser Gly Ala Gln Arg	
	165 170 175
Ile His Asp Pro Glu Leu Leu Glu Lys Arg Ala Arg Glu Cys Gly Ile	
	180 185 190
Asp Val Lys Thr Ile Ser Thr Tyr Ile Asp Ala Phe Arg Tyr Gly Xaa	
	195 200 205
Thr Thr Ser Arg Trp Ile Arg Ser Gly Ala Gly Ala Cys Gly Asn Ala	
	210 215 220
Leu Met Cys Pro Gln	
225	

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..759
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567489
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

gacccaaatc	tgacgcttct	ctctctcttt	ctggatatctg	cgtttgattc	ggagaaKdaa	60
aaaTaahhaa	aaMaaaaagg	caaagagaga	gcttcaatgg	agttagcttc	atccttggtg	120
gagctctggt	tgtttcgcta	tttcttctct	cgcgatggca	agagttcaat	gattttgggtg	180
aagatggtgg	ccgatcagct	aaatctttga	aacccaaatt	caatgccttt	gtaaaccatg	240
tgacaactca	cactggccag	caattgccac	cagtcgatat	gaagattctt	gttgctgctg	300
ctatagcctt	gaagggtatt	gggggactat	tgtttgctct	tggcagctca	ttgggagctt	360
atctcttgct	tctgcatcaa	gccgttgcca	ccccaaattct	gtatgatttc	tacaactacg	420
atgttgacag	aaaggaattc	ggccaactat	tttcaaaatt	tacacagagc	ttggctcttc	480
ttggaggact	gctcttcttc	attggaatga	aaaactcaag	gaaacacggg	aggcaactca	540
ggaaaaaggc	tccaaaggca	aaagcaaact	gaagaagcca	tatctttcat	cggttttatt	600
cggctctgtat	tttatcttca	ttttggaatc	caggatgggt	ttaaagagtc	tatctgatga	660
ggccattgaa	aggcaaaatc	tctgcaaatc	atcttgctta	cttcaagaag	cttttatgac	720
acttttttgt	agaaatatct	atggattatt	gtttcttag			

- (2) INFORMATION FOR SEQ ID NO:623:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567490
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

Met	Lys	Ile	Leu	Val	Ala	Ala	Ala	Ile	Ala	Leu	Lys	Gly	Ile	Gly	Gly
1				5					10					15	
Leu	Leu	Phe	Val	Phe	Gly	Ser	Ser	Leu	Gly	Ala	Tyr	Leu	Leu	Leu	Leu
			20					25					30		
His	Gln	Ala	Val	Ala	Thr	Pro	Ile	Leu	Tyr	Asp	Phe	Tyr	Asn	Tyr	Asp
		35					40					45			
Val	Asp	Arg	Lys	Glu	Phe	Gly	Gln	Leu	Phe	Ser	Lys	Phe	Thr	Gln	Ser
	50					55					60				
Leu	Ala	Leu	Leu	Gly	Gly	Leu	Leu	Phe	Phe	Ile	Gly	Met	Lys	Asn	Ser
	65					70				75				80	
Arg	Lys	His	Gly	Arg	Gln	Leu	Arg	Lys	Lys	Ala	Pro	Lys	Ala	Lys	Ala
			85					90						95	

Asn

- (2) INFORMATION FOR SEQ ID NO:624:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..397
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567501
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

aaaaacgcaa cgaagaacaa aatgggttca aagtcaccaa atattgtcgc acttgtgtta 60
cccctacttc ttatacttta cactctttcc tctcaagttg aagtcgtgga atctacaggg 120
cgaaaacttt cgttttgggg aaatcctatc gtgtggactc cacactcaaa ttcattgtgga 180
ggttctccag catcagttatt tgcttcttcc aagtggacga caggccgacc atgcagacgt 240
agtCgtNcct ccaggaacta atattcctgt ttctgatcaa tctccatagt actttaattt 300
gagtttgagt tactctgtgt tcgaatttta aagtatatgt ggttttctgt ttttagtttcg 360
tgtctcaact ctcaagtgtg gaggaataat ataaact

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1567502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

Lys Asn Ala Thr Lys Asn Lys Met Gly Ser Lys Ser Pro Asn Ile Val
1 5 10 15
Ala Leu Val Leu Pro Leu Leu Leu Ile Leu Tyr Thr Leu Ser Ser Gln
20 25 30
Val Glu Val Val Glu Ser Thr Gly Arg Lys Leu Ser Phe Trp Gly Asn
35 40 45
Pro Ile Val Trp Thr Pro His Ser Asn Ser Cys Gly Gly Ser Pro Ala
50 55 60
Ser Val Phe Ala Ser Ser Lys Trp Thr Thr Gly Arg Pro Cys Arg Arg
65 70 75 80
Ser Arg Xaa Ser Arg Asn
85

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1567503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Lys Thr Gln Arg Arg Thr Lys Trp Val Gln Ser His Gln Ile Leu Ser
1 5 10 15
His Leu Cys Tyr Pro Tyr Phe Leu Tyr Phe Thr Leu Phe Pro Leu Lys
20 25 30
Leu Lys Ser Trp Asn Leu Gln Gly Ala Asn Phe Arg Phe Gly Glu Ile
35 40 45
Leu Ser Cys Gly Leu His Thr Gln Ile His Val Glu Val Leu Gln His
50 55 60
Gln Tyr Leu Leu Leu Pro Ser Gly Arg Gln Ala Asp His Ala Asp Val
65 70 75 80
Val Xaa Pro Pro Gly Thr Asn Ile Pro Val Ser Asp Gln Ser Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..79
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567504
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

Met Gly Ser Lys Ser Pro Asn Ile Val Ala Leu Val Leu Pro Leu Leu
1 5 10 15
Leu Ile Leu Tyr Thr Leu Ser Ser Gln Val Glu Val Val Glu Ser Thr
 20 25 30
Gly Arg Lys Leu Ser Phe Trp Gly Asn Pro Ile Val Trp Thr Pro His
 35 40 45
Ser Asn Ser Cys Gly Gly Ser Pro Ala Ser Val Phe Ala Ser Ser Lys
 50 55 60
Trp Thr Thr Gly Arg Pro Cys Arg Arg Ser Arg Xaa Ser Arg Asn
65 70 75

(2) INFORMATION FOR SEQ ID NO:628:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..750
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

taatcaaaaa ataaaaagta attagtgaga gaattaagaa aaacaaagtc tattccatac 60
gaagaagagc ctcagggttaa ttttttaaaa gatgggttat tggaagtcga aggttggtcc 120
aaggatgaag aaattgttcg agaagagtc agcaaaaaag gaagttgttg aggaggagaa 180
gccacgagag gtggaagtcg tggaggaggt gtcgtgaaaa ccgaagaacc ggccaaggaa 240
ggagaaacta aaccggagga aataattgca accggcgaga aagagataga aatagttgaa 300
gagaagaaag aagaggctaa accggtggag gttccgggtcc tcgcagctgc ggaggagaag 360
aagccagccg tagaagagga gaagaagacg gcgccggttg aagagaagaa gccagctgtg 420
gaagaggaga agaagcctgc cgtggaagag aagaaacctg tggaggagga gaaaaaagaa 480
gttggtgccg ctgttccggt ggctgaaact ccttcgacta aggtctccga aactccggtg 540
gttgaaactc cgccaaggc tccggaaact ccggcgGctg cgccacaaaa ggcttgaatt 600
ttcttcatgg tacatttttc taaaaaaata ttgattgtct ttgtgtggat aattttattt 660
ctttgtttat ttgtcttatt atccatgtga atttcctcta taaattaatt tgcttgcttg 720
aattatatat tcttatgac caaatcctcc

(2) INFORMATION FOR SEQ ID NO:629:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..41
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

Met Gly Tyr Trp Lys Ser Lys Val Val Pro Arg Met Lys Lys Leu Phe
1 5 10 15
Glu Lys Ser Pro Ala Lys Lys Glu Val Val Glu Glu Glu Lys Pro Arg
 20 25 30
Glu Val Glu Val Val Glu Glu Val Ser
 35 40

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:

00000000-00000000

(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: / Ceres Seq. ID 1567515
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
Met Lys Lys Leu Phe Glu Lys Ser Pro Ala Lys Lys Glu Val Val Glu
1 5 10 15
Glu Glu Lys Pro Arg Glu Val Glu Val Glu Glu Val Ser
20 25 30
(2) INFORMATION FOR SEQ ID NO:631:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..591
(D) OTHER INFORMATION: / Ceres Seq. ID 1567520
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:
actcgggtccc atcatgcaag tagataaaca ctgaatcacc aaatcttggt tgagatttag 60
aaaaaaagga agctccaaga gatggcaaga gttgttaaaa tcgattctgc agagtcattgg 120
gatttctatg tgagtcaagc caagaatcag aattgtccca ttgtggctca tttcactgca 180
ttatggtgta ttccttctgt gtttatgaac tccttcttcg aagagcttgc gtttaactat 240
aaggatgctc tgtttctaata agttgatggt gatgaagtta aggaagtggc aagtcaacta 300
gaggtaaagg cgatgccaac tttcttggtc ttgaaggatg gtaatgcgat ggacaaactc 360
gtgggcgcaa accctgatga gattaagaaa cgggtcgtat gtttcgttca gtcctcacgt 420
gttggttcata ttgcttaaga gagatttata gatacgagca gaatactaaa taaagtttgt 480
gtgaagtgta attagtttgt aactttggtt tttggtttgt gtgaaAtatc aagtgttaagt 540
gtaaattttt ataaaagcaa gttytgttat aaacaagaac tggattttatt c
(2) INFORMATION FOR SEQ ID NO:632:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1567521
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:
Met Ala Arg Val Val Lys Ile Asp Ser Ala Glu Ser Trp Asp Phe Tyr
1 5 10 15
Val Ser Gln Ala Lys Asn Gln Asn Cys Pro Ile Val Ala His Phe Thr
20 25 30
Ala Leu Trp Cys Ile Pro Ser Val Phe Met Asn Ser Phe Phe Glu Glu
35 40 45
Leu Ala Phe Asn Tyr Lys Asp Ala Leu Phe Leu Ile Val Asp Val Asp
50 55 60
Glu Val Lys Glu Val Ala Ser Gln Leu Glu Val Lys Ala Met Pro Thr
65 70 75 80
Phe Leu Phe Leu Lys Asp Gly Asn Ala Met Asp Lys Leu Val Gly Ala
85 90 95
Asn Pro Asp Glu Ile Lys Lys Arg Val Asp Gly Phe Val Gln Ser Ser

100 105 110
Arg Val Val His Ile Ala
115

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Met Asn Ser Phe Phe Glu Glu Leu Ala Phe Asn Tyr Lys Asp Ala Leu
1 5 10 15
Phe Leu Ile Val Asp Val Asp Glu Val Lys Glu Val Ala Ser Gln Leu
20 25 30
Glu Val Lys Ala Met Pro Thr Phe Leu Phe Leu Lys Asp Gly Asn Ala
35 40 45
Met Asp Lys Leu Val Gly Ala Asn Pro Asp Glu Ile Lys Lys Arg Val
50 55 60
Asp Gly Phe Val Gln Ser Ser Arg Val Val His Ile Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

aatcagtaaa acgaaaagct aatccaaaac tctttaatta tttgtaacaa ctgatcaatg 60
gctgtaacaa gctcttcttc tacttgatgat gggttcttca tcatcagcct tattgtgtgc 120
gtttcttcat tgtttggggc atcatctgct cagttaaacg caacgtttta ctcaggcacg 180
tgccctaacg catctgccat cgttcgcagc actattcagc aagctcttca atccgatgca 240
agaatcggag gcagcctaatt ccgccttcat tttcagcact gttttgttaa tgggtgcgat 300
gggtcgctct tgcttgacga cacttcaagc atccagagcg agaagaacgc tcctgccaat 360
gcaaactcaa ctagaggatt caatgttgct gatagtatca agacagccct cgagaatgct 420
tgtcccggca ttgtttcttg ctctgacatt ttagctcttg cctcagaggc ctctgtgtct 480
ttggcaggag gaccttcattg gactgtgta ttaggaagaa gagatggct caccgcaaac 540
ttgtctggag ccaattcgtc tcttccctct cccttcgaag gccttaacaa catcacatca 600
aaatttgtag ctgtcgggct aaatacaacc gatgtagtat ccttgtctgg agcgcatagc 660
tttgggcgtg gtcaatgcgt aacCgttcaa caatagacta ttcaacttca acgggacagg 720
aaaccccgac ccgactctga actcaacact tctcagcagt cttcaacagc tatgtcctca 780
aaacggcagc aatacaggga tcaccaatct cgatctgagc acacctgatg cgttcgataa 840
caattacttc acgaaccttc agagtaacaa tgggcttctc cagtcagacc aggaactgtt 900
ctcaaacacc ggttcagcca ccgtcccgat tgtaattcc tttgcaagta accagaccct 960
gttttttgag gcgtttgttc agtctatgat caagatgggg aacattagtc ccttgactgg 1020
gagtagtgga gagattagac aagactgtaa ggtgggtaat ggacagtcac cagccactga 1080
agcaggggac attcagttac aatctgacgg accagtgagt gtagcagata tgtgaacaac 1140
gatgagatca gtttcaccgt ttgtttatca tatatgaata ataactccta ggccgaatca 1200
tttttgtaga aaaaataaag ttggttgagg agaaaataag tgagtggtag gggtgtgttt 1260
tacacttttg aaaaatttaa tattctaaaa cattattatg cctaaatata tgcatgcatg 1320
tataacgtct atcgttttga tacattttgt gg

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..212
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567527
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met Ala Val Thr Ser Ser Ser Thr Cys Asp Gly Phe Phe Ile Ile
1 5 10 15
Ser Leu Ile Val Val Val Ser Ser Leu Phe Gly Ala Ser Ser Ala Gln
 20 25 30
Leu Asn Ala Thr Phe Tyr Ser Gly Thr Cys Pro Asn Ala Ser Ala Ile
 35 40 45
Val Arg Ser Thr Ile Gln Gln Ala Leu Gln Ser Asp Ala Arg Ile Gly
50 55 60
Gly Ser Leu Ile Arg Leu His Phe His Asp Cys Phe Val Asn Gly Cys
65 70 75 80
Asp Gly Ser Leu Leu Leu Asp Asp Thr Ser Ser Ile Gln Ser Glu Lys
 85 90 95
Asn Ala Pro Ala Asn Ala Asn Ser Thr Arg Gly Phe Asn Val Val Asp
 100 105 110
Ser Ile Lys Thr Ala Leu Glu Asn Ala Cys Pro Gly Ile Val Ser Cys
115 120 125
Ser Asp Ile Leu Ala Leu Ala Ser Glu Ala Ser Val Ser Leu Ala Gly
130 135 140
Gly Pro Ser Trp Thr Val Leu Leu Gly Arg Arg Asp Gly Leu Thr Ala
145 150 155 160
Asn Leu Ser Gly Ala Asn Ser Ser Leu Pro Ser Pro Phe Glu Gly Leu
 165 170 175
Asn Asn Ile Thr Ser Lys Phe Val Ala Val Gly Leu Asn Thr Thr Asp
180 185 190
Val Val Ser Leu Ser Gly Ala His Thr Phe Gly Arg Gly Gln Cys Val
195 200 205
Thr Val Gln Gln
210

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..716
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567532
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

aagaattagg gtttctcttt gtcttcagca gtcagtgcgc atccgtagGa gaaaagtgtg 60
agaatctgcc accatgggtc gtatgcacag tcgaggaaag ggtatttcag cctctgcgtt 120
gccttacaag agatcgtctc caagctggct caagaccacc tctcaggatg ttgatgaatc 180
aatctgcaaa tttgccaaaa agggattgac cccttcccag attggtgtga ttctccgtga 240
ctctcacggg atccctcagg tcaagagtgt tactggaagc aagatottga ggataactcaa 300
agctcatggc cttgctcctg agatccctga ggatctgtac catctaatta agaaggctgt 360
tgccatccgt aaacatctcg agaggaacag gaaggacaag gattccaagt tcaggctcat 420
cttggttgag agcaggattc accgcctcgc tcgctattac aagaagacca agaagctccc 480
tcccgtctgg aagtacgaat ccactaccgc gagcaccctt gtggcttaag ctggagtctg 540
gaggaggatt ctactagtct gttgcttccc tttgttttga tgaattctca actttagtct 600

taatgtttca gcaggatttt tgtgtttgcc tctcttcttt ttccggaatc ttatgctccc 660
ttgtttaaga gaatcgatg atcttgaatt tactattgaa tatgcttttg catccc

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1567533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Met Gly Arg Met His Ser Arg Gly Lys Gly Ile Ser Ala Ser Ala Leu
1 5 10 15
Pro Tyr Lys Arg Ser Ser Pro Ser Trp Leu Lys Thr Thr Ser Gln Asp
20 25 30
Val Asp Glu Ser Ile Cys Lys Phe Ala Lys Lys Gly Leu Thr Pro Ser
35 40 45
Gln Ile Gly Val Ile Leu Arg Asp Ser His Gly Ile Pro Gln Val Lys
50 55 60
Ser Val Thr Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu
65 70 75 80
Ala Pro Glu Ile Pro Glu Asp Leu Tyr His Leu Ile Lys Lys Ala Val
85 90 95
Ala Ile Arg Lys His Leu Glu Arg Asn Arg Lys Asp Lys Asp Ser Lys
100 105 110
Phe Arg Leu Ile Leu Val Glu Ser Arg Ile His Arg Leu Ala Arg Tyr
115 120 125
Tyr Lys Lys Thr Lys Lys Leu Pro Pro Val Trp Lys Tyr Glu Ser Thr
130 135 140
Thr Ala Ser Thr Leu Val Ala
145 150

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1567534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Met His Ser Arg Gly Lys Gly Ile Ser Ala Ser Ala Leu Pro Tyr Lys
1 5 10 15
Arg Ser Ser Pro Ser Trp Leu Lys Thr Thr Ser Gln Asp Val Asp Glu
20 25 30
Ser Ile Cys Lys Phe Ala Lys Lys Gly Leu Thr Pro Ser Gln Ile Gly
35 40 45
Val Ile Leu Arg Asp Ser His Gly Ile Pro Gln Val Lys Ser Val Thr
50 55 60
Gly Ser Lys Ile Leu Arg Ile Leu Lys Ala His Gly Leu Ala Pro Glu
65 70 75 80
Ile Pro Glu Asp Leu Tyr His Leu Ile Lys Lys Ala Val Ala Ile Arg
85 90 95
Lys His Leu Glu Arg Asn Arg Lys Asp Lys Asp Ser Lys Phe Arg Leu
100 105 110
Ile Leu Val Glu Ser Arg Ile His Arg Leu Ala Arg Tyr Tyr Lys Lys

115 120 125
Thr Lys Lys Leu Pro Pro Val Trp Lys Tyr Glu Ser Thr Thr Ala Ser
130 135 140
Thr Leu Val Ala
145

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..675
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

aattcgacgt ctctcttttcg tctctgtatc gatttttttcg ccgcgaattt cgaataggtt 60
cttcaccata agcttgagat cttatttctc tactgtttctt tgctttcttct ctatcgatat 120
ggctggtaaa ggtgggaaag ggcttctagc tgcgaagacg acggcagcag ctgcaaacaa 180
agacagtgtt aagaagaaat ccattctctc ctcttctcgt gctgggtattc agtttccagt 240
gggtcgtatt catcgtcaac tcaagcaaag agtttcagca catggaagag ttggtgccac 300
tgctgctgtt tacactgcat caattctaga atacttgact gctgaagtac tcgagtttagc 360
tggaatgacg agcaaggatc tcaaagttaa gagaattaca ccaagacatt tgcagcttgc 420
aatcagagga gatgaggaac ttgacactct catcaaagga accattgcag gaggaggtgt 480
gatccctcac atccacaagt cccttgtcaa caaagtcacc aaggattgag tttcgccttc 540
tgagtcctaa gtctctatta tactatgtgc tcttttTota gacgccctca tgtgtatatg 600
ggttcattgt atctcttagg tctctcgttt tagactcata ctcttggtat tttgctaattg 660
cttacatgat tgagg

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

Ile Arg Arg Leu Ser Phe Val Ser Val Ser Ile Phe Ser Pro Arg Ile
1 5 10 15
Ser Asn Arg Phe Phe Thr Ile Ser Leu Arg Ser Tyr Phe Ser Thr Val
20 25 30
Leu Cys Phe Phe Ser Ile Asp Met Ala Gly Lys Gly Gly Lys Gly Leu
35 40 45
Leu Ala Ala Lys Thr Thr Ala Ala Ala Ala Asn Lys Asp Ser Val Lys
50 55 60
Lys Lys Ser Ile Ser Arg Ser Ser Arg Ala Gly Ile Gln Phe Pro Val
65 70 75 80
Gly Arg Ile His Arg Gln Leu Lys Gln Arg Val Ser Ala His Gly Arg
85 90 95
Val Gly Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu
100 105 110
Thr Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys
115 120 125
Val Lys Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp
130 135 140
Glu Glu Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val
145 150 155 160

Ile Pro His Ile His Lys Ser Leu Val Asn Lys Val Thr Lys Asp
165 170 175

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1567546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

Met Ala Gly Lys Gly Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala
1 5 10 15
Ala Ala Ala Asn Lys Asp Ser Val Lys Lys Lys Ser Ile Ser Arg Ser
20 25 30
Ser Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
35 40 45
Lys Gln Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
50 55 60
Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
65 70 75 80
Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
85 90 95
His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
100 105 110
Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
115 120 125
Leu Val Asn Lys Val Thr Lys Asp
130 135

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..566

(D) OTHER INFORMATION: / Ceres Seq. ID 1567547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

tcaagccgctc aacaatgtcg aagcgagggc gtggaggtac ctctggtaac aaattcagga 60
tgtcactggg tcttccggtg gcggcgacgg tgaactgtgc cgataacacc ggtgctaaga 120
atctctacat catttccgtg aaaggtatca aaggctcgtct taatcgatta ccttctgctt 180
gcgtcggaga catggtgatg gccaccgtca aaaagggtaa gcctgatctc aggaaaaagg 240
ttcttctctgc cgtcatcggtt aggcaacgca aaccatggcg ccgaaaggat ggtgttttca 300
tgtactttcga agataatgct ggagtcattg tcaaccccaa gggagaaatg aaaggttctg 360
caattactgg tcctattggg aaagagtgtg ctgatctttg gccaaaggatt gctagtgtctg 420
ccaatgccat tgtctaata tcatgatcaat caattgcttg tatttgatgg atatgtctag 480
atacaaattt gagaattttg gtagcaagat atttttattt tctgacaata tgtatctgac 540
attcaaata tttggctatt ttTgac

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1567548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Lys	Pro	Ser	Thr	Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn
1				5					10					15	
Lys	Phe	Arg	Met	Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys
			20					25					30		
Ala	Asp	Asn	Thr	Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly
		35					40					45			
Ile	Lys	Gly	Arg	Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met
	50					55					60				
Val	Met	Ala	Thr	Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val
65					70				75						80
Leu	Pro	Ala	Val	Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp
				85					90					95	
Gly	Val	Phe	Met	Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro
			100					105					110		
Lys	Gly	Glu	Met	Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu
		115					120					125			
Cys	Ala	Asp	Leu	Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val
	130					135						140			

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1567549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn	Lys	Phe	Arg	Met
1				5					10					15	
Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	Ala	Asp	Asn	Thr
			20					25					30		
Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	Ile	Lys	Gly	Arg
		35					40					45			
Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	Val	Met	Ala	Thr
	50					55					60				
Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val	Leu	Pro	Ala	Val
65					70				75						80
Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	Gly	Val	Phe	Met
			85						90					95	
Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	Lys	Gly	Glu	Met
			100					105					110		
Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	Cys	Ala	Asp	Leu
		115					120					125			
Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567550
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

```
Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn
1          5          10          15
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly
          20          25          30
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala
          35          40          45
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Leu Pro Ala
          50          55          60
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Phe
          65          70          75          80
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu
          85          90          95
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp
          100         105         110
Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val
          115         120         125
```

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..352
(D) OTHER INFORMATION: / Ceres Seq. ID 1567555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

```
cctagaaatt ttgtctctct cgccgccttg cgaaaagcat ttctgatctt actcttagga      60
taaaaaaatg tgcacagttg gagagcttgc ttgcagctac gctgttatga tcctcgagga      120
cgagggtatc gctatcacgg ctgacaaaat cgcgaccttg gtgaaagctg ctggtgttag      180
tattgagtca tactggccaa tgctattogc caagatggct gagaaacgta acgtgactga      240
tctcatcatg aacgttggtg ctggttggtg aggttggtgct ccggttgtag ctgctgctcc      300
agctgctggc ggtggtgcgg caSctgcaac cggagcacca ctctccacca cc
```

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1567556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

```
Met Ser Thr Val Gly Glu Leu Ala Cys Ser Tyr Ala Val Met Ile Leu
1          5          10          15
Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala Thr Leu Val
          20          25          30
Lys Ala Ala Gly Val Ser Ile Glu Ser Tyr Trp Pro Met Leu Phe Ala
          35          40          45
Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly
          50          55          60
Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala
```

(2) INFORMATION FOR SEQ ID NO:648:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1567557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

(2) INFORMATION FOR SEQ ID NO:649:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1567558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

(2) INFORMATION FOR SEQ ID NO:650:

(A) LENGTH: 1465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1465

(D) OTHER INFORMATION: / Ceres Seq. ID 1567563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

agattaaaaa ctctttaaaa actttttgtc ataaatcagg caaagaagta aaagaggctt 60
aaaactctct ctctctcttg gtcttctcga ctcttaacga aaatggactc totaacactc 120

ttcttcaccg gcgcactcgt cgccgtcggg atctactggg tctctcgcgt tctcgggtcca 180
gcagagcgta aaggcaaacg agccgtagat ctctctggcg gctcaatctc cgccgagaaa 240
gtccaagaca actacaaaca gtactgggtct ttcttccgcc gtccaaaaga aatcgaaacc 300
gccgagaaaag ttccagactt cgtcgacaca ttctacaatc tcgtcaccga catatacgag 360
tggggatggg gacaatcctt ccactttctca ccatcaatcc ccgaaaaatc tcacaaagac 420
gccacgcgcc tccacgaaga gatggccgta gatctgatcc aagtcaaacc tgggtcaaaag 480
atcctagacg tcggatdcgg cgtcggcggg bcgatgcgag cgattgcac tcaactcgca 540
gctaacgtag tcgggattac gataaacgag tatcagggtga acagagctcg tctccacaat 600
aagaaagctg gtctcgacgc gcttttgcgag gtcgtctgtg gtaacttctt ccagatgccg 660
ttcgatgaca acagtttcga cgggtgcttat tccatcgaag ccacgtgtca cgcgccgaag 720
ctggaggaag tgtacgcaga gatctacagg gtgttgaaac ccggatctat gtatgtgtcg 780
tacgagtggg ttacgacgga gaaatttaag gcggaggatg acgaaAcacg tggaggtaat 840
ccaaggGatt gagagagtg atgcgttacc tgggcttagg cttacgtgga tattgctgag 900
acggctaaaa aggttgggtt tgagatagtg aaggagaagg atctggcgag tccaccggct 960
gagccgtggg ggactaggct taagatgggt aggttgcctt attggaggaa tcacattgtg 1020
gttcagattt tgtcagcggg tggagttgct cctaaaggaa ctgttgatgt tcatgagatg 1080
ttgtttaaga ctgctgatta tttgaccaga ggaggtgaaa ccggaatatt ctctccgatg 1140
catatgattc tctgcagaaa accggagtc aaggaggaga gttcttgaga aaggtagaaa 1200
ggaaacatca ccgaaaaaag tatggagaat tttctcaatt tgtttttatt ttttaagttaa 1260
atcaacttgg ttattgtact atttttgtgt ttttaatttg tttgtgtttc aagaattatt 1320
agtttttttt tgttttgttg catatgagaa tcttactctt gatttctcgg ccgtagtgcc 1380
ggcgagacat aggggattat tagtattttt aagtgtgttt aagattgatt aacaagttag 1440
taaaataaaa tgtacttagg tgtcgc

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1567564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

Met	Asp	Ser	Leu	Thr	Leu	Phe	Phe	Thr	Gly	Ala	Leu	Val	Ala	Val	Gly
1			5					10						15	
Ile	Tyr	Trp	Phe	Leu	Cys	Val	Leu	Gly	Pro	Ala	Glu	Arg	Lys	Gly	Lys
			20					25					30		
Arg	Ala	Val	Asp	Leu	Ser	Gly	Gly	Ser	Ile	Ser	Ala	Glu	Lys	Val	Gln
			35				40						45		
Asp	Asn	Tyr	Lys	Gln	Tyr	Trp	Ser	Phe	Phe	Arg	Arg	Pro	Lys	Glu	Ile
			50			55				60					
Glu	Thr	Ala	Glu	Lys	Val	Pro	Asp	Phe	Val	Asp	Thr	Phe	Tyr	Asn	Leu
65					70					75				80	
Val	Thr	Asp	Ile	Tyr	Glu	Trp	Gly	Trp	Gly	Gln	Ser	Phe	His	Phe	Ser
			85					90						95	
Pro	Ser	Ile	Pro	Gly	Lys	Ser	His	Lys	Asp	Ala	Thr	Arg	Leu	His	Glu
			100					105					110		
Glu	Met	Ala	Val	Asp	Leu	Ile	Gln	Val	Lys	Pro	Gly	Gln	Lys	Ile	Leu
			115				120						125		
Asp	Val	Gly	Xaa	Gly	Val	Gly	Gly	Xaa	Met	Arg	Ala	Ile	Ala	Ser	His
			130			135				140					
Ser	Arg	Ala	Asn	Val	Val	Gly	Ile	Thr	Ile	Asn	Glu	Tyr	Gln	Val	Asn
145				150						155				160	
Arg	Ala	Arg	Leu	His	Asn	Lys	Lys	Ala	Gly	Leu	Asp	Ala	Leu	Cys	Glu
			165					170						175	
Val	Val	Cys	Gly	Asn	Phe	Leu	Gln	Met	Pro	Phe	Asp	Asp	Asn	Ser	Phe
			180					185					190		
Asp	Gly	Ala	Tyr	Ser	Ile	Glu	Ala	Thr	Cys	His	Ala	Pro	Lys	Leu	Glu
			195				200						205		

Glu Val Tyr Ala Glu Ile Tyr Arg Val Leu Lys Pro Gly Ser Met Tyr
210 215 220
Val Ser Tyr Glu Trp Val Thr Thr Glu Lys Phe Lys Ala Glu Asp Asp
225 230 235 240
Glu Thr Arg Gly Gly Asn Pro Arg Asp
245

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1567565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

Met Ala Val Asp Leu Ile Gln Val Lys Pro Gly Gln Lys Ile Leu Asp
1 5 10 15
Val Gly Xaa Gly Val Gly Gly Xaa Met Arg Ala Ile Ala Ser His Ser
20 25 30
Arg Ala Asn Val Val Gly Ile Thr Ile Asn Glu Tyr Gln Val Asn Arg
35 40 45
Ala Arg Leu His Asn Lys Lys Ala Gly Leu Asp Ala Leu Cys Glu Val
50 55 60
Val Cys Gly Asn Phe Leu Gln Met Pro Phe Asp Asp Asn Ser Phe Asp
65 70 75 80
Gly Ala Tyr Ser Ile Glu Ala Thr Cys His Ala Pro Lys Leu Glu Glu
85 90 95
Val Tyr Ala Glu Ile Tyr Arg Val Leu Lys Pro Gly Ser Met Tyr Val
100 105 110
Ser Tyr Glu Trp Val Thr Thr Glu Lys Phe Lys Ala Glu Asp Asp Glu
115 120 125
Thr Arg Gly Gly Asn Pro Arg Asp
130 135

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1629

(D) OTHER INFORMATION: / Ceres Seq. ID 1567581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

aattthtcTC gaacaccgaa aacactttcg aaccctaaaa gacagaacac tgtgtcaatt 60
ttcattacct gggaacaaaa cgcaaaatca aagacaataa ttttttcccc gagagagaaa 120
atgcagaggt tgaagcagca gcagcagcag caacaagtta tgatgcagca agctcttatg 180
cagcaacagt ctctctacca tcttggtctc ottgccccgc cacagataga accaatccca 240
agtggaaatc tcccccttg ttttgatcca agtacttgcc gcagtgtgta cgttggaac 300
atccatattc aggtgacgga acctctgctt caagaggttt ttgctggcac tggctcctgta 360
gaaagctgta aactaattag gaaagaaaag tcttcttatg ggtttgtgca ctactttgat 420
cgaagatcgg ctggtcttgc aatcctttct ctcaatggaa ggcatttggt tgggcaacct 480
atcaagggtta actgggctta tgcgagtggc cagagggagg atacatcaag tcacttcaat 540
atatttggtg gggatttgag tccggagggt actgatgcaa tgctgtttac ttgcttctct 600
gtctaccgga cttgctcgga tgcaagaggt atgtgggata agaaaactgg gcgttcaaga 660
ggatttggtt ttgtttcctt ccgtaaccaa caggatgccc agactgcaat agatgagata 720
actgggaaat ggcttggttc caggcagata cgttgcaact gggcgacaaa gggagccact 780

tctggtgagg acaaacagag ctctgattcc aaaagcgtcg tggaacttac cagtgggtgc 840
tcggaggatg gtaaagatac tactaatggt gaagtcctg agaacaatgc tcagtacaca 900
actgtttacg tcggtaatct tgctccagag gtgtcccagg ttgatcttca ccgccacttc 960
cattcccttg gtgctgggggt catagaggaa gtccgtgttc aaagagacaa aggtttcgga 1020
tttgtgagat actctactca tgtagaggca gccctcgcta ttcagatggg aaacacacat 1080
tcctacctta gtggcaggca aatgaagtgt tcttggggaa gcaagccaac tccagcagga 1140
acagcttcaa acccgcttcc tccaccagct cctgcaccaa tcccgggatt ctcagcgagt 1200
gatctcttgg cttacgagag gcaactagcg atgagcaaga tggcaggaat gaatccgatg 1260
atgcatcacc cgcagggaca acatgctttt aaacaagctg caatgggagc cactggttca 1320
aaccaggcaa tatatgacgg tggttaccag aacgcgcagc agctcatgta ctaccagtaa 1380
gatcttcctc ggagccggtta cttgagcgaa gagttctttc ttttcttctt ttttgttatg 1440
taacgtcttt attgtatctt tttcttttct totaacttat gttcttggtta taatgttatc 1500
atgtagctgt gggtttggg tttgtgttcc acgttttttc ttttgttaac tactacggtt 1560
tacgtttttg cacatcttca acttctttct ctttctcttt ctctaactta atcttattta 1620
ttgggtcgc

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1567582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Asn Xaa Ser Arg Thr Pro Lys Thr Leu Ser Asn Pro Lys Arg Gln Asn
1 5 10 15
Thr Val Ser Ile Phe Ile Thr Trp Glu Gln Asn Ala Lys Ser Lys Thr
20 25 30
Ile Ile Phe Ser Pro Arg Glu Lys Met Gln Arg Leu Lys Gln Gln Gln
35 40 45
Gln Gln Gln Gln Val Met Met Gln Gln Ala Leu Met Gln Gln Gln Ser
50 55 60
Leu Tyr His Pro Gly Leu Leu Ala Pro Pro Gln Ile Glu Pro Ile Pro
65 70 75 80
Ser Gly Asn Leu Pro Pro Gly Phe Asp Pro Ser Thr Cys Arg Ser Val
85 90 95
Tyr Val Gly Asn Ile His Ile Gln Val Thr Glu Pro Leu Leu Gln Glu
100 105 110
Val Phe Ala Gly Thr Gly Pro Val Glu Ser Cys Lys Leu Ile Arg Lys
115 120 125
Glu Lys Ser Ser Tyr Gly Phe Val His Tyr Phe Asp Arg Arg Ser Ala
130 135 140
Gly Leu Ala Ile Leu Ser Leu Asn Gly Arg His Leu Phe Gly Gln Pro
145 150 155 160
Ile Lys Val Asn Trp Ala Tyr Ala Ser Gly Gln Arg Glu Asp Thr Ser
165 170 175
Ser His Phe Asn Ile Phe Val Gly Asp Leu Ser Pro Glu Val Thr Asp
180 185 190
Ala Met Leu Phe Thr Cys Phe Ser Val Tyr Pro Thr Cys Ser Asp Ala
195 200 205
Arg Val Met Trp Asp Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly Phe
210 215 220
Val Ser Phe Arg Asn Gln Gln Asp Ala Gln Thr Ala Ile Asp Glu Ile
225 230 235 240
Thr Gly Lys Trp Leu Gly Ser Arg Gln Ile Arg Cys Asn Trp Ala Thr
245 250 255
Lys Gly Ala Thr Ser Gly Glu Asp Lys Gln Ser Ser Asp Ser Lys Ser
260 265 270

Val Val Glu Leu Thr Ser Gly Val Ser Glu Asp Gly Lys Asp Thr Thr
275 280 285
Asn Gly Glu Ala Pro Glu Asn Asn Ala Gln Tyr Thr Thr Val Tyr Val
290 295 300
Gly Asn Leu Ala Pro Glu Val Ser Gln Val Asp Leu His Arg His Phe
305 310 315 320
His Ser Leu Gly Ala Gly Val Ile Glu Glu Val Arg Val Gln Arg Asp
325 330 335
Lys Gly Phe Gly Phe Val Arg Tyr Ser Thr His Val Glu Ala Ala Leu
340 345 350
Ala Ile Gln Met Gly Asn Thr His Ser Tyr Leu Ser Gly Arg Gln Met
355 360 365
Lys Cys Ser Trp Gly Ser Lys Pro Thr Pro Ala Gly Thr Ala Ser Asn
370 375 380
Pro Leu Pro Pro Pro Ala Pro Ala Pro Ile Pro Gly Phe Ser Ala Ser
385 390 395 400
Asp Leu Leu Ala Tyr Glu Arg Gln Leu Ala Met Ser Lys Met Ala Gly
405 410 415
Met Asn Pro Met Met His His Pro Gln Gly Gln His Ala Phe Lys Gln
420 425 430
Ala Ala Met Gly Ala Thr Gly Ser Asn Gln Ala Ile Tyr Asp Gly Gly
435 440 445
Tyr Gln Asn Ala Gln Gln Leu Met Tyr Tyr Gln
450 455

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1567583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

Met Gln Arg Leu Lys Gln Gln Gln Gln Gln Gln Val Met Met Gln
1 5 10 15
Gln Ala Leu Met Gln Gln Gln Ser Leu Tyr His Pro Gly Leu Leu Ala
20 25 30
Pro Pro Gln Ile Glu Pro Ile Pro Ser Gly Asn Leu Pro Pro Gly Phe
35 40 45
Asp Pro Ser Thr Cys Arg Ser Val Tyr Val Gly Asn Ile His Ile Gln
50 55 60
Val Thr Glu Pro Leu Leu Gln Glu Val Phe Ala Gly Thr Gly Pro Val
65 70 75 80
Glu Ser Cys Lys Leu Ile Arg Lys Glu Lys Ser Ser Tyr Gly Phe Val
85 90 95
His Tyr Phe Asp Arg Arg Ser Ala Gly Leu Ala Ile Leu Ser Leu Asn
100 105 110
Gly Arg His Leu Phe Gly Gln Pro Ile Lys Val Asn Trp Ala Tyr Ala
115 120 125
Ser Gly Gln Arg Glu Asp Thr Ser Ser His Phe Asn Ile Phe Val Gly
130 135 140
Asp Leu Ser Pro Glu Val Thr Asp Ala Met Leu Phe Thr Cys Phe Ser
145 150 155 160
Val Tyr Pro Thr Cys Ser Asp Ala Arg Val Met Trp Asp Gln Lys Thr
165 170 175
Gly Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn Gln Gln Asp
180 185 190
Ala Gln Thr Ala Ile Asp Glu Ile Thr Gly Lys Trp Leu Gly Ser Arg

195	200	205
Gln Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Ser Gly Glu Asp		
210	215	220
Lys Gln Ser Ser Asp Ser Lys Ser Val Val Glu Leu Thr Ser Gly Val		
225	230	235
Ser Glu Asp Gly Lys Asp Thr Thr Asn Gly Glu Ala Pro Glu Asn Asn		
	245	250
Ala Gln Tyr Thr Thr Val Tyr Val Gly Asn Leu Ala Pro Glu Val Ser		
	260	265
Gln Val Asp Leu His Arg His Phe His Ser Leu Gly Ala Gly Val Ile		
	275	280
Glu Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe Val Arg Tyr		
	290	295
Ser Thr His Val Glu Ala Ala Leu Ala Ile Gln Met Gly Asn Thr His		
305	310	315
Ser Tyr Leu Ser Gly Arg Gln Met Lys Cys Ser Trp Gly Ser Lys Pro		
	325	330
Thr Pro Ala Gly Thr Ala Ser Asn Pro Leu Pro Pro Pro Ala Pro Ala		
	340	345
Pro Ile Pro Gly Phe Ser Ala Ser Asp Leu Leu Ala Tyr Glu Arg Gln		
	355	360
Leu Ala Met Ser Lys Met Ala Gly Met Asn Pro Met Met His His Pro		
	370	375
Gln Gly Gln His Ala Phe Lys Gln Ala Ala Met Gly Ala Thr Gly Ser		
385	390	395
Asn Gln Ala Ile Tyr Asp Gly Gly Tyr Gln Asn Ala Gln Gln Leu Met		
	405	410
		415
Tyr Tyr Gln		

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

Met Met Gln Gln Ala Leu Met Gln Gln Gln Ser Leu Tyr His Pro Gly	
1	5 10 15
Leu Leu Ala Pro Pro Gln Ile Glu Pro Ile Pro Ser Gly Asn Leu Pro	
	20 25 30
Pro Gly Phe Asp Pro Ser Thr Cys Arg Ser Val Tyr Val Gly Asn Ile	
	35 40 45
His Ile Gln Val Thr Glu Pro Leu Leu Gln Glu Val Phe Ala Gly Thr	
	50 55 60
Gly Pro Val Glu Ser Cys Lys Leu Ile Arg Lys Glu Lys Ser Ser Tyr	
65	70 75 80
Gly Phe Val His Tyr Phe Asp Arg Arg Ser Ala Gly Leu Ala Ile Leu	
	85 90 95
Ser Leu Asn Gly Arg His Leu Phe Gly Gln Pro Ile Lys Val Asn Trp	
	100 105 110
Ala Tyr Ala Ser Gly Gln Arg Glu Asp Thr Ser Ser His Phe Asn Ile	
	115 120 125
Phe Val Gly Asp Leu Ser Pro Glu Val Thr Asp Ala Met Leu Phe Thr	
	130 135 140
Cys Phe Ser Val Tyr Pro Thr Cys Ser Asp Ala Arg Val Met Trp Asp	
145	150 155 160

Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn
165 170 175
Gln Gln Asp Ala Gln Thr Ala Ile Asp Glu Ile Thr Gly Lys Trp Leu
180 185 190
Gly Ser Arg Gln Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Ser
195 200 205
Gly Glu Asp Lys Gln Ser Ser Asp Ser Lys Ser Val Val Glu Leu Thr
210 215 220
Ser Gly Val Ser Glu Asp Gly Lys Asp Thr Thr Asn Gly Glu Ala Pro
225 230 235 240
Glu Asn Asn Ala Gln Tyr Thr Thr Val Tyr Val Gly Asn Leu Ala Pro
245 250 255
Glu Val Ser Gln Val Asp Leu His Arg His Phe His Ser Leu Gly Ala
260 265 270
Gly Val Ile Glu Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe
275 280 285
Val Arg Tyr Ser Thr His Val Glu Ala Ala Leu Ala Ile Gln Met Gly
290 295 300
Asn Thr His Ser Tyr Leu Ser Gly Arg Gln Met Lys Cys Ser Trp Gly
305 310 315 320
Ser Lys Pro Thr Pro Ala Gly Thr Ala Ser Asn Pro Leu Pro Pro Pro
325 330 335
Ala Pro Ala Pro Ile Pro Gly Phe Ser Ala Ser Asp Leu Leu Ala Tyr
340 345 350
Glu Arg Gln Leu Ala Met Ser Lys Met Ala Gly Met Asn Pro Met Met
355 360 365
His His Pro Gln Gly Gln His Ala Phe Lys Gln Ala Ala Met Gly Ala
370 375 380
Thr Gly Ser Asn Gln Ala Ile Tyr Asp Gly Gly Tyr Gln Asn Ala Gln
385 390 395 400
Gln Leu Met Tyr Tyr Gln
405

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

agaaacccta	aaaatcctta	ttgtagcagc	tggagcaata	tatatcccaa	tttgccgcaa	60
ctagggtttt	ctcttctcca	cgcaaagcaa	tacatcgag	tctcccactg	attcagcagc	120
tctttgaact	actcttcgac	aatggcgga	cgtggtggag	aacgtggtgt	tgagcgtggt	180
ggagaacgtg	gtgatttcg	acgaggatc	ggaggccgtg	gaggtcgtgg	agatcgtgga	240
gggcgtggac	gtggaggccg	tgggtgctgt	cgtggagggc	gtgccagtga	agaagagaaa	300
tgggttccag	tgaccaagct	tggctgtcac	gtggcggtg	gtcatatcaa	gcagatagag	360
cagatctatc	ttcattcact	cccggttaag	gagtaccaga	tcattgatat	gctcatcggt	420
ccaacattga	aggatgaggt	aatgaaaatc	atgccggttc	agaaacaaac	cagggctggt	480
caaaggacta	gattcaaggc	ctttgttgtc	gttgagatg	gtaatggtca	tgttgggttg	540
ggagtgaat	gctctaagga	agttgctacg	gccattagag	gagcgattat	tctcgctaa	600
ctgtctgttg	ttccagtgag	gagagggtac	tggggtaaca	agattgggaa	gccacatacg	660
gttccttgta	agggtgactg	gaagtgtgga	tctgtgacag	tgaggatggt	tccagctcct	720
agaggttctg	gtattgtggc	tgctagagtt	cctaagaagg	ttcttcaatt	cgctggaatt	780
gatgatgttt	tacttctc	caggggatcc	accaaactc	ttggaaaCtt	cgtaaggct	840
acattcgatt	gccttcagaa	gacttacgga	ttccttacc	cagagttctg	gaaggagaca	900
agattctcta	gatcaccata	ccaagagcac	actgatttcc	tggcgtccaa	ggctctttcg	960
accagcaaac	ccgaccaggt	ggttgaagac	caagcctaaa	caatgcttcc	accttgtgtt	1020

(2) INFORMATION FOR SEQ ID NO:658:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1567590

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:
```

Met	Ala	Glu	Arg	Gly	Gly	Glu	Arg	Gly	Val	Glu	Arg	Gly	Gly	Glu	Arg
1				5					10					15	
Gly	Asp	Phe	Gly	Arg	Gly	Phe	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Asp	Arg
			20					25					30		
Gly	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Arg	Gly	Gly	Arg	Ala
		35					40					45			
Ser	Glu	Glu	Glu	Lys	Trp	Val	Pro	Val	Thr	Lys	Leu	Gly	Arg	His	Val
	50					55					60				
Ala	Ala	Gly	His	Ile	Lys	Gln	Ile	Glu	Gln	Ile	Tyr	Leu	His	Ser	Leu
65				70						75					80
Pro	Val	Lys	Glu	Tyr	Gln	Ile	Ile	Asp	Met	Leu	Ile	Gly	Pro	Thr	Leu
				85					90					95	
Lys	Asp	Glu	Val	Met	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala
			100					105					110		
Gly	Gln	Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Val	Val	Gly	Asp	Gly	Asn
			115				120					125			
Gly	His	Val	Gly	Leu	Gly	Val	Lys	Cys	Ser	Lys	Glu	Val	Ala	Thr	Ala
	130					135					140				
Ile	Arg	Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Val	Val	Pro	Val	Arg
145				150						155					160
Arg	Gly	Tyr	Trp	Gly	Asn	Lys	Ile	Gly	Lys	Pro	His	Thr	Val	Pro	Cys
				165					170					175	
Lys	Val	Thr	Gly	Lys	Cys	Gly	Ser	Val	Thr	Val	Arg	Met	Val	Pro	Ala
			180					185					190		
Pro	Arg	Gly	Ser	Gly	Ile	Val	Ala	Ala	Arg	Val	Pro	Lys	Lys	Val	Leu
		195					200					205			
Gln	Phe	Ala	Gly	Ile	Asp	Asp	Val	Phe	Thr	Ser	Ser	Arg	Gly	Ser	Thr
	210					215					220				
Lys	Thr	Leu	Gly	Asn	Phe	Val	Lys	Ala	Thr	Phe	Asp	Cys	Leu	Gln	Lys
225				230						235					240
Thr	Tyr	Gly	Phe	Leu	Thr	Pro	Glu	Phe	Trp	Lys	Glu	Thr	Arg	Phe	Ser
				245					250					255	
Arg	Ser	Pro	Tyr	Gln	Glu	His	Thr	Asp	Phe	Leu	Ala	Ser	Lys	Ala	Leu
			260					265					270		
Ser	Thr	Ser	Lys	Pro	Asp	Pro	Val	Val	Glu	Asp	Gln	Ala			
		275					280					285			

(2) INFORMATION FOR SEO ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1567591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Met Leu Ile Gly Pro Thr Leu Lys Asp Glu Val Met Lys Ile Met Pro
1 5 10 15
Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys Ala Phe
20 25 30
Val Val Val Gly Asp Gly Asn Gly His Val Gly Leu Gly Val Lys Cys
35 40 45
Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu Ala Lys
50 55 60
Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys Ile Gly
65 70 75 80
Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Lys Cys Gly Ser Val
85 90 95
Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser Gly Ile Val Ala Ala
100 105 110
Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly Ile Asp Asp Val Phe
115 120 125
Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly Asn Phe Val Lys Ala
130 135 140
Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe Leu Thr Pro Glu Phe
145 150 155 160
Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr Gln Glu His Thr Asp
165 170 175
Phe Leu Ala Ser Lys Ala Leu Ser Thr Ser Lys Pro Asp Pro Val Val
180 185 190
Glu Asp Gln Ala
195

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1567592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

Met Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr
1 5 10 15
Arg Phe Lys Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly
20 25 30
Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala
35 40 45
Ile Ile Leu Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp
50 55 60
Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly
65 70 75 80
Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser
85 90 95
Gly Ile Val Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly
100 105 110
Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly
115 120 125
Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe
130 135 140
Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr
145 150 155 160
Gln Glu His Thr Asp Phe Leu Ala Ser Lys Ala Leu Ser Thr Ser Lys

165 170 175
Pro Asp Pro Val Val Glu Asp Gln Ala
180 185
(2) INFORMATION FOR SEQ ID NO:661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1236
(D) OTHER INFORMATION: / Ceres Seq. ID 1567593
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:
aaacccaaca acataatttc acatatctct ctttctttct cttgaaggaa agacgaagat 60
ctccaagtcc caagttgtta acacaagacg taaacatggg tcatcttggg ttcttagtta 120
tgattatggt aggagtcatt gcttcttctg tgagcgtcta cgggtggcggg tggatcaacg 180
ctcacgccac tttttacggg ggtggtgatg cttccggcac aatgggtggt gcttgtggat 240
atggtaattc atatagccaa ggctacggga cgagcacggc ggctctaagc acagSctctc 300
ttcaacaatg gacttagctg tggttcttgc tttgagataa gatgtgaaaa cgatggtaaa 360
tggtgtttac ctggctcaat cgttgtaacc gctacaaact tctgcccggc aaataacgcg 420
ttagcgaaca ataatggcgg ttggtgtaat cctcctcttg aacactttga ccttgctcag 480
cctgtttttc aacgcattgc tcagtacaga gctggaatcg tccctgtttc ctacagaagg 540
gttccttgca ggagaagagg aggaataaga ttcacgataa acggccactc atacttcaac 600
cttgtgtctga tcacaaacgt cgggtggtgcc ggagacgttc actcggcggc gatcaagggg 660
tcaagaacag tgtggcaagc tatgtcaagg aactgggggc aaaattggca aagcaactct 720
tacctcaacg gtcaagcact ttcttttaag gtcaccacca gcgacggccg cacagtgtgc 780
tccttcaacg ccgctcctgc cggctggtct tatggccaga cttttgccgg tggacagttc 840
cgttaaaaag ggcaagttgg ttaatctctc ttccatttat ctaaagtaaa ctcatttgtg 900
tggttatatt gsyctcttga aaaaactcgg ttattgagag agtgatgcgt cgagggctcg 960
gttttgcaag aggccttgat gacgtctaatt ctttttttgg acctctttat ttttctttct 1020
tgaaactagt ttttgtaag aaagaaaaaa caagttatag tagttaatgt attactgatg 1080
cagaggtgga gttttaacta ccaccgcgta gtagtagtta tgagtttttt attttaagg 1140
gtgagagaga gatggattat caagatttgt caattttatt atgtttgttt gtaataatac 1200
aattctttac tccagttaat gaaaattggg ggattg

(2) INFORMATION FOR SEQ ID NO:662:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1567594
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:
Thr Gln Gln His Asn Phe Thr Tyr Leu Ser Phe Phe Leu Leu Lys Glu
1 5 10 15
Arg Arg Arg Ser Pro Ser Pro Lys Leu Leu Thr Gln Asp Val Asn Met
20 25 30
Gly His Leu Gly Phe Leu Val Met Ile Met Val Gly Val Met Ala Ser
35 40 45
Ser Val Ser Val Tyr Gly Gly Gly Trp Ile Asn Ala His Ala Thr Phe
50 55 60
Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala Cys Gly Tyr
65 70 75 80
Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Ser Thr Ala Ala Leu Ser
85 90 95
Thr Xaa Ser Leu Gln Gln Trp Thr

100

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met Gly His Leu Gly Phe Leu Val Met Ile Met Val Gly Val Met Ala
1 5 10 15
Ser Ser Val Ser Val Tyr Gly Gly Gly Trp Ile Asn Ala His Ala Thr
20 25 30
Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala Cys Gly
35 40 45
Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Ser Thr Ala Ala Leu
50 55 60
Ser Thr Xaa Ser Leu Gln Gln Trp Thr
65 70

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

Met Ile Met Val Gly Val Met Ala Ser Ser Val Ser Val Tyr Gly Gly
1 5 10 15
Gly Trp Ile Asn Ala His Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser
20 25 30
Gly Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly
35 40 45
Tyr Gly Thr Ser Thr Ala Ala Leu Ser Thr Xaa Ser Leu Gln Gln Trp
50 55 60
Thr
65

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..606
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

cagttcccag gaaacatggt ggaaggaagt ttctttgaag acttgaacat cccaaacaga 60
gcaaacaaca acaacagcag caacaatcaa acgttttttc aagggaacaa caacaacaac 120
aatgtgttta agttcgacac tgcagatcac aacaactttg aagctgcaca taacaacaac 180
aataacagta gcggcaacag gttccagctt gtgtttgatt ccacaccggt cgacatggcg 240

tcatttcgatt acagagatga tatgtcgaat ccaggagtag taggaacgat ggatggaatg 300
cagcagaagc agcaagatgt atccatatgg ttctaaagtc ttggtagtag atttcacatctt 360
ctcttatttt tatcttttgt gttctttacat tcaactcaacc atgtaatatatt ttttcctggg 420
tctctctgtc tctatcgctt gttatgatgt gtctgtaaga gtctctaaaa actctctgtt 480
actgtgtgtc tttgtctcgg cttggtgaat ctctctgtca tcatcagctt ttagttacac 540
acccgacttg gggatgaacg aacactaaat gtaagttttc ataataataa tatatttgca 600
Agctcc

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1567606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe Phe Glu Asp Leu Asn
1 5 10 15
Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser Asn Asn Gln Thr Phe
20 25 30
Phe Gln Gly Asn Asn Asn Asn Asn Val Phe Lys Phe Asp Thr Ala
35 40 45
Asp His Asn Asn Phe Glu Ala Ala His Asn Asn Asn Asn Ser Ser
50 55 60
Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr Pro Phe Asp Met Ala
65 70 75 80
Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro Gly Val Val Gly Thr
85 90 95
Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val Ser Ile Trp Phe
100 105 110

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1567607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

Met Val Glu Gly Ser Phe Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala
1 5 10 15
Asn Asn Asn Asn Ser Ser Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn
20 25 30
Asn Asn Asn Asn Val Phe Lys Phe Asp Thr Ala Asp His Asn Asn Phe
35 40 45
Glu Ala Ala His Asn Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln
50 55 60
Leu Val Phe Asp Ser Thr Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg
65 70 75 80
Asp Asp Met Ser Met Pro Gly Val Val Gly Thr Met Asp Gly Met Gln
85 90 95
Gln Lys Gln Gln Asp Val Ser Ile Trp Phe
100 105

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1448
(D) OTHER INFORMATION: / Ceres Seq. ID 1567608
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

aaaaagatgg tgcacttcag atgcttgcca caaatattga gtatgatgag cataaaggac 60
gcattgctat tggacgacta cacgcagggg tactgcgcaa aggaatggat gtcaggggtg 120
gcacttctga agattcctgt agatttgcaa gagttagtga gctttttgta tatgagaaat 180
tctacagagt acctactgat tcagtggag ctggagatat ttgcgctgta tgtggcatag 240
acaacattca gattggggag actattgctg ataaagtaca tgggaagcct ctacctacaa 300
tcaaagtaga agagccaact gtgaaaatgt ccttctctgt aaacacctct ccattttctg 360
gtcgtgaggg gaagtatgta acaagcagga acttaacgaga tcgtttaaac cgtgaacttg 420
aaagaaatct agctatgaaa gtggaagatg gtgagacagc agacacattc attgttagtg 480
ccgtggtaca ttacacatta ccatcctgat agaaaacatg cgaagagaag gatatgaatt 540
tatggttggc ccccgaaaag ttatcaacaa aagggttaac gataaattgc tggagccata 600
tgagatagca actggttgaag taccagaggc tcacatgggg cctggtgttg aacttcttgg 660
caaaaggcgt ggacagatgt ttgatatgca ggggtgttggg tcggaaggaa caacctttct 720
gcggtacaaa atcccaacac gtggacttct tggattgagg aacgcaattt taacagcttc 780
tcgcgggaca gctatcctta acactgtatt tgacagttTa tggaccttgg gccggtgata 840
ttagcacccg cgatctaggt tcgctgggtg cctttgaaga tggaaacatca acatcatatg 900
ccctggcgag tgcgcaggag agagggcaaa tgtttgtagg ttctggagtg gatgtataca 960
aaggtcagat agttgggagc caccGagaga cccggcgact tgggtcttaa tatctgcaag 1020
aagaaggcag cgacaaacat aagatccaac aaagatgtaa cagtgattct tgacactccc 1080
ttaacatata gtctggacga ctgcattgaa tacattgaag aggatgagtt ggtggaggtt 1140
acaccttcta gtattaggat gtgcaagaat cagaaaatgg caaagaaagg caggcagtaa 1200
aaccattttt tgcaagctgg gtttggagga aattgaagaa aagcttctac taaaaaaaat 1260
gaaagctagt ttctagtgtt atttataggc ttgtttgatt gttatacata gtcttattct 1320
tatagcaaag ggtgagtcct gatgttatcc aattaatgtt tttttggaat atctccatgc 1380
cctttgatca tctgatactt aaagctgtac aacttctgaa gttgtgcact agcagatatt 1440
aaagtgtg

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..168
(D) OTHER INFORMATION: / Ceres Seq. ID 1567609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

Lys Asp Gly Ala Leu Gln Met Leu Ala Thr Asn Ile Glu Tyr Asp Glu
1 5 10 15
His Lys Gly Arg Ile Ala Ile Gly Arg Leu His Ala Gly Val Leu Arg
20 25 30
Lys Gly Met Asp Val Arg Val Cys Thr Ser Glu Asp Ser Cys Arg Phe
35 40 45
Ala Arg Val Ser Glu Leu Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro
50 55 60
Thr Asp Ser Val Glu Ala Gly Asp Ile Cys Ala Val Cys Gly Ile Asp
65 70 75 80
Asn Ile Gln Ile Gly Glu Thr Ile Ala Asp Lys Val His Gly Lys Pro
85 90 95
Leu Pro Thr Ile Lys Val Glu Glu Pro Thr Val Lys Met Ser Phe Ser
100 105 110

Val Asn Thr Ser Pro Phe Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser
115 120 125
Arg Asn Leu Arg Asp Arg Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala
130 135 140
Met Lys Val Glu Asp Gly Glu Thr Ala Asp Thr Phe Ile Val Ser Ala
145 150 155 160
Val Val His Tyr Thr Leu Pro Ser
165

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1567610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met Leu Ala Thr Asn Ile Glu Tyr Asp Ser His Lys Gly Arg Ile Ala
1 5 10 15
Ile Gly Arg Leu His Ala Gly Val Leu Arg Lys Gly Met Asp Val Arg
20 25 30
Val Cys Thr Ser Glu Asp Ser Cys Arg Phe Ala Arg Val Ser Glu Leu
35 40 45
Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro Thr Asp Ser Val Glu Ala
50 55 60
Gly Asp Ile Cys Ala Val Cys Gly Ile Asp Asn Ile Gln Ile Gly Glu
65 70 75 80
Thr Ile Ala Asp Lys Val His Gly Lys Pro Leu Pro Thr Ile Lys Val
85 90 95
Glu Glu Pro Thr Val Lys Met Ser Phe Ser Val Asn Thr Ser Pro Phe
100 105 110
Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser Arg Asn Leu Arg Asp Arg
115 120 125
Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala Met Lys Val Glu Asp Gly
130 135 140
Glu Thr Ala Asp Thr Phe Ile Val Ser Ala Val Val His Tyr Thr Leu
145 150 155 160
Pro Ser

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1567611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

Met Asp Val Arg Val Cys Thr Ser Glu Asp Ser Cys Arg Phe Ala Arg
1 5 10 15
Val Ser Glu Leu Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro Thr Asp
20 25 30
Ser Val Glu Ala Gly Asp Ile Cys Ala Val Cys Gly Ile Asp Asn Ile
35 40 45
Gln Ile Gly Glu Thr Ile Ala Asp Lys Val His Gly Lys Pro Leu Pro

50 55 60
Thr Ile Lys Val Glu Glu Pro Thr Val Lys Met Ser Phe Ser Val Asn
65 70 75 80
Thr Ser Pro Phe Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser Arg Asn
85 90 95
Leu Arg Asp Arg Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala Met Lys
100 105 110
Val Glu Asp Gly Glu Thr Ala Asp Thr Phe Ile Val Ser Ala Val Val
115 120 125
His Tyr Thr Leu Pro Ser
130

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

gaaaatggat caagcaaagg gaaaagtctg tgttactggt gcttcaggct tcttggcttc 60
ttggcttgta aagaggcttc tacttgaagg atatgaagtt atcggaacag tcagagatcc 120
aggaaatgag aagaaacttg cgcacctatg gaagttggaa ggggcaaagg agagactacg 180
gttggtgaag gctgatttaa tggaagaagg aagttttgat aacgccataa tgggatgccca 240
aggagtgttc catactgctt ctccggtgct taaacctacc tctaattccag aggaggagat 300
tctgagacca gctatagaag gaacctgaa tgtactgcga tcatgcagga agaataccttc 360
cctgaagcgc gtgggttctca cctcatcctc ttcaacagtc aggatcagag atgattttga 420
tccaaaatc cctcttgaag aatcaatttg gacgtctgtg gaactctgca agcgcttcca 480
ggtctggtat gccttatcaa agacattagc ggaacaagct gcatggaaat tctctgaaga 540
aaatggtatt gacctogtca ctgttctacc atccttcctc gttggacca gtctgcctcc 600
tgattttatgt tctacagctt ccgatgtcct cggattactg aaaggagaaa cagagaagtt 660
ccaatggcat ggacaaatgg ggtatgttca tatcgatgac Gttgcacgaa cccacatagt 720
cgttttcgaa cacgaagcag ctcaaggcag atacatttgt agctctaacg ttatcagtct 780
agaggaactc gtttcattcc tatctgctcg ttacctatca ctccctatcc ccaagagggtt 840
tgagaaacta aatagggttc attacgactt tgacacctcg aagatacaga gtctcgggct 900
caagttcaag tcccttgaag agatgttcga tgactgcatt gcctcattag tcgagcaagg 960
ctatttatct actgttcttc cataactctt ggactagaga atatgtgcaa ataagattgg 1020
tctgaaatag tagtcatgtg gattcacaat gaaagaatgg gattggaaaa catgaaatca 1080
aagattacaa acgatataat ctttacttgt ttatgaacca aatcataaca tattttctct 1140
ccc

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..327
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

Lys Met Asp Gln Ala Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly
1 5 10 15
Phe Leu Ala Ser Trp Leu Val Lys Arg Leu Leu Leu Glu Gly Tyr Glu
20 25 30
Val Ile Gly Thr Val Arg Asp Pro Gly Asn Glu Lys Lys Leu Ala His
35 40 45

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Leu Trp Lys Leu Glu Gly Ala Lys Glu Arg Leu Arg Leu Val Lys Ala
 50          55          60
Asp Leu Met Glu Glu Gly Ser Phe Asp Asn Ala Ile Met Gly Cys Gln
 65          70          75          80
Gly Val Phe His Thr Ala Ser Pro Val Leu Lys Pro Thr Ser Asn Pro
          85          90          95
Glu Glu Glu Ile Leu Arg Pro Ala Ile Glu Gly Thr Leu Asn Val Leu
          100          105          110
Arg Ser Cys Arg Lys Asn Pro Ser Leu Lys Arg Val Val Leu Thr Ser
          115          120          125
Ser Ser Ser Thr Val Arg Ile Arg Asp Asp Phe Asp Pro Lys Ile Pro
          130          135          140
Leu Asp Glu Ser Ile Trp Thr Ser Val Glu Leu Cys Lys Arg Phe Gln
          145          150          155          160
Val Trp Trp Tyr Ala Leu Ser Lys Thr Leu Ala Glu Gln Ala Ala Trp Lys
          165          170          175
Phe Ser Glu Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro Ser Phe
          180          185          190
Leu Val Gly Pro Ser Leu Pro Pro Asp Leu Cys Ser Thr Ala Ser Asp
          195          200          205
Val Leu Gly Leu Leu Lys Gly Glu Thr Glu Lys Phe Gln Trp His Gly
          210          215          220
Gln Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Thr His Ile Val
          225          230          235          240
Val Phe Glu His Glu Ala Ala Gln Gly Arg Tyr Ile Cys Ser Ser Asn
          245          250          255
Val Ile Ser Leu Glu Glu Leu Val Ser Phe Leu Ser Ala Arg Tyr Pro
          260          265          270
Ser Leu Pro Ile Pro Lys Arg Phe Glu Lys Leu Asn Arg Leu His Tyr
          275          280          285
Asp Phe Asp Thr Ser Lys Ile Gln Ser Leu Gly Leu Lys Phe Lys Ser
          290          295          300
Leu Glu Glu Met Phe Asp Asp Cys Ile Ala Ser Leu Val Glu Gln Gly
          305          310          315          320
Tyr Leu Ser Thr Val Leu Pro
          325

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(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1567624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```

Met Asp Gln Ala Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe
 1          5          10          15
Leu Ala Ser Trp Leu Val Lys Arg Leu Leu Leu Glu Gly Tyr Glu Val
          20          25          30
Ile Gly Thr Val Arg Asp Pro Gly Asn Glu Lys Lys Leu Ala His Leu
          35          40          45
Trp Lys Leu Glu Gly Ala Lys Glu Arg Leu Arg Leu Val Lys Ala Asp
          50          55          60
Leu Met Glu Glu Gly Ser Phe Asp Asn Ala Ile Met Gly Cys Gln Gly
          65          70          75          80
Val Phe His Thr Ala Ser Pro Val Leu Lys Pro Thr Ser Asn Pro Glu
          85          90          95
Glu Glu Ile Leu Arg Pro Ala Ile Glu Gly Thr Leu Asn Val Leu Arg

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SEQUENCE 1014990

Met 1	Glu	Glu	Gly	Ser 5	Phe	Asp	Asn	Ala	Ile 10	Met	Gly	Cys	Gln	Gly 15	Val
Phe	His	Thr	Ala 20	Ser	Pro	Val	Leu	Lys 25	Pro	Thr	Ser	Asn	Pro 30	Glu	Glu
Glu	Ile	Leu	Arg 35	Pro	Ala	Ile	Glu 40	Gly	Thr	Leu	Asn	Val 45	Leu	Arg	Ser
Cys	Arg 50	Lys	Asn	Pro	Ser	Leu 55	Lys	Arg	Val	Val	Leu 60	Thr	Ser	Ser	Ser
Ser 65	Thr	Val	Arg	Ile 70	Arg	Asp	Asp	Phe	Asp 75	Pro	Lys	Ile	Pro	Leu 80	Asp
Glu	Ser	Ile	Trp 85	Thr	Ser	Val	Glu	Leu	Cys 90	Lys	Arg	Phe	Gln 95	Val	Trp
Tyr	Ala	Leu	Ser 100	Lys	Thr	Leu	Ala	Glu 105	Gln	Ala	Ala	Trp	Lys 110	Phe	Ser
Glu	Glu	Asn	Gly 115	Ile	Asp	Leu	Val 120	Thr	Val	Leu	Pro	Ser 125	Phe	Leu	Val
Gly	Pro 130	Ser	Leu	Pro	Pro	Asp 135	Leu	Cys	Ser	Thr	Ala 140	Ser	Asp	Val	Leu
Gly 145	Leu	Leu	Lys	Gly 150	Glu	Thr	Glu	Lys	Phe	Gln 155	Trp	His	Gly	Gln 160	Met

Gly Tyr Val His Ile Asp Asp Val Ala Arg Thr His Ile Val Val Phe
 165 170 175
Glu His Glu Ala Ala Gln Gly Arg Tyr Ile Cys Ser Ser Asn Val Ile
 180 185 190
Ser Leu Glu Glu Leu Val Ser Phe Leu Ser Ala Arg Tyr Pro Ser Leu
 195 200 205
Pro Ile Pro Lys Arg Phe Glu Lys Leu Asn Arg Leu His Tyr Asp Phe
 210 215 220
Asp Thr Ser Lys Ile Gln Ser Leu Gly Leu Lys Phe Lys Ser Leu Glu
225 230 235 240
Glu Met Phe Asp Asp Cys Ile Ala Ser Leu Val Glu Gln Gly Tyr Leu
 245 250 255
Ser Thr Val Leu Pro
 260

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

aaagtaggac	gacgtgcgtc	tgcttcgtct	cattacaaag	cagaagaaac	acaaacagag	60
tcagagatct	taagagttaa	agactaatcc	caacaatggc	gtctctcaaa	gtcccaagca	120
atgttcctct	tcccgaagat	gacgccgagc	aactccacaa	ggctttttca	ggatggggta	180
ccaacgagaa	gctgatacata	tcaatactag	ctcacaggaa	cgcagcacaa	cgagcttga	240
tccgcagcgt	ttatgcagct	acctacaatg	aggatcttct	caaagcatta	gacaaagagc	300
tttctagcga	ctttgagaga	gctgtgatgt	tgtggactct	tgatccacca	gagagagatg	360
cttatttggc	taaagaatcc	accaagatgt	tcaccaagaa	caattggggt	cttgttgaaa	420
tcgcttgac	aaggcctgct	cttgagctta	tcaaggtcaa	gcaagcttac	caagctcgat	480
acaagaaatc	aatcgaggaa	gatgtcgcgc	aacacacatc	tggtgacctt	cgtaagctct	540
tgcttcctct	tgtgagcaat	ttcaggtatg	aaggagatga	tgtgaacatg	atgcttgcaa	600
gatctgaagc	taagataact	cacgagaagg	tctcagagaa	atcctacagt	gacgatgact	660
tcatacagaat	cttgacaaca	agaagcaaag	cacagctcgg	tgcaacactc	aaccactaca	720
acaacgagta	tggaaacgcc	attaacaaga	acttgaagga	agagtcggac	gacaatgact	780
acatgaaact	actaagagct	gtaatcacat	gtttgacata	ccctgagaag	cattttgaga	840
aggttccttcg	tctatcaatc	aacaaaatgg	gaacagacga	atggggacta	acccgagtcg	900
tgactacaag	aactgaagtt	gacatggaac	gcatcaaaga	ggaatatcag	cgaagaaaca	960
gcattccttt	ggaccgtGct	atcgccaaag	acacttctgg	tgactatgag	gacatgcttg	1020
ttgctcttct	cggacatggc	gatgcttgaa	actgtttcaa	ctttcgagtt	cctcctttct	1080
cttactgcat	ggtttgtttt	aaataaaaaga	gttggtgaaac	tggttctgca	actattttatc	1140
aatgatcggt	tgagtttgtc					

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Met Ala Ser Leu Lys Val Pro Ser Asn Val Pro Leu Pro Glu Asp Asp
1 5 10 15
Ala Glu Gln Leu His Lys Ala Phe Ser Gly Trp Gly Thr Asn Glu Lys

20	25	30
Leu Ile Ile Ser Ile Leu Ala His Arg Asn Ala Ala Gln Arg Ser Leu		
35	40	45
Ile Arg Ser Val Tyr Ala Ala Thr Tyr Asn Glu Asp Leu Leu Lys Ala		
50	55	60
Leu Asp Lys Glu Leu Ser Ser Asp Phe Glu Arg Ala Val Met Leu Trp		
65	70	75
Thr Leu Asp Pro Pro Glu Arg Asp Ala Tyr Leu Ala Lys Glu Ser Thr		
85	90	95
Lys Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile Ala Cys Thr		
100	105	110
Arg Pro Ala Leu Glu Leu Ile Lys Val Lys Gln Ala Tyr Gln Ala Arg		
115	120	125
Tyr Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr Ser Gly Asp		
130	135	140
Leu Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg Tyr Glu Gly		
145	150	155
Asp Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys Ile Leu His		
165	170	175
Glu Lys Val Ser Glu Lys Ser Tyr Ser Asp Asp Asp Phe Ile Arg Ile		
180	185	190
Leu Thr Thr Arg Ser Lys Ala Gln Leu Gly Ala Thr Leu Asn His Tyr		
195	200	205
Asn Asn Glu Tyr Gly Asn Ala Ile Asn Lys Asn Leu Lys Glu Glu Ser		
210	215	220
Asp Asp Asn Asp Tyr Met Lys Leu Leu Arg Ala Val Ile Thr Cys Leu		
225	230	235
Thr Tyr Pro Glu Lys His Phe Glu Lys Val Leu Arg Leu Ser Ile Asn		
245	250	255
Lys Met Gly Thr Asp Glu Trp Gly Leu Thr Arg Val Val Thr Thr Arg		
260	265	270
Thr Glu Val Asp Met Glu Arg Ile Lys Glu Glu Tyr Gln Arg Arg Asn		
275	280	285
Ser Ile Pro Leu Asp Arg Ala Ile Ala Lys Asp Thr Ser Gly Asp Tyr		
290	295	300
Glu Asp Met Leu Val Ala Leu Leu Gly His Gly Asp Ala		
305	310	315

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1567631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Leu Trp Thr Leu Asp Pro Pro Glu Arg Asp Ala Tyr Leu Ala Lys	
1	15
Glu Ser Thr Lys Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile	
20	30
Ala Cys Thr Arg Pro Ala Leu Glu Ile Lys Val Lys Gln Ala Tyr	
35	45
Gln Ala Arg Tyr Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr	
50	60
Ser Gly Asp Leu Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg	
65	80
Tyr Glu Gly Asp Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys	
85	95

Ile	Leu	His	Glu	Lys	Val	Ser	Glu	Lys	Ser	Tyr	Ser	Asp	Asp	Asp	Phe
			100					105					110		
Ile	Arg	Ile	Leu	Thr	Thr	Arg	Ser	Lys	Ala	Gln	Leu	Gly	Ala	Thr	Leu
		115					120					125			
Asn	His	Tyr	Asn	Asn	Glu	Tyr	Gly	Asn	Ala	Ile	Asn	Lys	Asn	Leu	Lys
	130					135					140				
Glu	Glu	Ser	Asp	Asp	Asn	Asp	Tyr	Met	Lys	Leu	Leu	Arg	Ala	Val	Ile
145					150					155					160
Thr	Cys	Leu	Thr	Tyr	Pro	Glu	Lys	His	Phe	Glu	Lys	Val	Leu	Arg	Leu
			165						170					175	
Ser	Ile	Asn	Lys	Met	Gly	Thr	Asp	Glu	Trp	Gly	Leu	Thr	Arg	Val	Val
		180						185					190		
Thr	Thr	Arg	Thr	Glu	Val	Asp	Met	Glu	Arg	Ile	Lys	Glu	Glu	Tyr	Gln
	195						200					205			
Arg	Arg	Asn	Ser	Ile	Pro	Leu	Asp	Arg	Ala	Ile	Ala	Lys	Asp	Thr	Ser
	210					215					220				
Gly	Asp	Tyr	Glu	Asp	Met	Leu	Val	Ala	Leu	Leu	Gly	His	Gly	Asp	Ala
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1567632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

Met	Phe	Thr	Lys	Asn	Asn	Trp	Val	Leu	Val	Glu	Ile	Ala	Cys	Thr	Arg
1				5					10					15	
Pro	Ala	Leu	Glu	Leu	Ile	Lys	Val	Lys	Gln	Ala	Tyr	Gln	Ala	Arg	Tyr
		20						25					30		
Lys	Lys	Ser	Ile	Glu	Glu	Asp	Val	Ala	Gln	His	Thr	Ser	Gly	Asp	Leu
		35				40						45			
Arg	Lys	Leu	Leu	Leu	Pro	Leu	Val	Ser	Thr	Phe	Arg	Tyr	Glu	Gly	Asp
		50				55				60					
Asp	Val	Asn	Met	Met	Leu	Ala	Arg	Ser	Glu	Ala	Lys	Ile	Leu	His	Glu
65					70					75				80	
Lys	Val	Ser	Glu	Lys	Ser	Tyr	Ser	Asp	Asp	Asp	Phe	Ile	Arg	Ile	Leu
			85						90					95	
Thr	Thr	Arg	Ser	Lys	Ala	Gln	Leu	Gly	Ala	Thr	Leu	Asn	His	Tyr	Asn
		100						105					110		
Asn	Glu	Tyr	Gly	Asn	Ala	Ile	Asn	Lys	Asn	Leu	Lys	Glu	Glu	Ser	Asp
		115					120					125			
Asp	Asn	Asp	Tyr	Met	Lys	Leu	Leu	Arg	Ala	Val	Ile	Thr	Cys	Leu	Thr
	130					135					140				
Tyr	Pro	Glu	Lys	His	Phe	Glu	Lys	Val	Leu	Arg	Leu	Ser	Ile	Asn	Lys
145					150					155					160
Met	Gly	Thr	Asp	Glu	Trp	Gly	Leu	Thr	Arg	Val	Val	Thr	Thr	Arg	Thr
			165						170					175	
Glu	Val	Asp	Met	Glu	Arg	Ile	Lys	Glu	Glu	Tyr	Gln	Arg	Arg	Asn	Ser
		180						185					190		
Ile	Pro	Leu	Asp	Arg	Ala	Ile	Ala	Lys	Asp	Thr	Ser	Gly	Asp	Tyr	Glu
	195						200					205			
Asp	Met	Leu	Val	Ala	Leu	Leu	Gly	His	Gly	Asp	Ala				
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 628 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..628
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

ttgtcctctt	ctcaaacata	tctcaactta	ttgtttgaat	ataaaaagag	atatcaaaaa	60
gaagagaaga	ccaaaaacaa	aacaaaaatc	tctaataaaa	atggcttcca	aagctatctt	120
cttctctttc	tttgtcgtct	ccgccgtgtg	tttgtcttct	ctggcaggtt	tcgccgccgc	180
tgatgctgac	gacttcgatc	gtttccagat	tcaaggatca	gtttactgtg	acacttgccg	240
tgtccaattc	gttaccgcgc	tcagcaaatt	cctcgaaggc	gcgaaagtga	agttggagtg	300
caggagcaga	acaaacggaa	ccataacatt	gaccaaagaa	gctgttaccg	acaaaacagg	360
aagctacaaa	atggaagtaa	ccggtgacca	cgaggaagaa	gtttgcgagc	ttgttttggg	420
ccaatcacca	gacagtgggt	gcagtgatgt	cagcacagag	gcttacttac	gtaacgccgc	480
taagatcagt	ttaacggcga	atgacggaat	cgtctcccac	gagacacgta	ttgttaaccc	540
tctcggtttc	atggttcaga	ctcMAttggc	tgattgtcct	gctgccttca	aggagcttgg	600
tattgtccct	gacgtaacat	tctaagcg				

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..207
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

Cys	Pro	Leu	Leu	Lys	His	Ile	Ser	Thr	Tyr	Cys	Leu	Asn	Ile	Lys	Arg
1				5					10					15	
Asp	Ile	Lys	Lys	Lys	Arg	Arg	Pro	Lys	Thr	Lys	Gln	Lys	Ser	Leu	Ile
				20				25					30		
Lys	Met	Ala	Ser	Lys	Ala	Ile	Phe	Phe	Ser	Phe	Phe	Val	Val	Ser	Ala
				35			40					45			
Val	Cys	Leu	Ser	Ser	Leu	Ala	Gly	Phe	Ala	Ala	Ala	Asp	Ala	Asp	Asp
				50			55				60				
Phe	Asp	Arg	Phe	Gln	Ile	Gln	Gly	Ser	Val	Tyr	Cys	Asp	Thr	Cys	Arg
65					70				75					80	
Val	Gln	Phe	Val	Thr	Arg	Leu	Ser	Lys	Phe	Leu	Glu	Gly	Ala	Lys	Val
				85					90					95	
Lys	Leu	Glu	Cys	Arg	Ser	Arg	Thr	Asn	Gly	Thr	Ile	Thr	Leu	Thr	Lys
				100				105					110		
Glu	Ala	Val	Thr	Asp	Lys	Thr	Gly	Ser	Tyr	Lys	Met	Glu	Val	Thr	Gly
				115			120					125			
Asp	His	Glu	Glu	Glu	Val	Cys	Glu	Leu	Val	Leu	Val	Gln	Ser	Pro	Asp
				130			135				140				
Ser	Gly	Cys	Ser	Asp	Val	Ser	Thr	Glu	Ala	Tyr	Leu	Arg	Asn	Ala	Ala
145					150					155				160	
Lys	Ile	Ser	Leu	Thr	Ala	Asn	Asp	Gly	Ile	Val	Ser	His	Glu	Thr	Arg
				165				170						175	
Ile	Val	Asn	Pro	Leu	Gly	Phe	Met	Val	Gln	Thr	Xaa	Leu	Ala	Asp	Cys
				180				185					190		
Pro	Ala	Ala	Phe	Lys	Glu	Leu	Gly	Ile	Val	Pro	Asp	Val	Thr	Phe	
				195			200					205			

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

Met Ala Ser Lys Ala Ile Phe Phe Ser Phe Phe Val Val Ser Ala Val
1 5 10 15
Cys Leu Ser Ser Leu Ala Gly Phe Ala Ala Ala Asp Ala Asp Asp Phe
20 25 30
Asp Arg Phe Gln Ile Gln Gly Ser Val Tyr Cys Asp Thr Cys Arg Val
35 40 45
Gln Phe Val Thr Arg Leu Ser Lys Phe Leu Glu Gly Ala Lys Val Lys
50 55 60
Leu Glu Cys Arg Ser Arg Thr Asn Gly Thr Ile Thr Leu Thr Lys Glu
65 70 75 80
Ala Val Thr Asp Lys Thr Gly Ser Tyr Lys Met Glu Val Thr Gly Asp
85 90 95
His Glu Glu Glu Val Cys Glu Leu Val Leu Val Gln Ser Pro Asp Ser
100 105 110
Gly Cys Ser Asp Val Ser Thr Glu Ala Tyr Leu Arg Asn Ala Ala Lys
115 120 125
Ile Ser Leu Thr Ala Asn Asp Gly Ile Val Ser His Glu Thr Arg Ile
130 135 140
Val Asn Pro Leu Gly Phe Met Val Gln Thr Xaa Leu Ala Asp Cys Pro
145 150 155 160
Ala Ala Phe Lys Glu Leu Gly Ile Val Pro Asp Val Thr Phe
165 170

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..569
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

aaaatctcga aaccctaatt attctaagat tctaatttgt gaagtttgtg aggttttagg 60
gatgggttac aatttctaca tgagagtgtg tgaggttgtt gatgatgctt caacggatgc 120
aatcatatcg tggagcgaaa gcaacaacag tttcattatc tggaatgttg gagagtttta 180
cagaaggatt ctgcctaaat atgtagactt gggcacaaac ctctcacggt ttttctccaa 240
ccttcgttct catgggttca aaatagttaa aggaagaact ggagtattgg aatttgga 300
tgaagatttt gtcagagata aactggagct tatgaagaag atggttagcg ataaacgtaa 360
agcaaggaaa gcagctaaat ccaaagcaag gaaagctaga gttcaagtcg agtttctctt 420
ccaacacttg caaatttgat ccattaaatc agtcttcttt tttatgtata tattcatctc 480
caagtagatc aagtctaaga acttttcaat agtatgtatc tctctttata ggaaccctct 540
ttatatgcct agtctttgat Tcttctctc

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..145
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567675
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Lys Ser Arg Asn Pro Asn Tyr Ser Lys Ile Leu Ile Cys Glu Val Cys
1 5 10 15
Glu Val Leu Gly Met Gly Tyr Asn Phe Tyr Met Arg Val Tyr Glu Val
 20 25 30
Val Asp Asp Ala Ser Thr Asp Ala Ile Ile Ser Trp Ser Glu Ser Asn
 35 40 45
Asn Ser Phe Ile Ile Trp Asn Val Gly Glu Phe Tyr Arg Arg Ile Leu
50 55 60
Pro Lys Tyr Val Asp Leu Gly Thr Asn Leu Ser Arg Phe Phe Ser Asn
65 70 75 80
Leu Arg Ser His Gly Phe Lys Ile Val Lys Gly Arg Thr Gly Val Leu
 85 90 95
Glu Phe Gly His Glu Asp Phe Val Arg Asp Lys Leu Glu Leu Met Lys
 100 105 110
Lys Met Val Ser Asp Lys Arg Lys Ala Arg Lys Ala Ala Lys Ser Lys
 115 120 125
Ala Arg Lys Ala Arg Val Gln Val Glu Phe Leu Phe Gln His Leu Gln
130 135 140
Ile
145

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567676
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

Met Gly Tyr Asn Phe Tyr Met Arg Val Tyr Glu Val Val Asp Asp Ala
1 5 10 15
Ser Thr Asp Ala Ile Ile Ser Trp Ser Glu Ser Asn Asn Ser Phe Ile
 20 25 30
Ile Trp Asn Val Gly Glu Phe Tyr Arg Arg Ile Leu Pro Lys Tyr Val
 35 40 45
Asp Leu Gly Thr Asn Leu Ser Arg Phe Phe Ser Asn Leu Arg Ser His
50 55 60
Gly Phe Lys Ile Val Lys Gly Arg Thr Gly Val Leu Glu Phe Gly His
65 70 75 80
Glu Asp Phe Val Arg Asp Lys Leu Glu Leu Met Lys Lys Met Val Ser
 85 90 95
Asp Lys Arg Lys Ala Arg Lys Ala Ala Lys Ser Lys Ala Arg Lys Ala
 100 105 110
Arg Val Gln Val Glu Phe Leu Phe Gln His Leu Gln Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1567677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

Met Arg Val Tyr Glu Val Val Asp Asp Ala Ser Thr Asp Ala Ile Ile
1 5 10 15
Ser Trp Ser Glu Ser Asn Asn Ser Phe Ile Ile Trp Asn Val Gly Glu
20 25 30
Phe Tyr Arg Arg Ile Leu Pro Lys Tyr Val Asp Leu Gly Thr Asn Leu
35 40 45
Ser Arg Phe Phe Ser Asn Leu Arg Ser His Gly Phe Lys Ile Val Lys
50 55 60
Gly Arg Thr Gly Val Leu Glu Phe Gly His Glu Asp Phe Val Arg Asp
65 70 75 80
Lys Leu Glu Leu Met Lys Lys Met Val Ser Asp Lys Arg Lys Ala Arg
85 90 95
Lys Ala Ala Lys Ser Lys Ala Arg Lys Ala Arg Val Gln Val Glu Phe
100 105 110
Leu Phe Gln His Leu Gln Ile
115

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1133

(D) OTHER INFORMATION: / Ceres Seq. ID 1567687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

aacagatcaa ggatgaatta gatgtgtttt ccaaggaagc tgtgctttct gaagccaagc 60
gcatcaaagg tctaagagca gtgtttggag aagtctaccc cgatcccgtc agagtgggtg 120
caattgggag gaaggttgag gatctcttgg ctgatcctga aaacaatgaa tggtcattgc 180
tttcttccga gttttgtgga ggaaccacaca taacaaacac ccgcgaaGcc aaagcatttg 240
ctcttctatc ggagaaggga attgctaag gtattcgtag ggtaactgct gtgactactg 300
aatgtgcttt tgatgcattg aatgcggcgt ccttacttga aagagaagta gaggatgcct 360
ccagagcgga ggggaagtgc ttggaaaaga aagtttctgc tttgaaaagc cgagtagatg 420
cagcaattat cccagcagct aaaaaggcag atattaggac taagattgct tcgcttcaga 480
atgaagtaag aaaagctcag aagaaaatag cggaaacaaa cctgaaaaaa tctgtcaa 540
tagcaacaga ggcagctgag tccgcagcat cagatgggaa gactttctgc ataatccagc 600
tggatgtggg tcttgatgca gcagctgtgc gagaggccgt ttcaaaagtc atggaaaaga 660
agggtatgtc gataatggtg ttcagcacag atgaaagcac aaacaaggcg gttgtgtgtg 720
caggagtgcc agaaaaatca gaccagttaa agccgttaga cgtcactgaa tggttgacaa 780
ctgcattggg tcctctaaaa ggaaggtgcg ggaaagggaa aggtggtctt gcatcaggcg 840
aggaacgga tgcttctcaa gtgcaggcgg ctttgatat ggcttcatca tttgcatcaa 900
tgaagctcaa ctgatttggc cgggagggtta cataatctgt gaggtcagaa taacctctac 960
ttaatttgct ttcattgtac accgttttac acatgtttta agaattctgt aaatttctct 1020
gttcttgatg tggaaattgt ggtatgacac tcttttagtc aaagttacca atggctgtta 1080
taattccttg tgaaatgatc ctttcccgtt tgcgttgaaa tggttatttt ttt

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1567688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

Gln Ile Lys Asp Glu Leu Asp Val Phe Ser Lys Glu Ala Val Leu Ser
1 5 10 15
Glu Ala Lys Arg Ile Lys Gly Leu Arg Ala Val Phe Gly Glu Val Tyr
20 25 30
Pro Asp Pro Val Arg Val Val Ser Ile Gly Arg Lys Val Glu Asp Leu
35 40 45
Leu Ala Asp Pro Glu Asn Asn Glu Trp Ser Leu Leu Ser Ser Glu Phe
50 55 60
Cys Gly Gly Thr His Ile Thr Asn Thr Arg Glu Ala Lys Ala Phe Ala
65 70 75 80
Leu Leu Ser Glu Lys Gly Ile Ala Lys Gly Ile Arg Arg Val Thr Ala
85 90 95
Val Thr Thr Glu Cys Ala Phe Asp Ala Leu Asn Ala Ala Ser Leu Leu
100 105 110
Glu Arg Glu Val Glu Asp Ala Ser Arg Ala Glu Gly Ser Ala Leu Glu
115 120 125
Lys Lys Val Ser Ala Leu Lys Ser Arg Val Asp Ala Ala Ile Ile Pro
130 135 140
Ala Ala Lys Lys Ala Asp Ile Arg Thr Lys Ile Ala Ser Leu Gln Asn
145 150 155 160
Glu Val Arg Lys Ala Gln Lys Lys Ile Ala Glu Gln Asn Leu Lys Lys
165 170 175
Ser Val Lys Leu Ala Thr Glu Ala Ala Glu Ser Ala Ala Ser Asp Gly
180 185 190
Lys Thr Phe Cys Ile Ile Gln Leu Asp Val Gly Leu Asp Ala Ala Ala
195 200 205
Val Arg Glu Ala Val Ser Lys Val Met Glu Lys Lys Gly Met Ser Ile
210 215 220
Met Val Phe Ser Thr Asp Glu Ser Thr Asn Lys Ala Val Val Cys Ala
225 230 235 240
Gly Val Pro Glu Lys Ser Asp Gln Phe Lys Pro Leu Asp Val Thr Glu
245 250 255
Trp Leu Thr Thr Ala Leu Gly Pro Leu Lys Gly Arg Cys Gly Lys Gly
260 265 270
Lys Gly Gly Leu Ala Ser Gly Gln Gly Thr Asp Ala Ser Gln Val Gln
275 280 285
Ala Ala Leu Asp Met Ala Ser Ser Phe Ala Ser Met Lys Leu Asn
290 295 300

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1326

(D) OTHER INFORMATION: / Ceres Seq. ID 1567700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

aaaaagcact	ctgtgtgctt	ctgcaaatta	acaatttctt	cagaacaatt	acatttcgat	60
tcgattcgat	tctcttatct	tcttgatctc	tgtttggtca	tctgtggtgg	atctccagat	120
gttggttttg	agaattttgt	cgcgagtaac	ccgcaacgcg	ggcatacgct	catctctatc	180
cgccgtcact	cttccggcga	ggaatcagac	tcctgttttc	tcgagccggt	ttcactccct	240
agctcacgat	ttctcgcata	agcttggttc	agctcagatg	tctatgatgg	attcgtttgc	300
actgcaaagg	ttcaattttt	cttctcttac	ctcgcttgaa	tcagatgaga	agaagacca	360
cactgaggcc	tcaaagacaa	gtgaagagaa	acctacagct	gaggcaaacc	aaccaggtct	420
tgactctgaa	tctaaagatt	ctgtgacaga	ttctgcaaaa	agaaagcgga	aaggtgctaa	480

aggagctgca tcttcattctt ctgaatcaga ttctgagagt gatgatgatg aattgtcagc 540
cgatgatttg gtgaagctcg tagctgagaa ggaagagcta ctgtctgaga aggaagaaga 600
gattaagcag ttgaaagaca aagttcttcg cacttatgct gagatggaga atgtcatgga 660
cagaacaaga cgtgatgctg aaaacaccaa aaagtatgcc gtacagaatt ttgcaaagag 720
cctattggat gtggcggata atcttggaag agcttcttcg gttgtcaaag aaagcttctc 780
aaagcttgac acctcagaag attctgctgg agcagctcca ctattaaaga ccctttttaga 840
aggagtggag atgactgaga aacagcttgc tgaggtatctt aagaaatttg gtatggagaa 900
gtatgatcct ataaacgagc catttgatcc aaacagacat aacgcagtgt tccaagtccc 960
tgatgcttct aagccagaag gcacagttgc tcatgtcttg aagtctggat acacgctgta 1020
tgaccgagtt ataagaccag ctgaggttgg tgttaccag ggaggagaga accaagaaga 1080
aaagaaagag tctgatgctt aagaagaagt cagctgggtt tcataaattt tgttacgggt 1140
ctatgtttcc attaacatct tctcgagtct tcgagtcata gtthtctttt gtggtttggt 1200
tTattcatta gatgaacaag atctcccata agttTgctgg acatggcatt tgcaggggaa 1260
atcctgcttb tgtgtctgtt tBtctctatc tccatgctat aattgaacga ggaaaatatc 1320
attttt

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1567701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met Leu Val Leu Arg Ile Leu Ser Arg Val Thr Arg Asn Ala Gly Ile
1 5 10 15
Arg Ser Ser Leu Ser Ala Val Thr Leu Pro Ala Arg Asn Gln Thr Pro
20 25 30
Val Phe Ser Ser Arg Phe His Ser Leu Ala His Asp Phe Ser His Lys
35 40 45
Leu Val Pro Ala Gln Met Ser Met Met Asp Ser Phe Ala Leu Gln Arg
50 55 60
Phe Asn Phe Ser Ser Ser Thr Ser Pro Glu Ser Asp Glu Lys Lys Thr
65 70 75 80
His Thr Glu Ala Ser Lys Thr Ser Glu Glu Lys Pro Thr Ala Glu Ala
85 90 95
Asn Gln Pro Gly Leu Asp Ser Glu Ser Lys Asp Ser Val Thr Asp Ser
100 105 110
Ala Lys Arg Lys Arg Lys Gly Ala Lys Gly Ala Ala Ser Ser Ser Ser
115 120 125
Glu Ser Asp Ser Glu Ser Asp Asp Asp Glu Leu Ser Ala Asp Asp Leu
130 135 140
Val Lys Leu Val Ala Glu Lys Glu Glu Leu Leu Ser Glu Lys Glu Glu
145 150 155 160
Glu Ile Lys Gln Leu Lys Asp Lys Val Leu Arg Thr Tyr Ala Glu Met
165 170 175
Glu Asn Val Met Asp Arg Thr Arg Arg Asp Ala Glu Asn Thr Lys Lys
180 185 190
Tyr Ala Val Gln Asn Phe Ala Lys Ser Leu Leu Asp Val Ala Asp Asn
195 200 205
Leu Gly Arg Ala Ser Ser Val Val Lys Glu Ser Phe Ser Lys Leu Asp
210 215 220
Thr Ser Glu Asp Ser Ala Gly Ala Ala Pro Leu Leu Lys Thr Leu Leu
225 230 235 240
Glu Gly Val Glu Met Thr Glu Lys Gln Leu Ala Glu Val Phe Lys Lys
245 250 255
Phe Gly Met Glu Lys Tyr Asp Pro Ile Asn Glu Pro Phe Asp Pro Asn
260 265 270

Arg His Asn Ala Val Phe Gln Val Pro Asp Ala Ser Lys Pro Glu Gly
275 280 285
Thr Val Ala His Val Leu Lys Ser Gly Tyr Thr Leu Tyr Asp Arg Val
290 295 300
Ile Arg Pro Ala Glu Val Gly Val Thr Gln Gly Gly Glu Asn Gln Glu
305 310 315 320
Glu Lys Lys Glu Ser Asp Ala
325

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1567702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Met Ser Met Met Asp Ser Phe Ala Leu Gln Arg Phe Asn Phe Ser Ser
1 5 10 15
Ser Thr Ser Pro Glu Ser Asp Glu Lys Lys Thr His Thr Glu Ala Ser
20 25 30
Lys Thr Ser Glu Glu Lys Pro Thr Ala Glu Ala Asn Gln Pro Gly Leu
35 40 45
Asp Ser Glu Ser Lys Asp Ser Val Thr Asp Ser Ala Lys Arg Lys Arg
50 55 60
Lys Gly Ala Lys Gly Ala Ala Ser Ser Ser Ser Glu Ser Asp Ser Glu
65 70 75 80
Ser Asp Asp Asp Glu Leu Ser Ala Asp Asp Leu Val Lys Leu Val Ala
85 90 95
Glu Lys Glu Glu Leu Leu Ser Glu Lys Glu Glu Glu Ile Lys Gln Leu
100 105 110
Lys Asp Lys Val Leu Arg Thr Tyr Ala Glu Met Glu Asn Val Met Asp
115 120 125
Arg Thr Arg Arg Asp Ala Glu Asn Thr Lys Lys Tyr Ala Val Gln Asn
130 135 140
Phe Ala Lys Ser Leu Leu Asp Val Ala Asp Asn Leu Gly Arg Ala Ser
145 150 155 160
Ser Val Val Lys Glu Ser Phe Ser Lys Leu Asp Thr Ser Glu Asp Ser
165 170 175
Ala Gly Ala Ala Pro Leu Leu Lys Thr Leu Leu Glu Gly Val Glu Met
180 185 190
Thr Glu Lys Gln Leu Ala Glu Val Phe Lys Lys Phe Gly Met Glu Lys
195 200 205
Tyr Asp Pro Ile Asn Glu Pro Phe Asp Pro Asn Arg His Asn Ala Val
210 215 220
Phe Gln Val Pro Asp Ala Ser Lys Pro Glu Gly Thr Val Ala His Val
225 230 235 240
Leu Lys Ser Gly Tyr Thr Leu Tyr Asp Arg Val Ile Arg Pro Ala Glu
245 250 255
Val Gly Val Thr Gln Gly Gly Glu Asn Gln Glu Glu Lys Lys Glu Ser
260 265 270
Asp Ala

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..272
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567703
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

Met Met Asp Ser Phe Ala Leu Gln Arg Phe Asn Phe Ser Ser Ser Thr
1 5 10 15
Ser Pro Glu Ser Asp Glu Lys Lys Thr His Thr Glu Ala Ser Lys Thr
 20 25 30
Ser Glu Glu Lys Pro Thr Ala Glu Ala Asn Gln Pro Gly Leu Asp Ser
 35 40 45
Glu Ser Lys Asp Ser Val Thr Asp Ser Ala Lys Arg Lys Arg Lys Gly
 50 55 60
Ala Lys Gly Ala Ala Ser Ser Ser Ser Glu Ser Asp Ser Glu Ser Asp
65 70 75 80
Asp Asp Glu Leu Ser Ala Asp Asp Leu Val Lys Leu Val Ala Glu Lys
 85 90 95
Glu Glu Leu Leu Ser Glu Lys Glu Glu Ile Lys Gln Leu Lys Asp
 100 105 110
Lys Val Leu Arg Thr Tyr Ala Glu Met Glu Asn Val Met Asp Arg Thr
 115 120 125
Arg Arg Asp Ala Glu Asn Thr Lys Lys Tyr Ala Val Gln Asn Phe Ala
 130 135 140
Lys Ser Leu Leu Asp Val Ala Asp Asn Leu Gly Arg Ala Ser Ser Val
145 150 155 160
Val Lys Glu Ser Phe Ser Lys Leu Asp Thr Ser Glu Asp Ser Ala Gly
 165 170 175
Ala Ala Pro Leu Leu Lys Thr Leu Leu Glu Gly Val Glu Met Thr Glu
 180 185 190
Lys Gln Leu Ala Glu Val Phe Lys Lys Phe Gly Met Glu Lys Tyr Asp
 195 200 205
Pro Ile Asn Glu Pro Phe Asp Pro Asn Arg His Asn Ala Val Phe Gln
210 215 220
Val Pro Asp Ala Ser Lys Pro Glu Gly Thr Val Ala His Val Leu Lys
225 230 235 240
Ser Gly Tyr Thr Leu Tyr Asp Arg Val Ile Arg Pro Ala Glu Val Gly
 245 250 255
Val Thr Gln Gly Gly Glu Asn Gln Glu Glu Lys Lys Glu Ser Asp Ala
 260 265 270

(2) INFORMATION FOR SEQ ID NO:693:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1418
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

ataggactcg	acaaatagaa	gaagcagatt	cgttgctaac	gaaGtaaagg	atcttacttt	60
tttagtcttt	gcttttagaaa	taacttataa	ctacaagtca	gagaggggcc	gagtaaactcg	120
gaaagatgac	ggcgccgatg	atcctgaccg	gaagtggatc	ggcggcggag	agagacgctc	180
ggatggcgca	cactgctatg	gcgtttgttc	agctctttaa	tggtggatac	catgtgatta	240
ctaaagtagc	tcttaatggt	ggagtcaacc	agcttgtctt	ctgtgtatgc	cgtgatcttc	300
ttgctctctc	tattctcgct	cctcttgctt	acttcgcgca	aagaaagatc	agaactccaa	360

				245				250					255		
Ala	Phe	Phe	Met	Val	Lys	Glu	Pro	Leu	Asp	Trp	Lys	Leu	Thr	Gln	Ser
			260					265					270		
Glu	Val	Leu	Ala	Val	Ile	Tyr	Ala	Gly	Val	Ile	Ala	Ser	Ala	Leu	Asn
			275				280					285			
Tyr	Gly	Leu	Leu	Thr	Trp	Ser	Asn	Lys	Ile	Ile	Gly	Pro	Ala	Leu	Val
			290			295					300				
Ala	Leu	Tyr	Asn	Pro	Leu	Gln	Pro	Ala	Ala	Ser	Ala	Phe	Leu	Ser	Arg
305					310					315					320
Ile	Phe	Leu	Gly	Ser	Pro	Ile	Tyr	Leu	Gly	Ser	Val	Val	Gly	Gly	Phe
				325					330					335	
Phe	Ile	Ile	Leu	Gly	Leu	Tyr	Met	Val	Thr	Trp	Ala	Ser	Phe	Arg	Glu
			340					345					350		
Arg	Lys	Thr	Ala	Val	Ser	Gly	Ile	Gly	Ile	Ala	Pro	His	Gly	Leu	Lys
			355				360					365			
Thr	Ser	Glu	Pro	Leu	Ile	Phe	Asn	Gly	Thr	Val	Asn	Arg	Leu	Gly	Gln
			370			375					380				
Leu	Phe	Ser	Gly	Leu	Pro	Ser	Ser	Ser	Val	Lys	Ser	Ala	Asp		
385					390					395					

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1567706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

Met	Ile	Leu	Thr	Gly	Ser	Gly	Ser	Ala	Ala	Glu	Arg	Asp	Ala	Arg	Met
1				5				10					15		
Ala	His	Thr	Ala	Met	Ala	Phe	Val	Gln	Leu	Phe	Asn	Gly	Gly	Tyr	His
			20					25					30		
Val	Ile	Thr	Lys	Val	Ala	Leu	Asn	Val	Gly	Val	Asn	Gln	Leu	Val	Phe
			35				40					45			
Cys	Val	Cys	Arg	Asp	Leu	Leu	Ala	Leu	Ser	Ile	Leu	Ala	Pro	Leu	Ala
			50			55					60				
Tyr	Phe	Arg	Glu	Arg	Lys	Ile	Arg	Thr	Pro	Met	Asn	Lys	Ser	Leu	Leu
65					70					75				80	
Leu	Ser	Phe	Phe	Phe	Leu	Gly	Leu	Ala	Gly	Val	Phe	Gly	Asn	Gln	Leu
				85					90					95	
Leu	Phe	Leu	Ile	Gly	Leu	Thr	Tyr	Thr	Asn	Pro	Thr	Tyr	Ala	Ala	Ala
			100					105					110		
Ile	Gln	Pro	Ser	Ile	Pro	Val	Phe	Thr	Phe	Leu	Leu	Ala	Val	Met	Met
			115				120					125			
Gly	Thr	Glu	Arg	Val	Asn	Leu	Leu	Arg	Ile	Glu	Gly	Gln	Thr	Lys	Val
			130			135					140				
Gly	Gly	Thr	Leu	Val	Cys	Val	Met	Gly	Ala	Val	Phe	Met	Val	Val	Phe
145					150					155					160
Arg	Gly	Pro	Ala	Leu	Leu	Gly	Asp	Lys	Asp	Ala	Asp	Phe	Ala	Met	Asn
				165					170					175	
Asn	Glu	Ile	Ser	Ala	Lys	Gly	Gln	Pro	Glu	Pro	Thr	Gly	Trp	Leu	Val
			180					185					190		
Ser	Gly	Phe	Leu	Asp	Leu	Gly	Phe	Glu	Gln	Trp	His	Ile	Gly	Val	Leu
			195				200					205			
Cys	Leu	Ile	Gly	Asn	Cys	Met	Cys	Met	Ala	Thr	Phe	Leu	Ala	Ile	Gln
			210			215					220				
Ala	Pro	Leu	Leu	Lys	Lys	Tyr	Pro	Ala	Asn	Leu	Ser	Val	Ala	Ala	Leu
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:696:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1567707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

Met	Ala	His	Thr	Ala	Met	Ala	Phe	Val	Gln	Leu	Phe	Asn	Gly	Gly	Tyr
1				5				10						15	
His	Val	Ile	Thr	Lys	Val	Ala	Leu	Asn	Val	Gly	Val	Asn	Gln	Leu	Val
			20					25					30		
Phe	Cys	Val	Cys	Arg	Asp	Leu	Leu	Ala	Leu	Ser	Ile	Leu	Ala	Pro	Leu
			35				40					45			
Ala	Tyr	Phe	Arg	Glu	Arg	Lys	Ile	Arg	Thr	Pro	Met	Asn	Lys	Ser	Leu
	50					55					60				
Leu	Leu	Ser	Phe	Phe	Phe	Leu	Gly	Leu	Ala	Gly	Val	Phe	Gly	Asn	Gln
65					70					75					80
Leu	Leu	Phe	Leu	Ile	Gly	Leu	Thr	Tyr	Thr	Asn	Pro	Thr	Tyr	Ala	Ala
				85				90						95	
Ala	Ile	Gln	Pro	Ser	Ile	Pro	Val	Phe	Thr	Phe	Leu	Leu	Ala	Val	Met
			100					105					110		
Met	Gly	Thr	Glu	Arg	Val	Asn	Leu	Leu	Arg	Ile	Glu	Gly	Gln	Thr	Lys
			115				120					125			
Val	Gly	Gly	Thr	Leu	Val	Cys	Val	Met	Gly	Ala	Val	Phe	Met	Val	Val
			130			135					140				
Phe	Arg	Gly	Pro	Ala	Leu	Leu	Gly	Asp	Lys	Asp	Ala	Asp	Phe	Ala	Met
145					150					155					160
Asn	Asn	Glu	Ile	Ser	Ala	Lys	Gly	Gln	Pro	Glu	Pro	Thr	Gly	Trp	Leu
				165				170						175	
Val	Ser	Gly	Phe	Leu	Asp	Leu	Gly	Phe	Glu	Gln	Trp	His	Ile	Gly	Val
			180					185					190		
Leu	Cys	Leu	Ile	Gly	Asn	Cys	Met	Cys	Met	Ala	Thr	Phe	Leu	Ala	Ile
			195				200					205			
Gln	Ala	Pro	Leu	Leu	Lys	Lys	Tyr	Pro	Ala	Asn	Leu	Ser	Val	Ala	Ala
			210			215					220				
Leu	Ser	Tyr	Xaa	Phe	Gly	Thr	Val	Leu	Met	Cys	Thr	Thr	Ala	Phe	Phe

(2) INFORMATION FOR SEQ ID NO:697:

(A) LENGTH: 713 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1567711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

atcaagataa	gcttatagtt	atcactaaga	gttttgtcta	cgtacatttt	gtgatcaaac	60
aagtaatcaa	tcaaaagatg	gaaggcaaaa	ctgtgatctc	aagctctgctc	ataataagtc	120
ttgtcttagc	acagattcaa	gtagaagcaa	aaatctgctg	tcctaccaag	gatgatagat	180
ctgtgtattt	tgtatgcatg	ctttccgtgt	catcccaatt	ttattgtcta	ttaaagagta	240
aattgcaaaa	tacatctcag	acgatattgc	ctccgggata	tactaatgac	attctcgaaa	300
attctgtgta	tgtctgtcaat	gaatatgtgca	agctaggggtg	tgcattctct	gtgtgtgggtg	360
ccttgaccac	tctccaaaac	tttgacgcaa	gtaaagtatt	gagtgaagcg	gttgaacaat	420
gcaccaaggc	atgttcttct	gtctgcaccg	gagGatctac	cgccgcagtt	aaaagtgcc	480
aaacaagtat	atttaaaagt	gaagggtggt	catcattcag	agtggcgtga	ctgttttc	540
ggaataattg	tcgtctatcg	atgtattgtt	taaaaaaaa	tgctagacta	tgggtctagt	600
actgtttaat	aagttgtttc	cggtttgcca	atgtgtcatg	agagtttttg	attctagatt	660
gtatatccct	tctacttgct	ttttctctaaa	tataataataa	tgtgtccttc	tgc	

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1567712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Gln	Asp	Lys	Leu	Ile	Val	Ile	Thr	Lys	Ser	Phe	Val	Tyr	Val	His	Phe
1			5						10					15	
Val	Ile	Lys	Gln	Val	Ile	Asn	Gln	Lys	Met	Glu	Gly	Lys	Thr	Val	Ile
		20						25					30		
Ser	Ser	Leu	Leu	Ile	Ile	Ser	Leu	Val	Leu	Ala	Gln	Ile	Gln	Val	Glu
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:699:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(A) NAME

(B) LOCATION: 1..134

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:699:

Glu Gly Lys Thr Val Ile Ser Ser Leu Leu I

(2) INFORMATION FOR SEO ID NO:700:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAM

(B) LOCATION: 1..94

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:700:

Leu Ser Val Ser Ser Gln Phe Tyr Cys Leu L

1				5					10					15		
Lys	Asn	Thr	Ser	Gln	Thr	Ile	Cys	Pro	Pro	Gly	Tyr	Thr	Asn	Asp	Ile	
			20					25						30		
Leu	Glu	Asn	Ser	Gly	Asp	Ala	Val	Asn	Glu	Tyr	Cys	Lys	Leu	Gly	Cys	

35 40 45
Ala Ser Ser Val Cys Gly Ala Leu Thr Thr Leu Gln Asn Phe Asp Ala
50 55 60
Ser Lys Val Leu Ser Glu Ala Val Glu Gln Cys Thr Lys Ala Cys Ser
65 70 75 80
Ser Val Cys Thr Gly Gly Ser Thr Ala Ala Val Lys Ser Ala
85 90

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

atatataaca ataacacttt gggttttaga ctttagatac gaatcaaaaa catttgagat 60
aaaaAtcaga aaagtaaaga gacgaaaatg gcggatcaac aagcaggaac aatcgtcgga 120
ggagttcgcg atattgatgc aaatgctaag gatcttcaag tcgagagtct cgctcgtttc 180
gctgtcgatg agcataacaa gaacgagaac ttgactctgg agtacaagag gctccttggt 240
gcgaaaacac aggttgtggc aggaacaatg caccatctaa ctgtggaggt ggctgatggt 300
gagaccaata aggtctatga ggccaaggtt ttggagaaag cttgggagaa tctcaagcag 360
ttggagagtt tcaaccacct tcacgatgtt taatccgatg ccctgagctt tctctgcggc 420
ttgagtgagg tccttgtgtg ctctcagacc acgtgataag agttctggtt taaccaagtt 480
aacttcttta ataagtgaat tccagtccca tgtgtttgaa ctggtattgt gtgtatctct 540
tgactctcgt ttgtgtattg ctattagcaa actctcactt tttatcc

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Tyr Ile Thr Ile Thr Leu Trp Val Leu Asp Phe Arg Tyr Glu Ser Lys
1 5 10 15
Thr Phe Glu Ile Lys Ile Arg Lys Val Lys Arg Arg Lys Trp Arg Ile
20 25 30
Asn Lys Gln Glu Gln Ser Ser Glu Phe Ala Ile Leu Met Gln Met
35 40 45
Leu Met Ile Phe Lys Ser Arg Val Ser Leu Val Ser Leu Ser Met Ser
50 55 60
Ile Thr Arg Thr Arg Thr
65 70

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1567717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met Ala Asp Gln Gln Ala Gly Thr Ile Val Gly Gly Val Arg Asp Ile
1 5 10 15
Asp Ala Asn Ala Asn Asp Leu Gln Val Glu Ser Leu Ala Arg Phe Ala
20 25 30
Val Asp Glu His Asn Lys Asn Glu Asn Leu Thr Leu Glu Tyr Lys Arg
35 40 45
Leu Leu Gly Ala Lys Thr Gln Val Val Ala Gly Thr Met His His Leu
50 55 60
Thr Val Glu Val Ala Asp Gly Glu Thr Asn Lys Val Tyr Glu Ala Lys
65 70 75 80
Val Leu Glu Lys Ala Trp Glu Asn Leu Lys Gln Leu Glu Ser Phe Asn
85 90 95
His Leu His Asp Val
100

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1567721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

cttcgcgtctt atgtgtctct gcccaaat aaaaactcag aaaccctaga aaattccgat	60
tcatacaactg agagagaaga agaattgaga aatgatgaag cgtctgatcc caacgttcaa	120
ccgcatacttg gtgcagagag tcatccagcc cgctaaaacc gaaagcggca ttctcctacc	180
tgagaaaatcc tccaagctga actcaggcaa ggtgatagct gttggacctg gatcaaggga	240
taaggacggg aaattgattc cggctctctgt gaaggaaggc gacactgttc ttcttccaga	300
gtacgggtggt acacagggtca agctcggcga gaacgagtac catctcttcc gggacgagga	360
tgttttggga actttgcacg aggattgaaa aggctaagct tgccaactta accacgaggg	420
ttcatgttgg tgtttgtgtt atgaggagaa gtcatttata aattagttta tcttgaagat	480
gtggttggac tttgttgcg tttatcattg aatctacctt tatgaacctg tctttgaatt	540
tttacaatat ggcataatc acatggataa ccCaagtgtt gcatctt	

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1567722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

Leu Pro Ser Tyr Val Ser Leu Pro Gln Ile Lys Asn Ser Glu Thr Leu
1 5 10 15
Glu Asn Ser Asp Ser Ser Thr Glu Arg Glu Glu Glu Leu Arg Asn Asp
20 25 30
Glu Ala Ser Asp Pro Asn Val Gln Pro His Leu Gly Ala Glu Ser His
35 40 45
Pro Ala Arg
50

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met Met Lys Arg Leu Ile Pro Thr Phe Asn Arg Ile Leu Val Gln Arg
1 5 10 15
Val Ile Gln Pro Ala Lys Thr Glu Ser Gly Ile Leu Leu Pro Glu Lys
20 25 30
Ser Ser Lys Leu Asn Ser Gly Lys Val Ile Ala Val Gly Pro Gly Ser
35 40 45
Arg Asp Lys Asp Gly Lys Leu Ile Pro Val Ser Val Lys Glu Gly Asp
50 55 60
Thr Val Leu Leu Pro Glu Tyr Gly Gly Thr Gln Val Lys Leu Gly Glu
65 70 75 80
Asn Glu Tyr His Leu Phe Arg Asp Glu Asp Val Leu Gly Thr Leu His
85 90 95
Glu Asp

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567724
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met Lys Arg Leu Ile Pro Thr Phe Asn Arg Ile Leu Val Gln Arg Val
1 5 10 15
Ile Gln Pro Ala Lys Thr Glu Ser Gly Ile Leu Leu Pro Glu Lys Ser
20 25 30
Ser Lys Leu Asn Ser Gly Lys Val Ile Ala Val Gly Pro Gly Ser Arg
35 40 45
Asp Lys Asp Gly Lys Leu Ile Pro Val Ser Val Lys Glu Gly Asp Thr
50 55 60
Val Leu Leu Pro Glu Tyr Gly Gly Thr Gln Val Lys Leu Gly Glu Asn
65 70 75 80
Glu Tyr His Leu Phe Arg Asp Glu Asp Val Leu Gly Thr Leu His Glu
85 90 95
Asp

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1209
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567738
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ataccctcat	tttaattggcg	gagattacaa	gggaaagaga	caactccaat	tcaaagctct	60
gattttttcc	accaatcccc	atttttttccc	ttttacaatt	cttaagctag	ttttatactt	120
ttctttctcc	tttcatttgg	gttaagagaa	gccatggata	cagagtttct	ccgaacccta	180
gatcgtcaga	ttcttttggg	tgtcttcgtt	gcttttcgtc	ccgttggtgc	tggtgctgct	240
tattttctta	catcctccaa	gaaacgcaga	gtgtgtttgg	atccagagaa	tttcaaggag	300
ttcaagcttg	ttaagagaca	tcagcttagt	cacaatgtgg	ccaagtctgt	ttttgaactc	360
ccaacttcta	cttctgtgtt	gggtcttccc	attggacaac	acatcagttg	caggggaaag	420
gatggtcaag	gagaggatgt	tattaagcca	tacaccccga	ctacgttaga	ctctgacgtt	480
ggacgtttcg	aacttgtcat	taagatgtat	ccgcaaggac	ggatgtctca	tcatttcagg	540
gagatgcgtg	ttggagacca	tcttgccgta	aagggaccaa	agggtagggt	caagtatcaa	600
ccaggtcagt	ttagggcatt	tggaatgctt	gctggagggt	caggcatcac	tcccattgtt	660
caagtggcca	gagcaattct	agaaaaccca	acagacaaga	caaaggtgca	tctcatttac	720
gccaacgtca	catacgacga	cattctcttg	aaggaagaat	tggagggtct	tactaccaat	780
taccctgaac	aattttaa	cttctatgtt	ttgaaccagc	ctccggaagt	atgggatggt	840
ggtgttggat	ttgtatcaaa	ggaaatgatt	cagactcatt	gccctgcacc	tgcattctgat	900
attcagatcc	taagatgcgg	accaccgcca	atgaacaagg	ccatggctgc	aaaccttgaa	960
gctctgggat	actctccgga	gatgcaattc	cagttctgat	ctgaatatct	tcttttgggt	1020
gctctgaaac	ggaactcata	ataatttagt	tacaatccca	actacgagag	ttgtgtctta	1080
actgagtgag	agttgtat	ctgttgtgtg	tCttgttagc	ccacttgaaa	gtttccattg	1140
attggtttac	gaattgggta	Ygacattttg	gttcacctat	accgggttgg	tgcaaacact	1200
ttgatgctg						

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1567739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Met	Asp	Thr	Glu	Phe	Leu	Arg	Thr	Leu	Asp	Arg	Gln	Ile	Leu	Leu	Gly
1				5				10					15		
Val	Phe	Val	Ala	Phe	Val	Ala	Val	Gly	Ala	Gly	Ala	Ala	Tyr	Phe	Leu
			20					25					30		
Thr	Ser	Ser	Lys	Lys	Arg	Arg	Val	Cys	Leu	Asp	Pro	Glu	Asn	Phe	Lys
			35				40					45			
Glu	Phe	Lys	Leu	Val	Lys	Arg	His	Gln	Leu	Ser	His	Asn	Val	Ala	Lys
			50			55					60				
Phe	Val	Phe	Glu	Leu	Pro	Thr	Ser	Thr	Ser	Val	Leu	Gly	Leu	Pro	Ile
65					70				75					80	
Gly	Gln	His	Ile	Ser	Cys	Arg	Gly	Lys	Asp	Gly	Gln	Gly	Glu	Asp	Val
			85					90					95		
Ile	Lys	Pro	Tyr	Thr	Pro	Thr	Thr	Leu	Asp	Ser	Asp	Val	Gly	Arg	Phe
			100					105					110		
Glu	Leu	Val	Ile	Lys	Met	Tyr	Pro	Gln	Gly	Arg	Met	Ser	His	His	Phe
			115				120					125			
Arg	Glu	Met	Arg	Val	Gly	Asp	His	Leu	Ala	Val	Lys	Gly	Pro	Lys	Gly
			130			135					140				
Arg	Phe	Lys	Tyr	Gln	Pro	Gly	Gln	Phe	Arg	Ala	Phe	Gly	Met	Leu	Ala
145				150					155					160	
Gly	Gly	Ser	Gly	Ile	Thr	Pro	Met	Phe	Gln	Val	Ala	Arg	Ala	Ile	Leu
			165					170						175	
Glu	Asn	Pro	Thr	Asp	Lys	Thr	Lys	Val	His	Leu	Ile	Tyr	Ala	Asn	Val
			180					185					190		
Thr	Tyr	Asp	Asp	Ile	Leu	Leu	Lys	Glu	Glu	Leu	Glu	Gly	Leu	Thr	Thr
			195				200					205			
Asn	Tyr	Pro	Glu	Gln	Phe	Lys	Ile	Phe	Tyr	Val	Leu	Asn	Gln	Pro	Pro
			210				215					220			

Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln
225 230 235 240
Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly
245 250 255
Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly
260 265 270
Tyr Ser Pro Glu Met Gln Phe Gln Phe
275 280

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1567740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

Met Tyr Pro Gln Gly Arg Met Ser His Phe Arg Glu Met Arg Val
1 5 10 15
Gly Asp His Leu Ala Val Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln
20 25 30
Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala Gly Gly Ser Gly Ile
35 40 45
Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu Glu Asn Pro Thr Asp
50 55 60
Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val Thr Tyr Asp Asp Ile
65 70 75 80
Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr Asn Tyr Pro Glu Gln
85 90 95
Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro Glu Val Trp Asp Gly
100 105 110
Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln Thr His Cys Pro Ala
115 120 125
Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly Pro Pro Pro Met Asn
130 135 140
Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly Tyr Ser Pro Glu Met
145 150 155 160
Gln Phe Gln Phe

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1567741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Met Ser His His Phe Arg Glu Met Arg Val Gly Asp His Leu Ala Val
1 5 10 15
Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala
20 25 30
Phe Gly Met Leu Ala Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val
35 40 45
Ala Arg Ala Ile Leu Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu

50 55 60
Ile Tyr Ala Asn Val Thr Tyr Asp Asp Ile Leu Lys Glu Glu Leu
65 70 75 80
Glu Gly Leu Thr Thr Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val
85 90 95
Leu Asn Gln Pro Pro Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser
100 105 110
Lys Glu Met Ile Gln Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln
115 120 125
Ile Leu Arg Cys Gly Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn
130 135 140
Leu Glu Ala Leu Gly Tyr Ser Pro Glu Met Gln Phe Gln Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

ataaaaaacaa aaacaaaaaat ataattgtgga cttctaaaac cataagcttc actttcttca 60
tcacaacaat acttctcgcg tcttgcaacg catccgcaaa ggccaaaacg caaccgctgt 120
tcccagcgat tctaattcttt ggtgattcaa cagtcgacac aggcaacaat aactaccctt 180
cacaacaat cttcagagct aaacatgttc cttacggtat tgatctccca aaccactcac 240
ctaacggaag attctcaaac ggaaaaattt tctccgacat aatcgcaacc aaactcaaca 300
tcaaacagtt tgttctctcc ttcttacaac caaatctcac cgaccaagaa attgtaaccg 360
gagtcgtgtt tgcattcagca ggtgccgggtt acgatgacca aaccagtctc acgacacaag 420
cgattcgtgt ctcggaacaa ccaaatatgt tcaagagtta cattgctcgt cttaagagta 480
tcgtaggaga caagaaagcc atgaagatca taaacaatgc tttggtggtt gtgagtgcag 540
ggcctaataa tttcatcttg aattattacg aggttcccac atggcgtcgc atgtatccta 600
gcatttctga ttaccaagat tttgtttctta ataagcttaa caatttcgtg atggagcttt 660
acagcctagg ttgccggaaa attttggtcg gaggtttacc gccaatggga tgtttaccga 720
ttcaaattgc tgctcaattc cgcaacgtcc taaggttttg cttggaacaa gagaacagag 780
actctgtttt atacaatcag aaacttcaga agctcttacc tcagacacaa gcatctctta 840
caggaagcaa gatcctttac tctgatgtct atgacctat gatggagatg ctccaaaacc 900
ctagcaaata cgggttttaa gagacgacga gaggatgttg tggaacaggg ttcttgagga 960
cgagcttcat gtgtaattgt tattcttcca tgtgtgagaa tcgctcggag tttctgttct 1020
ttgactcgat tcatccatct gaagctacct acaattacat tggtaattgt ctggatacta 1080
agattcgtgg gtggcttaag gcttaagtta tcaagatttg caaagattga acaaaattat 1140
ctgttYtcat aatgtgacta tttgtggact Tcgtttgtta atcaactatt aactttggct 1200
ctt

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Lys Asn Lys Asn Lys Asn Ile Met Trp Thr Ser Lys Thr Ile Ser Phe
1 5 10 15
Thr Phe Phe Ile Thr Thr Ile Leu Leu Ala Ser Cys Asn Ala Ser Ala

Met	Trp	Thr	Ser	Lys	Thr	Ile	Ser	Phe	Thr	Phe	Phe	Ile	Thr	Thr	Ile
1				5					10					15	
Leu	Leu	Ala	Ser	Cys	Asn	Ala	Ser	Ala	Lys	Ala	Lys	Thr	Gln	Pro	Leu
			20					25					30		
Phe	Pro	Ala	Ile	Leu	Ile	Phe	Gly	Asp	Ser	Thr	Val	Asp	Thr	Gly	Asn
		35					40					45			

Asn	Asn	Tyr	Pro	Ser	Gln	Thr	Ile	Phe	Arg	Ala	Lys	His	Val	Pro	Tyr
50						55					60				
Gly	Ile	Asp	Leu	Pro	Asn	His	Ser	Pro	Asn	Gly	Arg	Phe	Ser	Asn	Gly
65					70				75						80
Lys	Ile	Phe	Ser	Asp	Ile	Ile	Ala	Thr	Lys	Leu	Asn	Ile	Lys	Gln	Phe
				85					90					95	
Val	Pro	Pro	Phe	Leu	Gln	Pro	Asn	Leu	Thr	Asp	Gln	Glu	Ile	Val	Thr
			100					105					110		
Gly	Val	Cys	Phe	Ala	Ser	Ala	Gly	Ala	Gly	Tyr	Asp	Asp	Gln	Thr	Ser
		115					120					125			
Leu	Thr	Thr	Gln	Ala	Ile	Arg	Val	Ser	Glu	Gln	Pro	Asn	Met	Phe	Lys
	130					135					140				
Ser	Tyr	Ile	Ala	Arg	Leu	Lys	Ser	Ile	Val	Gly	Asp	Lys	Lys	Ala	Met
145					150					155					160
Lys	Ile	Ile	Asn	Asn	Ala	Leu	Val	Val	Val	Ser	Ala	Gly	Pro	Asn	Asp
			165						170					175	
Phe	Ile	Leu	Asn	Tyr	Tyr	Glu	Val	Pro	Thr	Trp	Arg	Arg	Met	Tyr	Pro
			180					185					190		
Ser	Ile	Ser	Asp	Tyr	Gln	Asp	Phe	Val	Leu	Asn	Lys	Leu	Asn	Asn	Phe
	195						200					205			
Val	Met	Glu	Leu	Tyr	Ser	Leu	Gly	Cys	Arg	Lys	Ile	Leu	Val	Gly	Gly
	210					215					220				
Leu	Pro	Pro	Met	Gly	Cys	Leu	Pro	Ile	Gln	Met	Thr	Ala	Gln	Phe	Arg
225					230					235					240
Asn	Val	Leu	Arg	Phe	Cys	Leu	Glu	Gln	Glu	Asn	Arg	Asp	Ser	Val	Leu
				245					250					255	
Tyr	Asn	Gln	Lys	Leu	Gln	Lys	Leu	Leu	Pro	Gln	Thr	Gln	Ala	Ser	Leu
			260					265					270		
Thr	Gly	Ser	Lys	Ile	Leu	Tyr	Ser	Asp	Val	Tyr	Asp	Pro	Met	Met	Glu
	275						280					285			
Met	Leu	Gln	Asn	Pro	Ser	Lys	Tyr	Gly	Phe	Lys	Glu	Thr	Thr	Arg	Gly
	290					295					300				
Cys	Cys	Gly	Thr	Gly	Phe	Leu	Glu	Thr	Ser	Phe	Met	Cys	Asn	Ala	Tyr
305					310					315					320
Ser	Ser	Met	Cys	Glu	Asn	Arg	Ser	Glu	Phe	Leu	Phe	Phe	Asp	Ser	Ile
				325					330					335	
His	Pro	Ser	Glu	Ala	Thr	Tyr	Asn	Tyr	Ile	Gly	Asn	Val	Leu	Asp	Thr
			340					345					350		
Lys	Ile	Arg	Gly	Trp	Leu	Lys	Ala								
	355						360								

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1567753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met	Phe	Lys	Ser	Tyr	Ile	Ala	Arg	Leu	Lys	Ser	Ile	Val	Gly	Asp	Lys
1				5					10					15	
Lys	Ala	Met	Lys	Ile	Ile	Asn	Asn	Ala	Leu	Val	Val	Val	Ser	Ala	Gly
			20					25					30		
Pro	Asn	Asp	Phe	Ile	Leu	Asn	Tyr	Tyr	Glu	Val	Pro	Thr	Trp	Arg	Arg
			35				40					45			
Met	Tyr	Pro	Ser	Ile	Ser	Asp	Tyr	Gln	Asp	Phe	Val	Leu	Asn	Lys	Leu
	50					55				60					
Asn	Asn	Phe	Val	Met	Glu	Leu	Tyr	Ser	Leu	Gly	Cys	Arg	Lys	Ile	Leu

65 70 75 80
Val Gly Gly Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala
85 90 95
Gln Phe Arg Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp
100 105 110
Ser Val Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln
115 120 125
Ala Ser Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro
130 135 140
Met Met Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr
145 150 155 160
Thr Arg Gly Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys
165 170 175
Asn Ala Tyr Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe
180 185 190
Asp Ser Ile His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val
195 200 205
Leu Asp Thr Lys Ile Arg Gly Trp Leu Lys Ala
210 215

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

aatcgcattc	tccgatcgaa	tagccgacgg	agaaatgacc	aagttcagga	agctcggccg	60
cccagcaggt	caccgtatgt	ccatgctcag	gactatgggt	tctcaattgg	tgcaacacga	120
gcgaattgag	accactgtta	caaaggctat	agaagttcgt	cgtcttgctg	ataatatgat	180
tcaactcgga	aaagagggtt	cactagctgc	agcaagaaga	gctgctgggt	ttgttagagg	240
agatgatgta	cttcacaaga	tttttacaga	attggckcat	cgatacaaa	atagagctgg	300
tggatacaca	agaatgcttc	gtactcgcat	tcgtgttggt	gatgctgccc	caatggccta	360
tatcgagttt	atcgatagag	agaacgagct	aaggcaatca	aaaccagcta	ctcctcaacc	420
tccacctcga	gtgccacttg	atccatgggc	tagatcccg	ctcaccaggc	agtatgctcc	480
accaaaggag	gCaaaaaact	tctgattctg	acctataaat	agaagaagat	ctctctcgct	540
ctctcacacc	agaagatcat	gttttttttc	cccttgccca	tgttgtttct	ccttcaaccc	600
atagctttgt	atgtctggca	ccttattcat	cactgtcatt	cacaatgtgt	ttaaaacagt	660
ttaaattgtag	tttccttg					

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

Ile Ala Phe Ser Asp Arg Ile Ala Asp Gly Glu Met Thr Lys Phe Arg	
1 5 10 15	
Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser Met Leu Arg Thr Met	
20 25 30	
Val Ser Gln Leu Val Gln His Glu Arg Ile Glu Thr Val Thr Lys	
35 40 45	

Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met Ile Gln Leu Gly Lys
50 55 60
Glu Gly Ser Leu Ala Ala Arg Arg Ala Ala Gly Phe Val Arg Gly
65 70 75 80
Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu Xaa His Arg Tyr Lys
85 90 95
Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg Thr Arg Ile Arg Val
100 105 110
Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe Ile Asp Arg Glu Asn
115 120 125
Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln Pro Pro Arg Val
130 135 140
Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr Arg Gln Tyr Ala Pro
145 150 155 160
Pro Lys Glu Ala Lys Asn Phe
165

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1567764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser
1 5 10 15
Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg Ile Glu
20 25 30
Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met
35 40 45
Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala
50 55 60
Gly Phe Val Arg Gly Asp Val Leu His Lys Ile Phe Thr Glu Leu
65 70 75 80
Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg
85 90 95
Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe
100 105 110
Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln
115 120 125
Pro Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr
130 135 140
Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1567765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

Met Ser Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg

1 5 10 15
Ile Glu Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp
20 25 30
Asn Met Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg
35 40 45
Ala Ala Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr
50 55 60
Glu Leu Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met
65 70 75 80
Leu Arg Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile
85 90 95
Glu Phe Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr
100 105 110
Pro Gln Pro Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg
115 120 125
Leu Thr Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
130 135 140

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

acgcaggcaa atgtctcgta atttaatcta tagaagaac agagctctct gttttgtttt 60
aatcttgttc tgcttccctt accggtttgg cgctagaaac acgccggagg cggamcaatc 120
cacagcaaaa gcaactcaaa taatacacgt cagcaattcc acgtggcatg atttctctcg 180
tcttgtagat gtccaaatag gtagccacgt cagcggcgta tcagagctca aaagatacct 240
ccaccgattc gggtacgtca aggatggctc cgaaatattt tccgacgtgt tcgatgggtcc 300
tctggaatcg gcaatctctc tgtatcaaga aaatctcggt ttaccaataa ccggaagact 360
cgacacgagt acagttactc tcatgtcggt accgcgatgt ggcgtaggSg atacgcacat 420
gaccatcaac aacgatttcc tccacacaac ggcgcattat acgtatttca acggtaaacc 480
gaaatggaac cgtgatacgc taacctacgc tatctccaaa actcacaac tcgattactt 540
gacgtcagaa gacgtcaaaa ccgttttccg gcgagctttt tcacagtggg caagcgtgat 600
tccggtgagt ttcgaggaag tgcgacgatt cagcagcggt gatttaaaga tcggattcta 660
cgctggtgat cacggtgacg ggcttccggt tgacgggtgta cttggaactt tagcacacgc 720
ttttgcgccg gagaacggga ggcttcacct cgacgcggcg gagacgtgga tcgtcgacga 780
tgacttgaaa ggatcttcag aggtggccgt tgacttgag tctgtggcga ctcacgagat 840
cggtcacttg ttgggattag gacatagctc gcaggagtcg gcggttatgt atccgagtct 900
ccgaccgagg accaagaaaag ttgatcttac gggtgatgac gtggcagggt tacttaagct 960
atatggtccg aatcctaaac tacggttgga ttactaacg cagtcggaag attctattaa 1020
aaacggcacc gtatcacata gattcttgtc ggggaatttt atcggttatg ttctgttggt 1080
tgttgggttg attcttttcc tatagggtta taggcataaa aaatactgtt tttattcatt 1140
tatttttaat taaatgtaca tatatttttc aactatgtaa atgtaaatat atagttgaac 1200
aaaaaaagat gtacatatat agttaggctt ataattaggt ttatggtctt g

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567774

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

Arg Arg Gln Met Ser Arg Asn Leu Ile Tyr Arg Arg Asn Arg Ala Leu
1 5 10 15
Cys Phe Val Leu Ile Leu Phe Cys Phe Pro Tyr Arg Phe Gly Ala Arg
20 25 30
Asn Thr Pro Glu Ala Xaa Gln Ser Thr Ala Lys Ala Thr Gln Ile Ile
35 40 45
His Val Ser Asn Ser Thr Trp His Asp Phe Ser Arg Leu Val Asp Val
50 55 60
Gln Ile Gly Ser His Val Ser Gly Val Ser Glu Leu Lys Arg Tyr Leu
65 70 75 80
His Arg Phe Gly Tyr Val Lys Asp Gly Ser Glu Ile Phe Ser Asp Val
85 90 95
Phe Asp Gly Pro Leu Glu Ser Ala Ile Ser Leu Tyr Gln Glu Asn Leu
100 105 110
Gly Leu Pro Ile Thr Gly Arg Leu Asp Thr Ser Thr Val Thr Leu Met
115 120 125
Ser Leu Pro Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn Asn
130 135 140
Asp Phe Leu His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys Pro
145 150 155 160
Lys Trp Asn Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His Lys
165 170 175
Leu Asp Tyr Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg Ala
180 185 190
Phe Ser Gln Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val Asp
195 200 205
Asp Phe Thr Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His
210 215 220
Gly Asp Gly Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala
225 230 235 240
Phe Ala Pro Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp
245 250 255
Ile Val Asp Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu
260 265 270
Glu Ser Val Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His
275 280 285
Ser Ser Gln Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr
290 295 300
Lys Lys Val Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu
305 310 315 320
Tyr Gly Pro Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu
325 330 335
Asp Ser Ile Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn
340 345 350
Phe Ile Gly Tyr Val Leu Leu Val Gly Leu Ile Leu Phe Leu
355 360 365

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1567775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Met Ser Arg Asn Leu Ile Tyr Arg Arg Asn Arg Ala Leu Cys Phe Val
1 5 10 15

Leu Ile Leu Phe Cys Phe Pro Tyr Arg Phe Gly Ala Arg Asn Thr Pro
20 25 30
Glu Ala Xaa Gln Ser Thr Ala Lys Ala Thr Gln Ile Ile His Val Ser
35 40 45
Asn Ser Thr Trp His Asp Phe Ser Arg Leu Val Asp Val Gln Ile Gly
50 55 60
Ser His Val Ser Gly Val Ser Glu Leu Lys Arg Tyr Leu His Arg Phe
65 70 75 80
Gly Tyr Val Lys Asp Gly Ser Glu Ile Phe Ser Asp Val Phe Asp Gly
85 90 95
Pro Leu Glu Ser Ala Ile Ser Leu Tyr Gln Glu Asn Leu Gly Leu Pro
100 105 110
Ile Thr Gly Arg Leu Asp Thr Ser Thr Val Thr Leu Met Ser Leu Pro
115 120 125
Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn Asn Asp Phe Leu
130 135 140
His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys Pro Lys Trp Asn
145 150 155 160
Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His Lys Leu Asp Tyr
165 170 175
Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg Ala Phe Ser Gln
180 185 190
Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val Asp Asp Phe Thr
195 200 205
Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His Gly Asp Gly
210 215 220
Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala Phe Ala Pro
225 230 235 240
Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp Ile Val Asp
245 250 255
Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu Glu Ser Val
260 265 270
Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His Ser Ser Gln
275 280 285
Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr Lys Lys Val
290 295 300
Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu Tyr Gly Pro
305 310 315 320
Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu Asp Ser Ile
325 330 335
Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn Phe Ile Gly
340 345 350
Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu
355 360

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1567776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Met Ser Leu Pro Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn
1 5 10 15
Asn Asp Phe Leu His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys
20 25 30
Pro Lys Trp Asn Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His

35	40	45
Lys Leu Asp Tyr Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg		
50	55	60
Ala Phe Ser Gln Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val		
65	70	75
Asp Asp Phe Thr Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp		80
	85	90
His Gly Asp Gly Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His		95
	100	105
Ala Phe Ala Pro Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr		110
	115	120
Trp Ile Val Asp Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp		125
	130	140
Leu Glu Ser Val Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly		
145	150	155
His Ser Ser Gln Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg		160
	165	170
Thr Lys Lys Val Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys		175
	180	185
Leu Tyr Gly Pro Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser		190
	195	200
Glu Asp Ser Ile Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly		205
	210	220
Asn Phe Ile Gly Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu		
225	230	235
		240

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

agtgagaaaa	gaatcttctt	ttggcaaatg	cttcgatcct	caatttcgact	tctctatata	60
agaagaacca	gtcctctgct	tcgaagttta	tcatcatcat	catcattatc	atcaaaacga	120
ttcgattctg	cgaaccgat	tttcaattct	catcggactt	tttgtcttcc	tccaatctct	180
acaacgggag	ctaaactttc	tagatcggag	cattcaatgg	ctgcttcttc	cgaacctaaa	240
tctcttttacg	atttcaccgt	caaggatgct	aaggggaaacg	atgttgatct	aagcatctac	300
aaagggaagg	ttctcttgat	tgtgaacggt	gcttctcaat	gtggcttgac	taattcgaat	360
tatactgagC	ttgcgcaGct	gtatgagaag	tacaaaggcc	atggtttcga	gattcttgcg	420
tttccgtgta	acCagtttgg	gaatcaagag	cctgggacta	atgaagagat	tgttcagttt	480
gcttgacttc	gtttcaaggc	cgagtaccgc	attttcgaca	aggttgatgt	taacggtgac	540
aaagctgccc	cagtctacaa	gtttctgaaa	tcaagcaaaag	gcgggctctt	tggagacggc	600
attaagtgga	acttcgcaaa	gttcttggtt	gacaaagatg	gaaatgttgt	cgaccgtttc	660
gcaccaacta	cctcccctct	cagcattgag	aaggatttga	agaagttggt	gggagttact	720
gcttaagcaa	ggcaagattg	cataattaga	caaataaaaag	ctcattagta	ttgtattacc	780
aatactgtgt	agtaagctga	gttcgtgagt	gtgtgtgcct	ttgggaccgc	gtacaattat	840
aatccgtttt	ttagcggcca	aactatgtaa	taatcgtaaa	tctaaatata	agatttcctt	900
ttac						

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1567778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Ser Glu Lys Arg Ile Phe Phe Trp Gln Met Leu Arg Ser Ser Ile Arg
1 5 10 15
Leu Leu Tyr Ile Arg Arg Thr Ser Pro Leu Leu Arg Ser Leu Ser Ser
20 25 30
Ser Ser Ser Leu Ser Ser Lys Arg Phe Asp Ser Ala Lys Pro Ile Phe
35 40 45
Asn Ser His Arg Thr Phe Cys Leu Pro Pro Ile Ser Thr Thr Gly Ala
50 55 60
Lys Leu Ser Arg Ser Glu His Ser Met Ala Ala Ser Ser Glu Pro Lys
65 70 75 80
Ser Leu Tyr Asp Phe Thr Val Lys Asp Ala Lys Gly Asn Asp Val Asp
85 90 95
Leu Ser Ile Tyr Lys Gly Lys Val Leu Leu Ile Val Asn Val Ala Ser
100 105 110
Gln Cys Gly Leu Thr Asn Ser Asn Tyr Thr Glu Leu Ala Gln Leu Tyr
115 120 125
Glu Lys Tyr Lys Gly His Gly Phe Glu Ile Leu Ala Phe Pro Cys Asn
130 135 140
Gln Phe Gly Asn Gln Glu Pro Gly Thr Asn Glu Glu Ile Val Gln Phe
145 150 155 160
Ala Cys Thr Arg Phe Lys Ala Glu Tyr Pro Ile Phe Asp Lys Val Asp
165 170 175
Val Asn Gly Asp Lys Ala Ala Pro Val Tyr Lys Phe Leu Lys Ser Ser
180 185 190
Lys Gly Gly Leu Phe Gly Asp Gly Ile Lys Trp Asn Phe Ala Lys Phe
195 200 205
Leu Val Asp Lys Asp Gly Asn Val Val Asp Arg Phe Ala Pro Thr Thr
210 215 220
Ser Pro Leu Ser Ile Glu Lys Asp Leu Lys Lys Leu Leu Gly Val Thr
225 230 235 240
Ala

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1567779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Met Leu Arg Ser Ser Ile Arg Leu Leu Tyr Ile Arg Arg Thr Ser Pro
1 5 10 15
Leu Leu Arg Ser Leu Ser Ser Ser Ser Leu Ser Ser Lys Arg Phe
20 25 30
Asp Ser Ala Lys Pro Ile Phe Asn Ser His Arg Thr Phe Cys Leu Pro
35 40 45
Pro Ile Ser Thr Thr Gly Ala Lys Leu Ser Arg Ser Glu His Ser Met
50 55 60
Ala Ala Ser Ser Glu Pro Lys Ser Leu Tyr Asp Phe Thr Val Lys Asp
65 70 75 80
Ala Lys Gly Asn Asp Val Asp Leu Ser Ile Tyr Lys Gly Lys Val Leu

(2) INFORMATION FOR SEQ ID NO:727:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1567780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1418

(D) OTHER INFORMATION: / Ceres Seq. ID 1567785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

atccattgat	gagtatataa	ttttgtttgt	gggtattgct	ttgtttgatc	tgctaattgcg	60
tttactcttt	ctggaagaaa	gcttttgaag	atcagcctaa	aagtgatctc	tcataactgc	120
ttaaaagatt	gttgaaactc	gaagatgtct	ttggccgaga	taaacaagaa	tgaagtcgac	180
attgttattg	gggctcttaa	tgctgacctt	acacagtttt	tgaccagctg	gaggcctttc	240
ttctccggat	tccatctgat	tgttgtcaaa	gatcctgagc	tcaaggagga	actcaacata	300
ccagaaggct	ttgacgtaga	tgtctactct	aagactgaca	tggaaaagggt	tgtggggcgca	360
tccaattcca	ccatgttctc	tggctattct	tgcagatatt	tcggttatct	cgtatctaaa	420
aagaagtaca	ttgtctctat	tgatgatgat	tgtgtccctg	ctaaagatcc	gaagggggttc	480
ctagtggatg	ctgttactca	gcacgtgata	aaccttgaaa	acccagccac	gcctctcttc	540
ttcaacaccc	tttatgatcc	ttactgcgag	ggagcggatt	ttgtccgtgg	ataccctttc	600
agcctcagaa	gtgggtgtccc	ttgtgctgca	tcttgtgggc	tttggcttaa	tctagctgat	660
cttgatgctc	caacacaagc	tctcaagaca	gagaaaagga	acactgcata	tgttgatgcg	720
gttatgactg	tcccggccaa	ggctatgcta	cccataagcg	gaatcaacat	tgcttttaac	780
cgcgagttgg	tgggtccagc	tttgggtgct	gcactcagat	tggctggaga	agggaaaagt	840
agatgggaaa	cacttgaaga	tgtttgggtg	gggatgtgtc	tgaacatat	ctctgatcat	900
ttgggttatg	gtgtgaaaac	cggactgcct	tatgtgtgga	gaaacgagag	aggagatgca	960
gtggagagtt	tgaggaaagCa	aatgggaagg	aatgaagctg	atggagaaaa	gtgttccatt	1020
tttcgattca	ttgaaattgc	ccgagactgc	gcttaaaagtt	gaagattgtg	tgattgagct	1080
tgctaaagcg	gtgaaagagc	agttaggttc	agatgatcct	gcctttacgc	aagctgctga	1140
tgctatgggt	aagtgggtcc	agctctggaa	ttctgttaat	tctagcgctt	gaagttgaac	1200
aatctcttga	ggttaggttc	cittatcact	tctaagcata	ttatcatgtc	tcagagattt	1260
acccaagtcg	ttttctttct	tttagtatca	tcatgtttat	tttctctttt	tatctaaatt	1320
ataagcatgt	gtttttgaga	cactcaataa	tgtaacctga	tgaaacccat	ctgctttgac	1380
tcgatgatat	taatatctat	tgcttagctt	ttttactt			

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1567786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met	Ser	Leu	Ala	Glu	Ile	Asn	Lys	Asn	Glu	Val	Asp	Ile	Val	Ile	Gly
1				5				10						15	
Ala	Leu	Asn	Ala	Asp	Leu	Thr	Gln	Phe	Leu	Thr	Ser	Trp	Arg	Pro	Phe
		20						25					30		
Phe	Ser	Gly	Phe	His	Leu	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Lys	Glu
		35					40					45			
Glu	Leu	Asn	Ile	Pro	Glu	Gly	Phe	Asp	Val	Asp	Val	Tyr	Ser	Lys	Thr
		50				55					60				
Asp	Met	Glu	Lys	Val	Val	Gly	Ala	Ser	Asn	Ser	Thr	Met	Phe	Ser	Gly
65					70				75					80	
Tyr	Ser	Cys	Arg	Tyr	Phe	Gly	Tyr	Leu	Val	Ser	Lys	Lys	Lys	Tyr	Ile
		85						90						95	
Val	Ser	Ile	Asp	Asp	Asp	Cys	Val	Pro	Ala	Lys	Asp	Pro	Lys	Gly	Phe
		100						105					110		
Leu	Val	Asp	Ala	Val	Thr	Gln	His	Val	Ile	Asn	Leu	Glu	Asn	Pro	Ala
		115				120						125			
Thr	Pro	Leu	Phe	Phe	Asn	Thr	Leu	Tyr	Asp	Pro	Tyr	Cys	Glu	Gly	Ala
		130				135					140				
Asp	Phe	Val	Arg	Gly	Tyr	Pro	Phe	Ser	Leu	Arg	Ser	Gly	Val	Pro	Cys
145					150				155					160	
Ala	Ala	Ser	Cys	Gly	Leu	Trp	Leu	Asn	Leu	Ala	Asp	Leu	Asp	Ala	Pro

				165					170					175	
Thr	Gln	Ala	Leu	Lys	Thr	Glu	Lys	Arg	Asn	Thr	Ala	Tyr	Val	Asp	Ala
			180					185					190		
Val	Met	Thr	Val	Pro	Ala	Lys	Ala	Met	Leu	Pro	Ile	Ser	Gly	Ile	Asn
		195					200					205			
Ile	Ala	Phe	Asn	Arg	Glu	Leu	Val	Gly	Pro	Ala	Leu	Val	Pro	Ala	Leu
	210					215				220					
Arg	Leu	Ala	Gly	Glu	Gly	Lys	Val	Arg	Trp	Glu	Thr	Leu	Glu	Asp	Val
225					230					235				240	
Trp	Cys	Gly	Met	Cys	Leu	Lys	His	Ile	Ser	Asp	His	Leu	Gly	Tyr	Gly
			245						250				255		
Val	Lys	Thr	Gly	Leu	Pro	Tyr	Val	Trp	Arg	Asn	Glu	Arg	Gly	Asp	Ala
		260						265				270			
Val	Glu	Ser	Leu	Arg	Lys	Gln	Met	Gly	Arg	Asn	Glu	Ala	Asp	Gly	Glu
	275					280					285				
Lys	Cys	Ser	Ile	Phe	Arg	Phe	Ile	Glu	Ile	Ala	Arg	Asp	Cys	Ala	
290						295				300					

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1567787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

Met	Glu	Lys	Val	Val	Gly	Ala	Ser	Asn	Ser	Thr	Met	Phe	Ser	Gly	Tyr
1			5					10					15		
Ser	Cys	Arg	Tyr	Phe	Gly	Tyr	Leu	Val	Ser	Lys	Lys	Lys	Tyr	Ile	Val
		20					25					30			
Ser	Ile	Asp	Asp	Asp	Cys	Val	Pro	Ala	Lys	Asp	Pro	Lys	Gly	Phe	Leu
	35				40					45					
Val	Asp	Ala	Val	Thr	Gln	His	Val	Ile	Asn	Leu	Glu	Asn	Pro	Ala	Thr
50					55					60					
Pro	Leu	Phe	Phe	Asn	Thr	Leu	Tyr	Asp	Pro	Tyr	Cys	Glu	Gly	Ala	Asp
65				70				75						80	
Phe	Val	Arg	Gly	Tyr	Pro	Phe	Ser	Leu	Arg	Ser	Gly	Val	Pro	Cys	Ala
		85					90					95			
Ala	Ser	Cys	Gly	Leu	Trp	Leu	Asn	Leu	Ala	Asp	Leu	Asp	Ala	Pro	Thr
		100					105				110				
Gln	Ala	Leu	Lys	Thr	Glu	Lys	Arg	Asn	Thr	Ala	Tyr	Val	Asp	Ala	Val
	115					120					125				
Met	Thr	Val	Pro	Ala	Lys	Ala	Met	Leu	Pro	Ile	Ser	Gly	Ile	Asn	Ile
130					135					140					
Ala	Phe	Asn	Arg	Glu	Leu	Val	Gly	Pro	Ala	Leu	Val	Pro	Ala	Leu	Arg
145				150				155						160	
Leu	Ala	Gly	Glu	Gly	Lys	Val	Arg	Trp	Glu	Thr	Leu	Glu	Asp	Val	Trp
			165					170				175			
Cys	Gly	Met	Cys	Leu	Lys	His	Ile	Ser	Asp	His	Leu	Gly	Tyr	Gly	Val
		180						185				190			
Lys	Thr	Gly	Leu	Pro	Tyr	Val	Trp	Arg	Asn	Glu	Arg	Gly	Asp	Ala	Val
	195					200					205				
Glu	Ser	Leu	Arg	Lys	Gln	Met	Gly	Arg	Asn	Glu	Ala	Asp	Gly	Glu	Lys
210					215					220					
Cys	Ser	Ile	Phe	Arg	Phe	Ile	Glu	Ile	Ala	Arg	Asp	Cys	Ala		
225					230					235					

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..227
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567788
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

Met Phe Ser Gly Tyr Ser Cys Arg Tyr Phe Gly Tyr Leu Val Ser Lys
1 5 10 15
Lys Lys Tyr Ile Val Ser Ile Asp Asp Cys Val Pro Ala Lys Asp
20 25 30
Pro Lys Gly Phe Leu Val Asp Ala Val Thr Gln His Val Ile Asn Leu
35 40 45
Glu Asn Pro Ala Thr Pro Leu Phe Phe Asn Thr Leu Tyr Asp Pro Tyr
50 55 60
Cys Glu Gly Ala Asp Phe Val Arg Gly Tyr Pro Phe Ser Leu Arg Ser
65 70 75 80
Gly Val Pro Cys Ala Ala Ser Cys Gly Leu Trp Leu Asn Leu Ala Asp
85 90 95
Leu Asp Ala Pro Thr Gln Ala Leu Lys Thr Glu Lys Arg Asn Thr Ala
100 105 110
Tyr Val Asp Ala Val Met Thr Val Pro Ala Lys Ala Met Leu Pro Ile
115 120 125
Ser Gly Ile Asn Ile Ala Phe Asn Arg Glu Leu Val Gly Pro Ala Leu
130 135 140
Val Pro Ala Leu Arg Leu Ala Gly Glu Gly Lys Val Arg Trp Glu Thr
145 150 155 160
Leu Glu Asp Val Trp Cys Gly Met Cys Leu Lys His Ile Ser Asp His
165 170 175
Leu Gly Tyr Gly Val Lys Thr Gly Leu Pro Tyr Val Trp Arg Asn Glu
180 185 190
Arg Gly Asp Ala Val Glu Ser Leu Arg Lys Gln Met Gly Arg Asn Glu
195 200 205
Ala Asp Gly Glu Lys Cys Ser Ile Phe Arg Phe Ile Glu Ile Ala Arg
210 215 220
Asp Cys Ala
225

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1304
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567789
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

atctttcttc tctctctatc tctcctcttt gaaccctaaa aactotttct ttacaaggat 60
tgatcttttt gtatttttga ttttgacatt tgctttgtgt tcgatctctg ttttgatgcg 120
atttctctgt ttttaaagcc atttgataga ttgtttccgg taaagctcag cgagagaaga 180
agaagaacaa caatggagtt tacagatttc tcaaagacga gtttttacta cccgtcgtca 240
caaagcgttt gggatttcgg agatttagcg gcggcgagaga ggcattcttt agggttcatg 300
gagttattaa gttctcagca gcatcaagac tttgctactg tttctctca ttccttctt 360
ctccaaacgt ctcaaccgca aacgcaaacg caaccatcgg cgaagCtgtc ttcaagtatc 420
attcaagctc caccgtcaga gcaattagtg acgtcaaagg tggagtcttt gtgttcggat 480
catttgttga taaaccCacc ggcgactcct aactcgtcac cgatttcgtc tgcttcaaga 540

gaggctctaa atgaagagaa accgaaaaca gaagacaatg aagaagaagg aggtgaagat 600
caacaagaga agagtcatac taagaaacag ttgaaagcaa agaagaataa tcagaagaga 660
cagagagagg caagagtcgc attcatgaca aagagtgaag ttgatcatct cgaagatggt 720
tatcgctggc gaaaatatgg tcaaaaagct gtcaaaaaca gtccttttcc caggagttac 780
taccgttgca caacggcttc atgtaacgtg aagaagagag tggagagatc attcagagat 840
ccaagcactg tggttacaac ctacgaaggt caacacactc acattagtc actcacgtct 900
cgtcctatct cactggagg tttcttcgga tcgtcaggag ctgcttcgag tctcggtaat 960
ggttgctttg ggtttcctat tgatggctcc acgttaatct ctctcagtt ccaacagctt 1020
gtccaatacc atcaccaaca gcagcaacaa gaactcatgt cttgttttgg aggagtcaac 1080
gagtaccta atagccacgc taatgagtat ggtgatgata atcgtgtgaa gaagagtcga 1140
gttttggtta aagataatgg acttctgcaa gatgttggtc cgtatcatat gttgaaggaa 1200
gagtagtagt atatatatag tcttatagtt ttYaatctag ttttttttg tataattgtc 1260
taaaagaaac ggatcttttg ttctgatgaa gaagatgttt tctc

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..337

(D) OTHER INFORMATION: / Ceres Seq. ID 1567790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

Met Glu Phe Thr Asp Phe Ser Lys Thr Ser Phe Tyr Tyr Pro Ser Ser
1 5 10 15
Gln Ser Val Trp Asp Phe Gly Asp Leu Ala Ala Ala Glu Arg His Ser
20 25 30
Leu Gly Phe Met Glu Leu Leu Ser Gln Gln His Gln Asp Phe Ala
35 40 45
Thr Val Ser Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr
50 55 60
Gln Thr Gln Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro
65 70 75 80
Pro Ser Glu Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp
85 90 95
His Leu Leu Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser
100 105 110
Ser Ala Ser Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp
115 120 125
Asn Glu Glu Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys
130 135 140
Lys Gln Leu Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala
145 150 155 160
Arg Val Ala Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly
165 170 175
Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe
180 185 190
Pro Arg Ser Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys
195 200 205
Arg Val Glu Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr
210 215 220
Glu Gly Gln His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser
225 230 235 240
Thr Gly Gly Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn
245 250 255
Gly Cys Phe Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln
260 265 270
Phe Gln Gln Leu Val Gln Tyr His His Gln Gln Gln Gln Gln Glu Leu
275 280 285

Met Ser Cys Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn
290 295 300
Glu Tyr Gly Asp Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys
305 310 315 320
Asp Asn Gly Leu Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu
325 330 335
Glu

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1567791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

Met Glu Leu Leu Ser Ser Gln Gln His Gln Asp Phe Ala Thr Val Ser
1 5 10 15
Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr Gln Thr Gln
20 25 30
Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro Pro Ser Glu
35 40 45
Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp His Leu Leu
50 55 60
Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser Ser Ala Ser
65 70 75 80
Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp Asn Glu Glu
85 90 95
Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys Lys Gln Leu
100 105 110
Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala Arg Val Ala
115 120 125
Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp
130 135 140
Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe Pro Arg Ser
145 150 155 160
Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys Arg Val Glu
165 170 175
Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr Glu Gly Gln
180 185 190
His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser Thr Gly Gly
195 200 205
Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn Gly Cys Phe
210 215 220
Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln Phe Gln Gln
225 230 235 240
Leu Val Gln Tyr His His Gln Gln Gln Gln Glu Leu Met Ser Cys
245 250 255
Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn Glu Tyr Gly
260 265 270
Asp Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys Asp Asn Gly
275 280 285
Leu Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu Glu
290 295 300

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..173
(D) OTHER INFORMATION: / Ceres Seq. ID 1567792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg
1 5 10 15
Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe Pro Arg Ser Tyr
20 25 30
Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys Arg Val Glu Arg
35 40 45
Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr Glu Gly Gln His
50 55 60
Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser Thr Gly Gly Phe
65 70 75 80
Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn Gly Cys Phe Gly
85 90 95
Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln Phe Gln Gln Leu
100 105 110
Val Gln Tyr His His Gln Gln Gln Gln Gln Glu Leu Met Ser Cys Phe
115 120 125
Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn Glu Tyr Gly Asp
130 135 140
Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys Asp Asn Gly Leu
145 150 155 160
Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu Glu
165 170

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..853
(D) OTHER INFORMATION: / Ceres Seq. ID 1567797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

agaatttgag attgcctctg caaagagtaa aatggcgaat cctaaagtct tcttcgacat 60
cttgattggt aagatgaagg cagggcgtgt tgtaatggag ttatttgcag atgtgactcc 120
gagaacagct aataatttcc gtgctttgtg cactggggag aatggtattg ggaaagcagg 180
gaaggcttta cactacaaag gctcagcctt tcaccgtata atcccagggt tcatgtgtca 240
aggtggagat ttactctgtg ggaatggaac tggaggagaa tctatttacg ggtctaaatt 300
tgaagatgag aacttcaagt tgaagcacac tgggtccaggg attttgtcta tggctaactc 360
tgggtccaac actagtgggt ctcagttctt catctgcaca gagaagactt cgtggcttga 420
tgggaaacat gttgttttctg ggaaagttgt tgatggatac aatgtgggtca aggcaatgga 480
ggatgttGgg ctctgacatg ggaaatcctt ctgaacgagt tgtgattgaa gatttgtggtg 540
agctcaagaa cccaagttca taagttctta aaacattggg tgggttgatc ttgacaggtt 600
attctatcat atgctgtgaa gcagagacag catcttagcg ttaaggtcaa tctagttctg 660
gatgcactac tttgggtttt actatatcat atgaacctta ggaagtggtc catccttgta 720
agttgttttc ttaaaactct tgtgtgagac taggatggat gataataatg gttagtttct 780
ttatgaagac atttggtttt gtagctttct tattttgggtg tagttaatat gaatgaacca 840
aactcttctt agg

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1567798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

Glu Phe Glu Ile Ala Ser Ala Lys Ser Lys Met Ala Asn Pro Lys Val
1 5 10 15
Phe Phe Asp Ile Leu Ile Gly Lys Met Lys Ala Gly Arg Val Val Met
20 25 30
Glu Leu Phe Ala Asp Val Thr Pro Arg Thr Ala Asn Asn Phe Arg Ala
35 40 45
Leu Cys Thr Gly Glu Asn Gly Ile Gly Lys Ala Gly Lys Ala Leu His
50 55 60
Tyr Lys Gly Ser Ala Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln
65 70 75 80
Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr Gly Gly Glu Ser Ile Tyr
85 90 95
Gly Ser Lys Phe Glu Asp Glu Asn Phe Lys Leu Lys His Thr Gly Pro
100 105 110
Gly Ile Leu Ser Met Ala Asn Ser Gly Pro Asn Thr Ser Gly Ser Gln
115 120 125
Phe Phe Ile Cys Thr Glu Lys Thr Ser Trp Leu Asp Gly Lys His Val
130 135 140
Val Phe Gly Lys Val Val Asp Gly Tyr Asn Val Val Lys Ala Met Glu
145 150 155 160
Asp Val Gly Leu

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1567799
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

Met Ala Asn Pro Lys Val Phe Phe Asp Ile Leu Ile Gly Lys Met Lys
1 5 10 15
Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Val Thr Pro Arg Thr
20 25 30
Ala Asn Asn Phe Arg Ala Leu Cys Thr Gly Glu Asn Gly Ile Gly Lys
35 40 45
Ala Gly Lys Ala Leu His Tyr Lys Gly Ser Ala Phe His Arg Ile Ile
50 55 60
Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr
65 70 75 80
Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu Asp Glu Asn Phe Lys
85 90 95
Leu Lys His Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ser Gly Pro
100 105 110
Asn Thr Ser Gly Ser Gln Phe Phe Ile Cys Thr Glu Lys Thr Ser Trp
115 120 125
Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Asp Gly Tyr Asn
130 135 140

Val Val Lys Ala Met Glu Asp Val Gly Leu
145 150

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1567800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

Met Lys Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Val Thr Pro
1 5 10 15
Arg Thr Ala Asn Asn Phe Arg Ala Leu Cys Thr Gly Glu Asn Gly Ile
20 25 30
Gly Lys Ala Gly Lys Ala Leu His Tyr Lys Gly Ser Ala Phe His Arg
35 40 45
Ile Ile Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn
50 55 60
Gly Thr Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu Asp Glu Asn
65 70 75 80
Phe Lys Leu Lys His Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ser
85 90 95
Gly Pro Asn Thr Ser Gly Ser Gln Phe Phe Ile Cys Thr Glu Lys Thr
100 105 110
Ser Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Asp Gly
115 120 125
Tyr Asn Val Val Lys Ala Met Glu Asp Val Gly Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1033

(D) OTHER INFORMATION: / Ceres Seq. ID 1567812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

ctcaatttct tttttcttc cagaaatttc ctccgatttc aaaattttcc ggtgaaatcg 60
aaaaaaaaag cgagatcttc ttctctaattg ggcacgacct taagcagaga tcaatatgtc 120
tacatggcga aGctcgccga gcaagccgag cgttacgaag agatgggttca attcatggaa 180
cagctcgtaa gtggagctac accggccggt gagctgaccg tagaagagag gaatcttctc 240
tcggctcgct ataaaaacgt gattggatct ctctgtgagg catggagaat cgtgtcttcg 300
attgagcaaa aggaagagag caggaagaac gaagaacacg tgtcgcttgt taaggattac 360
agatctaaag ttgagactga gctttcttcg atctgttctg ggattctcag gttacttgat 420
tcgcatctga ttccttcagc tactgccagt gagtctaagg ttttttacct gaagatgaaa 480
ggagattatc atcgttatct ggctgagttt aaatctggtg atgagaggaa aactgctgct 540
gaagatacta tgatcgctta caaagctgct caggacgttg cagttgctga tctagcacct 600
acacatccga tcaggcttgg tttggctctt aaactctcag tgttttacta cgagattctc 660
aactcttcag agaaaagctg tagcatggcg aaacaggctt ttgaagaagc cattgctgag 720
ctggacacat tgggagagga gtcatacaag gacagtaact tcatcatgca gttgctaagg 780
gacaatctaa ccttttgac ctccgatatg caggagcaga tggatgaggc ctgaaggtct 840
aatggaagaa aagacggtta tgtaatgtac ctgcaaccgt aaccgaaaat ctgagttcaa 900
cctcctttgc tgtaaaactt gTtcgaaaag aaaagtttgt ttttttatga cagattatgt 960
gcacagcttt ggtgttatct gctgctctgt atcaactctg tttttgtttg gtaatttatc 1020

ctcatctttg etc

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..277

(D) OTHER INFORMATION: / Ceres Seq. ID 1567813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Leu Asn Phe Phe Phe Ser Ser Arg Asn Phe Leu Arg Phe Gln Asn Phe
1 5 10 15
Pro Val Lys Ser Lys Lys Lys Ala Arg Ser Ser Ser Leu Met Ala Thr
20 25 30
Thr Leu Ser Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu Ala Glu Gln
35 40 45
Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln Leu Val Ser
50 55 60
Gly Ala Thr Pro Ala Gly Glu Leu Thr Val Glu Glu Arg Asn Leu Leu
65 70 75 80
Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala Ala Trp Arg
85 90 95
Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu
100 105 110
His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu Thr Glu Leu
115 120 125
Ser Ser Ile Cys Ser Gly Ile Leu Arg Leu Leu Asp Ser His Leu Ile
130 135 140
Pro Ser Ala Thr Ala Ser Glu Ser Lys Val Phe Tyr Leu Lys Met Lys
145 150 155 160
Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ser Gly Asp Glu Arg
165 170 175
Lys Thr Ala Ala Glu Asp Thr Met Ile Ala Tyr Lys Ala Ala Gln Asp
180 185 190
Val Ala Val Ala Asp Leu Ala Pro Thr His Pro Ile Arg Leu Gly Leu
195 200 205
Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Ser Glu
210 215 220
Lys Ala Cys Ser Met Ala Lys Gln Ala Phe Glu Glu Ala Ile Ala Glu
225 230 235 240
Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met
245 250 255
Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Glu
260 265 270
Gln Met Asp Glu Ala
275

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1567814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

Met Ala Thr Thr Leu Ser Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu
1 5 10 15
Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln
20 25 30
Leu Val Ser Gly Ala Thr Pro Ala Gly Glu Leu Thr Val Glu Glu Arg
35 40 45
Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala
50 55 60
Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys
65 70 75 80
Asn Glu Glu His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu
85 90 95
Thr Glu Leu Ser Ser Ile Cys Ser Gly Ile Leu Arg Leu Leu Asp Ser
100 105 110
His Leu Ile Pro Ser Ala Thr Ala Ser Glu Ser Lys Val Phe Tyr Leu
115 120 125
Lys Met Lys Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ser Gly
130 135 140
Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Ile Ala Tyr Lys Ala
145 150 155 160
Ala Gln Asp Val Ala Val Ala Asp Leu Ala Pro Thr His Pro Ile Arg
165 170 175
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn
180 185 190
Ser Ser Glu Lys Ala Cys Ser Met Ala Lys Gln Ala Phe Glu Glu Ala
195 200 205
Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr
210 215 220
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp
225 230 235 240
Met Gln Glu Gln Met Asp Glu Ala
245

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1567815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln
1 5 10 15
Phe Met Glu Gln Leu Val Ser Gly Ala Thr Pro Ala Gly Glu Leu Thr
20 25 30
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
35 40 45
Ser Leu Arg Ala Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu
50 55 60
Glu Ser Arg Lys Asn Glu Glu His Val Ser Leu Val Lys Asp Tyr Arg
65 70 75 80
Ser Lys Val Glu Thr Glu Leu Ser Ser Ile Cys Ser Gly Ile Leu Arg
85 90 95
Leu Leu Asp Ser His Leu Ile Pro Ser Ala Thr Ala Ser Glu Ser Lys
100 105 110
Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr Leu Ala Glu
115 120 125
Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Ile

130	135	140
Ala Tyr Lys Ala Ala Gln Asp Val Ala Val Ala Asp Leu Ala Pro Thr		
145	150	155
His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr		160
	165	170
Glu Ile Leu Asn Ser Ser Glu Lys Ala Cys Ser Met Ala Lys Gln Ala		175
	180	185
Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr		190
	195	200
Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu		205
	210	215
Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala		220
225	230	235

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1854
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

attttctcgat aagcaacgcg ctagagacgg atctcacata atcaccagat caatthttctc	60
gagaaaaaga aaatgtgatt atccattcga ttttttcgca gaagaagacg aaagagagaa	120
gaagagaaaag agatttgaaa tcatggcgaa tgtagtggga cagctaaaac gaggaatctc	180
gagacaattc tcaactggat cgcttcgctg tacgcttagt cgtcaattca cgcgtcaagc	240
ttcacatgat cctcgccgga acaatatgcg atttagtttt ggtagacaat cgtctttaga	300
tccgattcgt cggagtcctg atggtttctaa cgggtccgcag cttgctgtac cggataatct	360
cgacgctact atgcagcttc tattttgtggc ttgtagaggt gatgttgaaag gtgttcagga	420
tctgcttgat gaaggtattg atgttaatag tatcgatctt gatggtcgta cggctcttca	480
tatcgctgct tgtgaaggtc atgtcgatgt tgtcaagctt cttcttacta ggaaggctaa	540
tattgatgct cgtgatcggt ggggaagcac ggcagctgct gatgctaagt attatggtaa	600
catggatggt ttcaacattt tgaaagcccg tggagctaaa gttccgaaaa ccaaaaggac	660
acccatgggt gtggcgaaatc ctctgtgaagt tcctgagtac gagttaaatc cgcaggaact	720
tcaagttcgg aaagctgatg gtatctcaaa gggaatatat caagtggcta aatggaatgg	780
gactaagggt tctgtaaaga tacttgataa ggatctctac aaggattctg acactataaa	840
tgccctcaaa cacgaactta ctttattcga gaaggtacgt catcctaagt ttgtgcaatt	900
tggtggagct gttactcaaa atgtcccat gatgattgtg tccgagtatc atcctaaagg	960
ggaccttggt agctatcttc aaaaaaaagg tcgtctttct ccagccaaag ttctaagatt	1020
tgccctcgat atagccaggg gaatgaatta tcttcacgag tgtaaaccag aaccagtaat	1080
ccactgtgat ctaaaaccca aaaatattat gctcgatagt ggaggacatc tgaaggtggc	1140
Ggggatttgg tttgataagt tttgcaaagt tatcatctga taaatcaaaa atccttaac	1200
acggggccca tatagatcct tcaaattact gtatggcacc tgaggtttac aaagatgaaa	1260
tatttgacag gagtgtggat tcttactctt ttggtgtcgt attatatgag atgattgaag	1320
gagtacaacc tttccatcct aaacccccag aagaggcagt gaagctaagt tgtttagaag	1380
gaagaagacc ttcgttttaa gccaaagtcca aaagttgtcc ccaagagatg agagaattga	1440
ttgaggaatg ctgggatacg gaaacttttg ttagaccaac attttctgag atcatagttc	1500
gattggacaa gatctttgta cactgctcaa aacagggatg gtggaaagat acattcaagt	1560
tcccttgaa atagtacata agaacgtgag aggtttactc aggaacacga gaaactccac	1620
aattcaagag ctctcttctc atgtttacaa taaactcgat acaaagaata caaaaagaaa	1680
cggccctctc cgatttgta ttgtcttctc gtgtaacagt gtacaatgta aaccccaaaa	1740
agtactttca tcgagctata tagacttctc tactgcacag aactgagcat tttgagatac	1800
aatgtatcat atttatataa gtatcaagaa agctctttat tcttgttatg ctcc	

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

(2) INFORMATION FOR SEQ ID NO:746:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..345
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567837
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:
Met Ala Asn Val Val Gly Gln Leu Lys Arg Gly Ile Ser Arg Gln Phe
1 5 10 15
Ser Thr Gly Ser Leu Arg Arg Thr Leu Ser Arg Gln Phe Thr Arg Gln
 20 25 30
Ala Ser His Asp Pro Arg Arg Asn Met Arg Phe Ser Phe Gly Arg
 35 40 45
Gln Ser Ser Leu Asp Pro Ile Arg Arg Ser Pro Asp Gly Ser Asn Gly
50 55 60
Pro Gln Leu Ala Val Pro Asp Asn Leu Asp Ala Thr Met Gln Leu Leu
65 70 75 80
Phe Val Ala Cys Arg Gly Asp Val Glu Gly Val Gln Asp Leu Leu Asp
 85 90 95
Glu Gly Ile Asp Val Asn Ser Ile Asp Leu Asp Gly Arg Thr Ala Leu
 100 105 110
His Ile Ala Ala Cys Glu Gly His Val Asp Val Val Lys Leu Leu Leu
115 120 125
Thr Arg Lys Ala Asn Ile Asp Ala Arg Asp Arg Trp Gly Ser Thr Ala
130 135 140
Ala Ala Asp Ala Lys Tyr Tyr Gly Asn Met Asp Val Phe Asn Ile Leu
145 150 155 160
Lys Ala Arg Gly Ala Lys Val Pro Lys Thr Lys Arg Thr Pro Met Val
 165 170 175
Val Ala Asn Pro Arg Glu Val Pro Glu Tyr Glu Leu Asn Pro Gln Glu
180 185 190
Leu Gln Val Arg Lys Ala Asp Gly Ile Ser Lys Gly Ile Tyr Gln Val
195 200 205
Ala Lys Trp Asn Gly Thr Lys Val Ser Val Lys Ile Leu Asp Lys Asp
210 215 220
Leu Tyr Lys Asp Ser Asp Thr Ile Asn Ala Phe Lys His Glu Leu Thr
225 230 235 240
Leu Phe Glu Lys Val Arg His Pro Asn Val Val Gln Phe Val Gly Ala
 245 250 255
Val Thr Gln Asn Val Pro Met Met Ile Val Ser Glu Tyr His Pro Lys
260 265 270
Gly Asp Leu Gly Ser Tyr Leu Gln Lys Lys Gly Arg Leu Ser Pro Ala
275 280 285
Lys Val Leu Arg Phe Ala Leu Asp Ile Ala Arg Gly Met Asn Tyr Leu
290 295 300
His Glu Cys Lys Pro Glu Pro Val Ile His Cys Asp Leu Lys Pro Lys
305 310 315 320
Asn Ile Met Leu Asp Ser Gly Gly His Leu Lys Val Ala Gly Ile Trp
 325 330 335
Phe Asp Lys Phe Cys Lys Val Ile Ile
340 345

- (2) INFORMATION FOR SEQ ID NO:747:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

U.S. PAT. & TM. OFF.

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1567838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

Met Arg Phe Ser Phe Gly Arg Gln Ser Ser Leu Asp Pro Ile Arg Arg
1 5 10 15
Ser Pro Asp Gly Ser Asn Gly Pro Gln Leu Ala Val Pro Asp Asn Leu
20 25 30
Asp Ala Thr Met Gln Leu Leu Phe Val Ala Cys Arg Gly Asp Val Glu
35 40 45
Gly Val Gln Asp Leu Leu Asp Glu Gly Ile Asp Val Asn Ser Ile Asp
50 55 60
Leu Asp Gly Arg Thr Ala Leu His Ile Ala Ala Cys Glu Gly His Val
65 70 75 80
Asp Val Val Lys Leu Leu Thr Arg Lys Ala Asn Ile Asp Ala Arg
85 90 95
Asp Arg Trp Gly Ser Thr Ala Ala Ala Asp Ala Lys Tyr Tyr Gly Asn
100 105 110
Met Asp Val Phe Asn Ile Leu Lys Ala Arg Gly Ala Lys Val Pro Lys
115 120 125
Thr Lys Arg Thr Pro Met Val Val Ala Asn Pro Arg Glu Val Pro Glu
130 135 140
Tyr Glu Leu Asn Pro Gln Glu Leu Gln Val Arg Lys Ala Asp Gly Ile
145 150 155 160
Ser Lys Gly Ile Tyr Gln Val Ala Lys Trp Asn Gly Thr Lys Val Ser
165 170 175
Val Lys Ile Leu Asp Lys Asp Leu Tyr Lys Asp Ser Asp Thr Ile Asn
180 185 190
Ala Phe Lys His Glu Leu Thr Leu Phe Glu Lys Val Arg His Pro Asn
195 200 205
Val Val Gln Phe Val Gly Ala Val Thr Gln Asn Val Pro Met Met Ile
210 215 220
Val Ser Glu Tyr His Pro Lys Gly Asp Leu Gly Ser Tyr Leu Gln Lys
225 230 235 240
Lys Gly Arg Leu Ser Pro Ala Lys Val Leu Arg Phe Ala Leu Asp Ile
245 250 255
Ala Arg Gly Met Asn Tyr Leu His Glu Cys Lys Pro Glu Pro Val Ile
260 265 270
His Cys Asp Leu Lys Pro Lys Asn Ile Met Leu Asp Ser Gly Gly His
275 280 285
Leu Lys Val Ala Gly Ile Trp Phe Asp Lys Phe Cys Lys Val Ile Ile
290 295 300

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1884

(D) OTHER INFORMATION: / Ceres Seq. ID 1567843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

acagcttctg atctcactag tggtcgtcat ctttggttga ttgaagtttg ggaagtgggtg 60
atggtaatag gagcagcagc gcgtgtagcc atcggcggNt tgcgaaagc tcgtctcgtc 120
acatacctcc ctctctctcg tctcttctca gtgtcgccag atgagtatgg acgcacaaag 180
cgtttctgaa aagcttagga gttctggtct attacgaact caaggtctaa ttggaggcaa 240
gtggcttgac tcgtatgaca ataagacaat caaggttaac aatccagcaa ccggtgaaat 300
tatactgat gttgcatgta tgggaacaaa agagacaaat gatgctattg cttcttctta 360

tgaagcattt	acctcttggg	gcagattgac	tgctggagag	aggagtaaag	ttttacggag	420
atgggtatgac	ctcctgattg	cacacaagga	agaacttgga	caacttataa	ctttggagca	480
aggaaaacca	ctcaaggaag	ccatcggaga	ggtagcatat	ggggcaagtt	ttattgagta	540
ctatgctggag	gaggcaaaac	gtgtatatgg	tgatataaatt	cctccgaatc	tgtctgatcg	600
ccgactgttg	gttctaaaaac	agcctgtcgg	tattgttggt	gcaattaccc	cttggaaactt	660
cccttagacc	atgattactc	ggaaggtcgg	ccctgtctct	gcttctggat	gcacggtggt	720
tgtaaacca	tctgaactta	cgccctaacc	agcacttget	gcggtcgaac	ttgcacttca	780
agctggagtt	cctccggggg	cacttaattgt	ggatcatggga	aatgctcctg	aaattggggg	840
tgctttgctt	acgagtccac	aggtgagaaa	aatcacgttc	acgggatcaa	cagcagttgg	900
gaagaagttg	atggcagctg	ctgcacctac	cgtcaagaag	gtttctctag	aacttggcgg	960
caacgcaccc	tctatagtat	ttgatgatgc	agacctggat	gtagctgtaa	aaggaacgct	1020
tgcagcgaaa	tttaggaata	gtggtcagac	atgtgtttgt	gcgaacagag	tacttgtgca	1080
agatggtatc	tatgataaat	ttgctgaggc	cttttctgaa	gcggttcaaa	aattagaagt	1140
aggagatggg	tttagggatg	ggacaacca	gggtccactt	ataaatgatg	cagcagtgca	1200
aaaggtagag	acatttgtac	aagatgctgt	ttctaaggga	gcaaaaatca	tcattggtgg	1260
caaaaggcac	agtctagggg	tgactttcta	tgagcctact	gttatccgcg	atgtttcggg	1320
taacatgatc	atgtctaagg	aggagatttt	tggacctgta	gctcccctta	ttcgggttcaa	1380
aaccgaggag	gacgctatca	gaattgctaa	tgacacaatt	gcaggacttg	ctgcttatat	1440
attcacaaaac	agtgtccaaa	gatcttggcg	tgtattttgaa	gcacttgaat	atggacttgt	1500
aggggtgaac	gaaggactca	tatcaacaga	gggtggctcca	ttcggggggg	tgaagcagtc	1560
tggtcttggg	aggggaaggat	ccaagtatgg	tatggacgaa	taccttgaga	tcaaatatcgt	1620
atgcttggga	gatatgaata	gacactgatt	tggtttgttt	gaaaagcttt	agaaattgta	1680
agtttttctc	ctccactcgt	atccttctaa	taaaagctta	ctgtggaaca	taataaggat	1740
tcggaggata	cttcttaaga	aataaagatt	tggtctacga	ccaattgtta	gcatgatttt	1800
tagataataa	tttgggggtt	ccattttatt	tatctttgtt	tacgttattt	ttttctttgt	1860
tttacgttaa	tttttgaat	tcgg				

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Met	Ser	Met	Asp	Ala	Gln	Ser	Val	Ser	Glu	Lys	Leu	Arg	Ser	Ser	Gly
1				5					10					15	
Leu	Leu	Arg	Thr	Gln	Gly	Leu	Ile	Gly	Gly	Lys	Trp	Leu	Asp	Ser	Tyr
			20					25					30		
Asp	Asn	Lys	Thr	Ile	Lys	Val	Asn	Asn	Pro	Ala	Thr	Gly	Glu	Ile	Ile
		35				40						45			
Ala	Asp	Val	Ala	Cys	Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala
	50				55					60					
Ser	Ser	Tyr	Glu	Ala	Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu
65				70					75					80	
Arg	Ser	Lys	Val	Leu	Arg	Arg	Trp	Tyr	Asp	Leu	Leu	Ile	Ala	His	Lys
			85					90					95		
Glu	Glu	Leu	Gly	Gln	Leu	Ile	Thr	Leu	Glu	Gln	Gly	Lys	Pro	Leu	Lys
		100						105					110		
Glu	Ala	Ile	Gly	Glu	Val	Ala	Tyr	Gly	Ala	Ser	Phe	Ile	Glu	Tyr	Tyr
	115				120						125				
Ala	Glu	Glu	Ala	Lys	Arg	Val	Tyr	Gly	Asp	Ile	Ile	Pro	Pro	Asn	Leu
	130				135					140					
Ser	Asp	Arg	Arg	Leu	Leu	Val	Leu	Lys	Gln	Pro	Val	Gly	Ile	Val	Gly
145				150					155					160	
Ala	Ile	Thr	Pro	Trp	Asn	Phe	Pro	Leu	Ala	Met	Ile	Thr	Arg	Lys	Val
			165					170					175		
Gly	Pro	Ala	Leu	Ala	Ser	Gly	Cys	Thr	Val	Val	Val	Lys	Pro	Ser	Glu

Variable	Mean	SD	Min	Max
Age	34.5	10.5	18	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	9	16
Income	15.5	10.5	5	45
Occupation	1.5	1.5	0	3
Health status	1.5	1.5	0	3
Stress level	2.5	1.5	0	4
Life satisfaction	3.5	1.5	1	5
Resilience	2.5	1.5	0	4
Optimism	3.5	1.5	1	5
Gratitude	3.5	1.5	1	5
Forgiveness	3.5	1.5	1	5
Empathy	3.5	1.5	1	5
Compassion	3.5	1.5	1	5
Kindness	3.5	1.5	1	5
Generosity	3.5	1.5	1	5
Patience	3.5	1.5	1	5
Self-control	3.5	1.5	1	5
Emotional stability	3.5	1.5	1	5
Psychological well-being	3.5	1.5	1	5
Life purpose	3.5	1.5	1	5
Meaning in life	3.5	1.5	1	5
Existential well-being	3.5	1.5	1	5
Transcendental well-being	3.5	1.5	1	5
Overall well-being	3.5	1.5	1	5

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

(x1) SEQUENCE DESCRIPTION: 322															
Met	Asp	Ala	Gln	Ser	Val	Ser	Glu	Lys	Leu	Arg	Ser	Ser	Gly	Leu	Leu
1				5					10					15	
Arg	Thr	Gln	Gly	Leu	Ile	Gly	Gly	Lys	Trp	Leu	Asp	Ser	Tyr	Asp	Asn
			20					25					30		
Lys	Thr	Ile	Lys	Val	Asn	Asn	Pro	Ala	Thr	Gly	Glu	Ile	Ile	Ala	Asp
			35				40					45			
Val	Ala	Cys	Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala	Ser	Ser
	50					55					60				
Tyr	Glu	Ala	Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu	Arg	Ser
65					70					75					80

[illegible]

- (2) INFORMATION FOR SEQ ID NO:751:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1567846

(X1) SEQUENCE DESCRIPTION: 522																
Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala	Ser	Ser	Tyr	Glu	Ala	
1				5					10					15		
Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu	Arg	Ser	Lys	Val	Leu	
			20					25					30			
Arg	Arg	Trp	Tyr	Asp	Leu	Leu	Ile	Ala	His	Lys	Glu	Glu	Leu	Gly	Gln	
		35					40					45				
Leu	Ile	Thr	Leu	Glu	Gln	Gly	Lys	Pro	Leu	Lys	Glu	Ala	Ile	Gly	Glu	
	50					55					60					
Val	Ala	Tyr	Gly	Ala	Ser	Phe	Ile	Glu	Tyr	Tyr	Ala	Glu	Glu	Ala	Lys	
65					70					75					80	
Arg	Val	Tyr	Gly	Asp	Ile	Ile	Pro	Pro	Asn	Leu	Ser	Asp	Arg	Arg	Leu	
				85					90					95		
Leu	Val	Leu	Lys	Gln	Pro	Val	Gly	Ile	Val	Gly	Ala	Ile	Thr	Pro	Trp	
			100					105					110			
Asn	Phe	Pro	Leu	Ala	Met	Ile	Thr	Arg	Lys	Val	Gly	Pro	Ala	Leu	Ala	
	115						120					125				
Ser	Gly	Cys	Thr	Val	Val	Val	Lys	Pro	Ser	Glu	Leu	Thr	Pro	Leu	Thr	
	130					135					140					
Ala	Leu	Ala	Ala	Ala	Glu	Leu	Ala	Leu	Gln	Ala	Gly	Val	Pro	Pro	Gly	
145					150					155					160	
Ala	Leu	Asn	Val	Val	Met	Gly	Asn	Ala	Pro	Glu	Ile	Gly	Asp	Ala	Leu	
				165					170					175		
Leu	Thr	Ser	Pro	Gln	Val	Arg	Lys	Ile	Thr	Phe	Thr	Gly	Ser	Thr	Ala	
			180					185					190			
Val	Gly	Lys	Lys	Leu	Met	Ala	Ala	Ala	Ala	Pro	Thr	Val	Lys	Lys	Val	
	195					200						205				
Ser	Leu	Glu	Leu	Gly	Gly	Asn	Ala	Pro	Ser	Ile	Val	Phe	Asp	Asp	Ala	
	210					215					220					
Asp	Leu	Asp	Val	Ala	Val	Lys	Gly	Thr	Leu	Ala	Ala	Lys	Phe	Arg	Asn	
225					230					235					240	
Ser	Gly	Gln	Thr	Cys	Val	Cys	Ala	Asn	Arg	Val	Leu	Val	Gln	Asp	Gly	
				245					250					255		
Ile	Tyr	Asp	Lys	Phe	Ala	Glu	Ala	Phe	Ser	Glu	Ala	Val	Gln	Lys	Leu	
			260					265					270			
Glu	Val	Gly	Asp	Gly	Phe	Arg	Asp	Gly	Thr	Thr	Gln	Gly	Pro	Leu	Ile	
	275						280					285				
Asn	Asp	Ala	Ala	Val	Gln	Lys	Val	Glu	Thr	Phe	Val	Gln	Asp	Ala	Val	
	290					295					300					
Ser	Lys	Gly	Ala	Lys	Ile	Ile	Ile	Gly	Gly	Lys	Arg	His	Ser	Leu	Gly	
305					310					315					320	
Met	Thr	Phe	Tyr	Glu	Pro	Thr	Val	Ile	Arg	Asp	Val	Ser	Asp	Asn	Met	
				325					330					335		
Ile	Met	Ser	L													

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1386

(D) OTHER INFORMATION: / Ceres Seq. ID 1567877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

aaacctttct	cttctctgct	aacgagaaaa	caaaagctat	cgtctttgct	actactacta	60
ctgctattat	tacattgaat	cctttgtggt	cttcttcttc	agctgctact	ttgttcgagt	120
gctttcttac	atgccgtcgg	agattgttga	caggaaaagg	aagtctcgtg	gaacacGaga	180
Ntgtagctga	gattctaagg	caatggagag	agtacaatga	gcagattgag	gcagaatctt	240
gtatcgatgg	tgggtgtcca	aaatcaatcc	gaaagcctcc	tccaaaaggt	tcgaggaagg	300
gttgatgaa	aggtaaagg	ggacctgaaa	acgggatttg	tgactataga	gaagttagac	360
agaggagatg	gggtaaattg	gttgctgaga	tccgtgagcc	agacggaggt	gctagggttg	420
ggctcggtag	tttctccagt	tcatatgaag	ctgcattggc	ttatgacgag	gcggccaaa	480
ctatatatgg	tcagttctgc	agactcaatc	ttcccagagat	cacaaatcgc	tcttcttcga	540
ctgctgccac	tgccactgtg	tcagggtcgg	ttactgcatt	ttctgatgaa	tctgaagttt	600
gtgcacgtga	ggatacaaat	gcaagttcag	gttttggtca	ggtgaaacta	gaggattgta	660
gcgatgaata	tgttctctta	gatatgtctc	agtgtattaa	agaggagctg	aaaggaaaa	720
aggaagtgag	ggaagaacat	aacttggctg	ttggttttgg	aattggacag	gactcgaaaa	780
gggagacttt	ggatgcttgg	ttgatgggaa	atggcaatga	acaagaacca	ttggagtttg	840
gtgtggatga	aacgtttgat	attaatgagc	tattgggtat	attaaacgac	aacaatgtgt	900
ctggtcaaga	gacaatgcag	tatcaagtgg	atagacaccc	aaatttcagt	taccaaacgc	960
agtttccaaa	ttctaacttg	ctcgggagcc	tcaaccctat	ggagattgct	caaccaggag	1020
ttgattatgg	atgtccttat	gtgcagccca	gtgatatgga	gaactatggt	attgatttag	1080
accatcgtag	gttcaatgat	cttgacatac	aggacttgga	ttttggagga	gacaaagatg	1140
ttcatggatc	tacataagat	ttcaaatttc	gtttgactgt	cctaagtttg	tgattctgct	1200
ccgagacggt	gtagctgtta	ctagctagaa	gctgcccttc	tttgaagcta	ctgatacttt	1260
ctgatattaa	tggttgtgag	acgtagtaca	tgtagttagg	taatgtagga	caagttcaaa	1320
tatgattcct	tctttctttt	tcttgtgaat	acatatgaca	tatgaagaag	ttcaaacgtt	1380

gggtcc

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1567878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Thr	Phe	Leu	Phe	Ser	Ala	Asn	Glu	Lys	Thr	Lys	Ala	Ile	Val	Phe	Ala
1				5					10					15	
Thr	Thr	Thr	Thr	Ala	Ile	Ile	Thr	Leu	Asn	Pro	Leu	Cys	Ser	Ser	Ser
				20				25					30		
Ser	Ala	Ala	Thr	Leu	Phe	Glu	Cys	Phe	Leu	Thr	Cys	Arg	Arg	Arg	Leu
				35			40					45			
Leu	Thr	Gly	Lys	Gly	Ser	Leu	Val	Glu	His	Glu	Xaa	Val	Ala	Glu	Ile
				50			55				60				
Leu	Arg	Gln	Trp	Arg	Glu	Tyr	Asn	Glu	Gln	Ile	Glu	Ala	Glu	Ser	Cys
65				70					75					80	
Ile	Asp	Gly	Gly	Gly	Pro	Lys	Ser	Ile	Arg	Lys	Pro	Pro	Pro	Lys	Gly
				85					90					95	
Ser	Arg	Lys	Gly	Cys	Met	Lys	Gly	Lys	Gly	Gly	Pro	Glu	Asn	Gly	Ile
				100				105					110		
Cys	Asp	Tyr	Arg	Glu	Val	Arg	Gln	Arg	Arg	Trp	Gly	Lys	Trp	Val	Ala

115 120 125
Glu Ile Arg Glu Pro Asp Gly Gly Ala Arg Leu Trp Leu Gly Thr Phe
130 135 140
Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp Glu Ala Ala Lys Ala
145 150 155 160
Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro Glu Ile Thr Asn Arg
165 170 175
Ser Ser Ser Thr Ala Ala Thr Ala Thr Val Ser Gly Ser Val Thr Ala
180 185 190
Phe Ser Asp Glu Ser Glu Val Cys Ala Arg Glu Asp Thr Asn Ala Ser
195 200 205
Ser Gly Phe Gly Gln Val Lys Leu Glu Asp Cys Ser Asp Glu Tyr Val
210 215 220
Leu Leu Asp Ser Ser Gln Cys Ile Lys Glu Glu Leu Lys Gly Lys Glu
225 230 235 240
Glu Val Arg Glu Glu His Asn Leu Ala Val Gly Phe Gly Ile Gly Gln
245 250 255
Asp Ser Lys Arg Glu Thr Leu Asp Ala Trp Leu Met Gly Asn Gly Asn
260 265 270
Glu Gln Glu Pro Leu Glu Phe Gly Val Asp Glu Thr Phe Asp Ile Asn
275 280 285
Glu Leu Leu Gly Ile Leu Asn Asp Asn Asn Val Ser Gly Gln Glu Thr
290 295 300
Met Gln Tyr Gln Val Asp Arg His Pro Asn Phe Ser Tyr Gln Thr Gln
305 310 315 320
Phe Pro Asn Ser Asn Leu Leu Gly Ser Leu Asn Pro Met Glu Ile Ala
325 330 335
Gln Pro Gly Val Asp Tyr Gly Cys Pro Tyr Val Gln Pro Ser Asp Met
340 345 350
Glu Asn Tyr Gly Ile Asp Leu Asp His Arg Arg Phe Asn Asp Leu Asp
355 360 365
Ile Gln Asp Leu Asp Phe Gly Gly Asp Lys Asp Val His Gly Ser Thr
370 375 380

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..283

(D) OTHER INFORMATION: / Ceres Seq. ID 1567879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

Met Lys Gly Lys Gly Gly Pro Glu Asn Gly Ile Cys Asp Tyr Arg Glu
1 5 10 15
Val Arg Gln Arg Arg Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
20 25 30
Asp Gly Gly Ala Arg Leu Trp Leu Gly Thr Phe Ser Ser Ser Tyr Glu
35 40 45
Ala Ala Leu Ala Tyr Asp Glu Ala Ala Lys Ala Ile Tyr Gly Gln Ser
50 55 60
Ala Arg Leu Asn Leu Pro Glu Ile Thr Asn Arg Ser Ser Ser Thr Ala
65 70 75 80
Ala Thr Ala Thr Val Ser Gly Ser Val Thr Ala Phe Ser Asp Glu Ser
85 90 95
Glu Val Cys Ala Arg Glu Asp Thr Asn Ala Ser Ser Gly Phe Gly Gln
100 105 110

Val Lys Leu Glu Asp Cys Ser Asp Glu Tyr Val Leu Leu Asp Ser Ser
115 120 125
Gln Cys Ile Lys Glu Glu Leu Lys Gly Lys Glu Glu Val Arg Glu Glu
130 135 140
His Asn Leu Ala Val Gly Phe Gly Ile Gly Gln Asp Ser Lys Arg Glu
145 150 155 160
Thr Leu Asp Ala Trp Leu Met Gly Asn Gly Asn Glu Gln Glu Pro Leu
165 170 175
Glu Phe Gly Val Asp Glu Thr Phe Asp Ile Asn Glu Leu Leu Gly Ile
180 185 190
Leu Asn Asp Asn Asn Val Ser Gly Gln Glu Thr Met Gln Tyr Gln Val
195 200 205
Asp Arg His Pro Asn Phe Ser Tyr Gln Thr Gln Phe Pro Asn Ser Asn
210 215 220
Leu Leu Gly Ser Leu Asn Pro Met Glu Ile Ala Gln Pro Gly Val Asp
225 230 235 240
Tyr Gly Cys Pro Tyr Val Gln Pro Ser Asp Met Glu Asn Tyr Gly Ile
245 250 255
Asp Leu Asp His Arg Arg Phe Asn Asp Leu Asp Ile Gln Asp Leu Asp
260 265 270
Phe Gly Gly Asp Lys Asp Val His Gly Ser Thr
275 280

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

aaaatagctg atcatttttg agggaagctt cacttgggtt acatgctgat ccgcgacaaa	60
ttggcagagc ttcaggagga gaagaacaaa gttcacaagg aacgggtcga agaaaggaga	120
tcaaaggaga ggagtagaga gcgagaatca agtaaagaca gagacggagg agatagccgt	180
gaccgaggaa gagatgttga ccgcagGagt agagatcgtg acaggcacca tgaccaccga	240
gaacatgaca gaaactataa ccagtcacgt ggctatgact caagaagccg gcgcagttca	300
cggccccggt ctagggaaag accgagggat catgatcgcc gcagacgcca tgaccgctac	360
taagacctg ccaaagatgg ttgcacctgg tttaagaggt tcttacagat gcgttttagga	420
tctattttggG agttacaaac actttctttt ttctttgctc aagtgtttta aggattttt	480
agattgtaac ttactttaag tttgtaAgag gagcttcttc agatatcttt aatttgttt	540
ttatgttggt gacatcaaag acttgcgagt ag	

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Lys Ile Ala Asp His Phe Gly Gly Lys Leu His Leu Gly Tyr Met Leu
1 5 10 15
Ile Arg Asp Lys Leu Ala Glu Leu Gln Glu Glu Lys Asn Lys Val His
20 25 30
Lys Glu Arg Val Glu Glu Arg Arg Ser Lys Glu Arg Ser Arg Glu Arg

35 40 45
Glu Ser Ser Lys Asp Arg Asp Gly Gly Asp Ser Arg Asp Arg Gly Arg
50 55 60
Asp Val Asp Arg Arg Ser Arg Asp Arg Asp Arg His His Asp His Arg
65 70 75 80
Glu His Asp Arg Asn Tyr Asn Gln Ser Arg Gly Tyr Asp Ser Arg Ser
85 90 95
Arg Arg Ser Ser Arg Ser Arg Ser Arg Glu Arg Pro Arg Asp His Asp
100 105 110
Arg Arg Arg Arg His Asp Arg Tyr
115 120

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

Met Leu Ile Arg Asp Lys Leu Ala Glu Leu Gln Glu Glu Lys Asn Lys
1 5 10 15
Val His Lys Glu Arg Val Glu Glu Arg Arg Ser Lys Glu Arg Ser Arg
20 25 30
Glu Arg Glu Ser Ser Lys Asp Arg Asp Gly Gly Asp Ser Arg Asp Arg
35 40 45
Gly Arg Asp Val Asp Arg Arg Ser Arg Asp Arg Asp Arg His His Asp
50 55 60
His Arg Glu His Asp Arg Asn Tyr Asn Gln Ser Arg Gly Tyr Asp Ser
65 70 75 80
Arg Ser Arg Arg Ser Ser Arg Ser Arg Ser Arg Glu Arg Pro Arg Asp
85 90 95
His Asp Arg Arg Arg Arg His Asp Arg Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

Met Leu Thr Ala Gly Val Glu Ile Val Thr Gly Thr Met Thr Thr Glu
1 5 10 15
Asn Met Thr Glu Thr Ile Thr Ser His Val Ala Met Thr Gln Glu Ala
20 25 30
Gly Ala Val His Gly Pro Gly Leu Gly Lys Asp Arg Gly Ile Met Ile
35 40 45
Ala Ala Asp Ala Met Thr Ala Thr Lys Thr Leu Pro Lys Met Val Ala
50 55 60
Pro Gly Leu Arg Gly Ser Tyr Arg Cys Val
65 70

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1148

(D) OTHER INFORMATION: / Ceres Seq. ID 1567896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

caaagggtttt	caatgagtag	catgacaagt	aaactcaagt	acggtcttgt	tccccttctt	60
aatcattttg	ctgaggaagg	aacaactctt	gacttgcaaa	gcgtcttcgg	gaggttcaact	120
ttcgatacaa	ttttcatcct	tataactggg	tctgaccta	gatctctctc	cattgaaatg	180
cctgaagacg	aatttgctaa	agctctcgac	gatgttgagg	aagggattct	ttataggcat	240
tttaaaccac	ggttcttgtg	gaagctgcaa	aactggatag	gattcggaca	agagaagaag	300
ctcactgaag	ctaatagcaac	ttttgaccgc	gtgtgtgcc	aatacatatc	agccaagaga	360
gaagagatta	aaagatcaca	agggacttcc	aatggaggaa	gtcaggatct	tttaacttcc	420
ttcataaagc	tagacacgac	caagtacaag	ctcttgaatc	cgagtgcaga	taagttcctt	480
agagacaaca	tcttagcttt	cattctagcg	ggaagagaca	caacagccac	cgctctctct	540
tgttcttctt	ggcttctctc	tgaatatcca	catgtggtag	ccaagattca	tcaagagatc	600
aacatcaaca	ctgatctatc	aagaacagga	aatagccaag	agaatgtaga	caagttggtg	660
tattttacatg	gtgcgttgtg	tgaagcaatg	agactctacc	caccagtttc	Cttcggacgc	720
aagtcctcaa	tcaaatcaga	tgtgcttcca	agtggccata	aagttgatgc	aaactctaag	780
attattatct	gtctttatgc	attggggagg	atgcgagcgg	tttggggaga	agatgcacgc	840
cagttcaagc	cagagagatg	gatttcggag	aatggaggca	taaaacatga	gccttccttc	900
aagtttttgt	cgtttaaatgc	cggtccaaga	acttgtctag	gtaaacaatc	agctatgact	960
caaatagaag	tagtggcagt	ggagatatta	cgaaactacg	acattaaggt	tctccaagga	1020
cagaagattg	tgccagctct	tggttttata	ttgtcaatga	aacatgggtc	tcaaatcact	1080
gttactaaga	gatgttctgc	ttgaaattat	tcatgtatta	aataaaaaaa	tcattttggg	1140
ttggtttt						

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1567897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

Gln	Arg	Phe	Ser	Met	Ser	Thr	Met	Thr	Ser	Lys	Leu	Lys	Tyr	Gly	Leu
1				5					10					15	
Val	Pro	Leu	Leu	Asn	His	Phe	Ala	Glu	Glu	Gly	Thr	Thr	Leu	Asp	Leu
		20						25					30		
Gln	Ser	Val	Phe	Gly	Arg	Phe	Thr	Phe	Asp	Thr	Ile	Phe	Ile	Leu	Ile
		35					40				45				
Thr	Gly	Ser	Asp	Pro	Arg	Ser	Leu	Ser	Ile	Glu	Met	Pro	Glu	Asp	Glu
	50					55				60					
Phe	Ala	Lys	Ala	Leu	Asp	Asp	Val	Gly	Glu	Gly	Ile	Leu	Tyr	Arg	His
65					70				75					80	
Phe	Lys	Pro	Arg	Phe	Leu	Trp	Lys	Leu	Gln	Asn	Trp	Ile	Gly	Phe	Gly
			85					90					95		
Gln	Glu	Lys	Lys	Leu	Thr	Glu	Ala	Asn	Ala	Thr	Phe	Asp	Arg	Val	Cys
		100						105				110			
Ala	Lys	Tyr	Ile	Ser	Ala	Lys	Arg	Glu	Glu	Ile	Lys	Arg	Ser	Gln	Gly
		115				120						125			
Thr	Ser	Asn	Gly	Gly	Ser	Gln	Asp	Leu	Leu	Thr	Ser	Phe	Ile	Lys	Leu
	130					135					140				
Asp	Thr	Thr	Lys	Tyr	Lys	Leu	Leu	Asn	Pro	Ser	Asp	Asp	Lys	Phe	Leu

Met	Ser	Thr	Met	Thr	Ser	Lys	Leu	Lys	Tyr	Gly	Leu	Val	Pro	Leu	Leu
1				5					10					15	
Asn	His	Phe	Ala	Glu	Glu	Gly	Thr	Thr	Leu	Asp	Leu	Gln	Ser	Val	Phe
			20					25					30		
Gly	Arg	Phe	Thr	Phe	Asp	Thr	Ile	Phe	Ile	Leu	Ile	Thr	Gly	Ser	Asp
		35				40						45			
Pro	Arg	Ser	Leu	Ser	Ile	Glu	Met	Pro	Glu	Asp	Glu	Phe	Ala	Lys	Ala
	50					55					60				
Leu	Asp	Asp	Val	Gly	Glu	Gly	Ile	Leu	Tyr	Arg	His	Phe	Lys	Pro	Arg
65				70					75					80	
Phe	Leu	Trp	Lys	Leu	Gln	Asn	Trp	Ile	Gly	Phe	Gly	Gln	Glu	Lys	Lys
			85						90					95	
Leu	Thr	Glu	Ala	Asn	Ala	Thr	Phe	Asp	Arg	Val	Cys	Ala	Lys	Tyr	Ile
			100					105					110		
Ser	Ala	Lys	Arg	Glu	Glu	Ile	Lys	Arg	Ser	Gln	Gly	Thr	Ser	Asn	Gly
		115				120						125			
Gly	Ser	Gln	Asp	Leu	Leu	Thr	Ser	Phe	Ile	Lys	Leu	Asp	Thr	Thr	Lys
	130					135					140				
Tyr	Lys	Leu	Leu	Asn	Pro	Ser	Asp	Asp	Lys	Phe	Leu	Arg	Asp	Asn	Ile
145				150					155					160	
Leu	Ala	Phe	Ile	Leu	Ala	Gly	Arg	Asp	Thr	Thr	Ala	Thr	Ala	Leu	Ser
			165					170						175	

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 1																
Met	Thr	Ser	Lys	Leu	Lys	Tyr	Gly	Leu	Val	Pro	Leu	Leu	Asn	His	Phe	
1				5					10					15		
Ala	Glu	Glu	Gly	Thr	Thr	Leu	Asp	Leu	Gln	Ser	Val	Phe	Gly	Arg	Phe	
			20					25					30			
Thr	Phe	Asp	Thr	Ile	Phe	Ile	Leu	Ile	Thr	Gly	Ser	Asp	Pro	Arg	Ser	
		35				40					45					
Leu	Ser	Ile	Glu	Met	Pro	Glu	Asp	Glu	Phe	Ala	Lys	Ala	Leu	Asp	Asp	
	50					55					60					
Val	Gly	Glu	Gly	Ile	Leu	Tyr	Arg	His	Phe	Lys	Pro	Arg	Phe	Leu	Trp	
65				70						75					80	
Lys	Leu	Gln	Asn	Trp	Ile	Gly	Phe	Gly	Gln	Glu	Lys	Lys	Leu	Thr	Glu	
			85						90					95		
Ala	Asn	Ala	Thr	Phe	Asp	Arg	Val	Cys	Ala	Lys	Tyr	Ile	Ser	Ala	Lys	
			100					105					110			
Arg	Glu	Glu	Ile	Lys	Arg	Ser	Gln	Gly	Thr	Ser	Asn	Gly	Gly	Ser	Gln	
		115					120					125				
Asp	Leu	Leu	Thr	Ser	Phe	Ile	Lys	Leu	Asp	Thr	Thr	Lys	Tyr	Lys	Leu	
	130					135					140					
Leu	Asn	Pro	Ser	Asp	Asp	Lys	Phe	Leu	Arg	Asp	Asn	Ile	Leu	Ala	Phe	
145				150						155				160		
Ile	Leu	Ala	Gly	Arg	Asp	Thr	Thr	Ala	Thr	Ala	Leu	Ser	Trp	Phe	Phe	
			165						170					175		
Trp	Leu	Leu	Ser	Glu	Asn	Pro	His	Val	Val	Ala	Lys	Ile	His	Gln	Glu	
		180						185					190			
Ile	Asn	Ile	Asn	Thr	Asp	Leu	Ser	Arg	Thr	Gly	Asn	Ser	Gln	Glu	Asn	

195	200	205
Val Asp Lys Leu Val Tyr Leu His Gly Ala Leu Cys Glu Ala Met Arg		
210	215	220
Leu Tyr Pro Pro Val Ser Phe Gly Arg Lys Ser Pro Ile Lys Ser Asp		
225	230	235
Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Ile Ile		
245	250	255
Cys Leu Tyr Ala Leu Gly Arg Met Arg Ala Val Trp Gly Glu Asp Ala		
260	265	270
Ser Gln Phe Lys Pro Glu Arg Trp Ile Ser Glu Asn Gly Gly Ile Lys		
275	280	285
His Glu Pro Ser Phe Lys Phe Leu Ser Phe Asn Ala Gly Pro Arg Thr		
290	295	300
Cys Leu Gly Lys His Leu Ala Met Thr Gln Met Lys Ile Val Ala Val		
305	310	315
Glu Ile Leu Arg Asn Tyr Asp Ile Lys Val Leu Gln Gly Gln Lys Ile		
325	330	335
Val Pro Ala Leu Gly Phe Ile Leu Ser Met Lys His Gly Leu Gln Ile		
340	345	350
Thr Val Thr Lys Arg Cys Ser Ala		
355	360	

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

ggcttgctgc	agaagttggg	attcgtcttt	ttataatttg	ccctgaaaac	gaaaacgaaa	60
ataaaaagcg	gagagagaga	tggctagata	cgatcgagca	attactgtct	tctccccga	120
cggtcacctc	tttcaagtcg	aatacgccct	tgaagccgto	cgcaagggtg	acgccgccgt	180
cgggtgtccgc	ggtaccgaca	ccgttgctct	cgccgtcgag	aagaagtcca	cccccaagct	240
tcaggattct	agatcagcca	gaaaaattgt	gagccttgac	aatcacattg	ccttggcatg	300
cgcggggctc	aaggctgatg	cccagctctt	gattaacaaa	gcaaggatcg	agtgtcaaag	360
ccacaggctt	acacttgagg	accctgtcac	tgttgagtac	atcactcgct	acattgctgg	420
ccttcaacag	aagtataccc	aaagtgggtg	tgtcagaccc	ttcgggtctt	ctactcttat	480
cgttggtctt	gacccttact	ctcgctccc	ttccctatat	cagactgatc	cttctgggac	540
tttctctgct	tggaaagcta	atgctaccgg	cagaaactcc	aactctatta	gggaattcct	600
cgagaagaac	tacaaagaat	cctctggcca	agaaactatt	aaactcgcta	tccgtgctct	660
gcttgaggta	gttgagagtg	gcggaaagaa	cattgagggt	gccgtaatga	cacggggagga	720
aactGggCtg	cgccagctag	aagaagctga	aattgatgca	atcgtggcca	agatcgaagc	780
tgaaggcggc	cgcagaagca	gccaagaaag	gccctccaaa	ggaaacttga	taaaacaata	840
actgtttctg	tttctcaatc	tgaacttacc	ttcttcgctg	cttctgtttc	tcaatcttgt	900
tttgactoga	gccaaactct	tggcaaaaga	agaacctgac	cccacgtttt	tgtaaacttg	960
aaaatgctcc	aaaaaaaaac	tgaagaaagg	gtttaaaatt	cgcttgatct	tgatcaaacc	1020
aaggataaat	ttgctgttgc	tcattgttag	atagagaagt	gactctccat	tttctattta	1080
taagtaagca	gaacaattag	tggt				

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1567905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

Met Ala Arg Tyr Asp Arg Ala Ile Thr Val Phe Ser Pro Asp Gly His
1 5 10 15
Leu Phe Gln Val Glu Tyr Ala Leu Glu Ala Val Arg Lys Gly Asn Ala
20 25 30
Ala Val Gly Val Arg Gly Thr Asp Thr Val Val Leu Ala Val Glu Lys
35 40 45
Lys Ser Thr Pro Lys Leu Gln Asp Ser Arg Ser Ala Arg Lys Ile Val
50 55 60
Ser Leu Asp Asn His Ile Ala Leu Ala Cys Ala Gly Leu Lys Ala Asp
65 70 75 80
Ala Arg Val Leu Ile Asn Lys Ala Arg Ile Glu Cys Gln Ser His Arg
85 90 95
Leu Thr Leu Glu Asp Pro Val Thr Val Glu Tyr Ile Thr Arg Tyr Ile
100 105 110
Ala Gly Leu Gln Gln Lys Tyr Thr Gln Ser Gly Gly Val Arg Pro Phe
115 120 125
Gly Leu Ser Thr Leu Ile Val Gly Phe Asp Pro Tyr Ser Arg Leu Pro
130 135 140
Ser Leu Tyr Gln Thr Asp Pro Ser Gly Thr Phe Ser Ala Trp Lys Ala
145 150 155 160
Asn Ala Thr Gly Arg Asn Ser Asn Ser Ile Arg Glu Phe Leu Glu Lys
165 170 175
Asn Tyr Lys Glu Ser Ser Gly Gln Glu Thr Ile Lys Leu Ala Ile Arg
180 185 190
Ala Leu Leu Glu Val Val Glu Ser Gly Gly Lys Asn Ile Glu Val Ala
195 200 205
Val Met Thr Arg Glu Glu Thr Gly Leu Arg Gln Leu Glu Glu Ala Glu
210 215 220
Ile Asp Ala Ile Val Ala Lys Ile Glu Ala Glu Gly Gly Arg Arg Ser
225 230 235 240
Ser Gln Glu Arg Pro Ser Lys Gly Asn Leu Ile Lys Gln
245 250

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1956

(D) OTHER INFORMATION: / Ceres Seq. ID 1567929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

ctctcatttt Gctactcttc ttcaaaagca cactcaatat ttcgagatcc tctcggttg 60
ttcgttcttc gtgaacgata ccatctattg tttctcgctg gtctcagatt cgactaactt 120
ggatatctcc gatactgaag aagcctcctt cttctttttc cgctcttccc gatgccgata 180
gataagatct tcaaagatga tgctagtga gagaaggag aacgtgcgag gatggcatca 240
tttggttggtg caatggctat cagtgatctg gttaagtcta ctttagggcc aaagggcatg 300
gataaaatct tacaatctac tggtagaggt catgcggtca ctgttactaa cgatggtgct 360
actattctca agtcaacttca catagacaac cctgcagcta aagttcttgt tgacatctcg 420
aaagttcaag atgatgaggt tggatgatga actaccttg ttgttgctt gccggcgag 480
cttctgaggg aagcagaaaa gcttggtggt tctaagattc accctatgac catcatagca 540
ggttacagaa tggcttcgga atgtgctcgt aatgctttac tgaaaagagt cattgataac 600
aaggacaatg cagagaagtt taggtcagac ttgttgaaga ttgcgatgac tactttatgt 660
tccaaaattc tctcacagga caaggaacat ttgacagaaa tggccgtgga tgctgttttc 720
aggctaaagg gaagcacaaa cttggaagct attcagatca tcaaaaaacc tggagggtct 780
ctgaaggatt cgtttttgga tgaagggttt attcttgaca agaaaatagg aattgggcag 840

Parameter	Value	Unit
α	0.001	
β	0.001	
γ	0.001	
δ	0.001	
ϵ	0.001	
ζ	0.001	
η	0.001	
θ	0.001	
ι	0.001	
κ	0.001	
λ	0.001	
μ	0.001	
ν	0.001	
ξ	0.001	
\omicron	0.001	
π	0.001	
ρ	0.001	
σ	0.001	
τ	0.001	
υ	0.001	
ϕ	0.001	
χ	0.001	
ψ	0.001	
ω	0.001	
Ω	0.001	
Θ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	
\Omicron	0.001	
Π	0.001	
\Rho	0.001	
Σ	0.001	
Υ	0.001	
Φ	0.001	
Ψ	0.001	
Ξ	0.001	

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..527

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567930

	(10)	(20)														
Met	Pro	Ile	Asp	Lys	Ile	Phe	Lys	Asp	Ala	Ser	Glu	Glu	Lys	Gly		
1				5				10					15			
Glu	Arg	Ala	Arg	Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser		
			20					25					30	Asp		
Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu		
		35					40					45		Gln		
Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala		
	50					55					60			Thr		
Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu		
65					70					75				80		
Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr		
			85					90					95	Ser		
Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Val		
			100					105					110			
Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met		
		115					120					125		Ala		
Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn		
	130					135					140			Lys		
Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met		
145					150					155				160		
Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala		
			165						170					175		
Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu		
			180					185					190	Glu		
Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser		
		195					200					205		Phe		
Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln		
	210					215					220			Pro		
Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met		
225					230					235				240		

```

Thr Asp Lys Val Lys Ile Tyr Gly Ala Arg Val Arg Val Asp Ser Met
                245                250                255
Thr Lys Val Ala Glu Ile Glu Gly Ala Glu Lys Glu Lys Met Lys Asp
                260                265                270
Lys Val Lys Lys Ile Ile Gly His Gly Ile Asn Cys Phe Val Asn Arg
                275                280                285
Gln Leu Ile Tyr Asn Phe Pro Glu Glu Leu Phe Ala Asp Ala Gly Ile
                290                295                300
Leu Ala Ile Glu His Ala Asp Phe Glu Gly Ile Glu Arg Leu Gly Leu
305                310                315                320
Val Thr Gly Gly Glu Ile Ala Ser Thr Phe Asp Asn Pro Glu Ser Val
                325                330                335
Lys Leu Gly His Cys Lys Leu Ile Glu Glu Ile Met Ile Gly Glu Asp
                340                345                350
Lys Leu Ile His Phe Ser Gly Cys Glu Met Gly Gln Ala Cys Ser Ile
                355                360                365
Val Leu Arg Gly Ala Ser His His Val Leu Asp Glu Ala Glu Arg Ser
370                375                380
Leu His Asp Ala Leu Cys Val Leu Ser Gln Thr Val Asn Asp Thr Arg
385                390                395                400
Val Leu Leu Gly Gly Trp Pro Glu Met Val Met Ala Lys Glu Val
                405                410                415
Asp Glu Leu Ala Arg Lys Thr Ala Gly Lys Lys Ser His Ala Ile Glu
                420                425                430
Ala Phe Ser Arg Ala Leu Val Ala Ile Pro Thr Thr Ile Ala Asp Asn
                435                440                445
Ala Gly Leu Asp Ser Ala Glu Leu Val Ala Gln Leu Arg Ala Glu His
                450                455                460
His Thr Glu Gly Cys Asn Ala Gly Ile Asp Val Ile Thr Gly Ala Val
465                470                475                480
Gly Asp Met Glu Glu Arg Gly Ile Tyr Glu Ala Phe Lys Val Lys Gln
                485                490                495
Ala Val Leu Leu Ser Ala Thr Glu Ala Ser Glu Met Ile Leu Arg Val
                500                505                510
Asp Glu Ile Ile Thr Cys Ala Pro Arg Arg Arg Glu Asp Arg Met
                515                520                525

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 507 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..507

(D) OTHER INFORMATION: / Ceres Seq. ID 1567931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

```

Met Ala Ser Phe Val Gly Ala Met Ala Ile Ser Asp Leu Val Lys Ser
1          5          10          15
Thr Leu Gly Pro Lys Gly Met Asp Lys Ile Leu Gln Ser Thr Gly Arg
          20          25          30
Gly His Ala Val Thr Val Thr Asn Asp Gly Ala Thr Ile Leu Lys Ser
          35          40          45
Leu His Ile Asp Asn Pro Ala Lys Val Leu Val Asp Ile Ser Lys
          50          55          60
Val Gln Asp Asp Glu Val Gly Asp Gly Thr Thr Ser Val Val Val Leu
65          70          75          80
Ala Gly Glu Leu Leu Arg Glu Ala Glu Lys Leu Val Ala Ser Lys Ile
          85          90          95
His Pro Met Thr Ile Ile Ala Gly Tyr Arg Met Ala Ser Glu Cys Ala

```

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
2	2	1	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
3	3	2	1	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
4	4	3	2	1	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
5	5	4	3	2	1	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80																				

(i) SEQUENCE CHARACTERISTICS:

- ```
(i) SEQUENCE INFORMATION:
 (A) LENGTH: 500 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..500
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

|                                         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Met                                     | Ala | Ile | Ser | Asp | Leu | Val | Lys | Ser | Thr | Leu | Gly | Pro | Lys | Gly | Met |  |
| 1                                       |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp                                     | Lys | Ile | Leu | Gln | Ser | Thr | Gly | Arg | Gly | His | Ala | Val | Thr | Val | Thr |  |
|                                         |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn                                     | Asp | Gly | Ala | Thr | Ile | Leu | Lys | Ser | Leu | His | Ile | Asp | Asn | Pro | Ala |  |
|                                         |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala                                     | Lys | Val | Leu | Val | Asp | Ile | Ser | Lys | Val | Gln | Asp | Asp | Glu | Val | Gly |  |
|                                         | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp                                     | Gly | Thr | Thr | Ser | Val | Val | Val | Leu | Ala | Gly | Glu | Leu | Leu | Arg | Glu |  |
| 65                                      |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ala                                     | Glu | Lys | Leu | Val | Ala | Ser | Lys | Ile | His | Pro | Met | Thr | Ile | Ile | Ala |  |
|                                         |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly                                     | Tyr | Arg | Met | Ala | Ser | Glu | Cys | Ala | Arg | Asn | Ala | Leu | Leu | Lys | Arg |  |
|                                         |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val                                     | Ile | Asp | Asn | Lys | Asp | Asn | Ala | Glu | Lys | Phe | Arg | Ser | Asp | Leu | Leu |  |
|                                         |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys                                     | Ile | Ala | Met | Thr | Thr | Leu | Cys | Ser | Lys | Ile | Leu | Ser | Gln | Asp | Lys |  |
|                                         | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu                                     | His | Phe | Ala | Glu | Met | Ala | Val | Asp | Ala | Val | Phe | Arg | Leu | Lys | Gly |  |
| 145                                     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Ser                                     | Thr | Asn | Leu | Glu | Ala | Ile | Gln | Ile | Ile | Lys | Lys | Pro | Gly | Gly | Ser |  |
|                                         |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu                                     | Lys | Asp | Ser | Phe | Leu | Asp | Glu | Gly | Phe | Ile | Leu | Asp | Lys | Lys | Ile |  |
|                                         |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly                                     | Ile | Gly | Gln | Pro | Lys | Arg | Ile | Glu | Asn | Ala | Asn | Ile | Leu | Val | Ala |  |
|                                         |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Asn                                     | Thr | Ala | Met | Asp | Thr | Asp | Lys | Val | Lys | Ile | Tyr | Gly | Ala | Arg | Val |  |
|                                         | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Arg                                     | Val | Asp | Ser | Met | Thr | Lys | Val | Ala | Glu | Ile | Glu | Gly | Ala | Glu | Lys |  |
| 225                                     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Glu                                     | Lys | Met | Lys | Asp | Lys | Val | Lys | Lys | Ile | Ile | Gly | His | Gly | Ile | Asn |  |
|                                         |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Cys                                     | Phe | Val | Asn | Arg | Gln | Leu | Ile | Tyr | Asn | Phe | Pro | Glu | Glu | Leu | Phe |  |
|                                         |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ala                                     | Asp | Ala | Gly | Ile | Leu | Ala | Ile | Glu | His | Ala | Asp | Phe | Glu | Gly | Ile |  |
|                                         |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Glu                                     | Arg | Leu | Gly | Leu | Val | Thr | Gly | Gly | Glu | Ile | Ala | Ser | Thr | Phe | Asp |  |
|                                         | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Asn                                     | Pro | Glu | Ser | Val | Lys | Leu | Gly | His | Cys | Lys | Leu | Ile | Glu | Glu | Ile |  |
| 305                                     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Met                                     | Ile | Gly | Glu | Asp | Lys | Leu | Ile | His | Phe | Ser | Gly | Cys | Glu | Met | Gly |  |
|                                         |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Gln                                     | Ala | Cys | Ser |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:769:

(A) LENGTH: 1504 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1504

(D) OTHER INFORMATION: / Ceres Seq. ID 1567933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

| (X1) SEQUENCE ALIGNMENT: 111 |            |            |             |            |             |      |
|------------------------------|------------|------------|-------------|------------|-------------|------|
| atcttoagctt                  | gcttcctcct | caaaaggtga | aaaattagag  | cgagagagat | agagagagat  | 60   |
| ttcaaaaacga                  | aaatccagag | aaagggtctt | gccagtttag  | ggcatccttg | tgggtgagag  | 120  |
| agcgattgag                   | agattttcaa | aggaggaaga | ggaagatacg  | agtgtgagag | agatttagag  | 180  |
| ggagagaaga                   | aagagagatt | ctttttgagt | gtgttagggt  | ttcatttctc | ctgcagatct  | 240  |
| acatttatct                   | cttctcatgg | aacggaagct | tgtggttttg  | ggaatcccgt | gggatattga  | 300  |
| ttccgatggg                   | cttaaggatt | acatgtcaaa | atttgagac   | ttggaggatt | gtattgtcat  | 360  |
| gaaggatcga                   | tcaactggaa | gatctcgtg  | atttgatat   | gtcacttttg | cttcagccga  | 420  |
| agatgcaaa                    | aatgctttga | aaggtgaaca | ctttttagg   | aacagatctc | tggaagttaa  | 480  |
| agtggctaca                   | ccaaaggaag | agatgagaca | gcctgcaaaa  | aaagtgcga  | ggatcttcgt  | 540  |
| tgctcgatac                   | ccttcacag  | tctctgaatc | agatttccga  | agccattttg | agaggtatgg  | 600  |
| ggaaataaca                   | gacttataca | tgctaagga  | ctacaactcg  | aagcagcacc | gacgaatagg  | 660  |
| gtttatcaca                   | ttctctagt  | ctgattcagt | ggaggatctg  | atggaggaca | ctcatgatct  | 720  |
| gggaggtaca                   | acagttgctg | ttgatcgggc | aacaccaaaa  | gaggatgatc | atccgcctag  | 780  |
| gccaccgcc                    | gtggctagaa | tgtcgcgcc  | acccgtaggt  | attgcaggtg | gattttggagc | 840  |
| tccaggtggt                   | tatggagctt | atgatgctta | catttctgca  | gctacaagat | acgcagcgtc  | 900  |
| tggtgcccc                    | actttgtatg | ataatcccc  | cacgttttat  | ggaagagggg | aaccaaccac  | 960  |
| aaggggaata                   | ggaacaaga  | tctttgttgg | acggcttctc  | caagaagcat | ccgttgatga  | 1020 |
| tcttcgcat                    | tattttggga | gatttggcca | tattcaagat  | gcttatattc | caaaggaccc  | 1080 |
| aaagagaagt                   | ggacatagag | gttttggatt | tgttaccttt  | gctgaaaatg | gtgttcgaga  | 1140 |
| tcgtgtagcc                   | cgaagatctc | atgaaatctg | tggaacaagag | gtagcaatag | attcagcaac  | 1200 |
| gcctcttgat                   | gaagctggac | ctagcgctgg | cgcaagttcc  | atgttaagt  | cttctcgctc  | 1260 |
| tgaatatttt                   | ggtggctatg | gaggtcctat | gcgcgcattt  | ggtcgaatgt | atggaggcat  | 1320 |
| gagcttgac                    | gattggggat | atggaatgcc | aaacgcaaga  | ccatcaagac | cagaccggag  | 1380 |
| gtaccggcca                   | tactaatgca | gcagaccaac | atttcattag  | ctttgctttt | gtctttttat  | 1440 |
| agaaacttca                   | ctttgtcaga | tctattttaa | ttgaagcttt  | tgtttttgtt | ttacctctgg  | 1500 |
| aacc                         |            |            |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1567934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

| (X1) SEQUENCE DESCRIPTION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                       | Glu | Arg | Lys | Leu | Val | Val | Leu | Gly | Ile | Pro | Trp | Asp | Ile | Asp | Ser |
| 1                         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp                       | Gly | Leu | Lys | Asp | Tyr | Met | Ser | Lys | Phe | Gly | Asp | Leu | Glu | Asp | Cys |
|                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile                       | Val | Met | Lys | Asp | Arg | Ser | Thr | Gly | Arg | Ser | Arg | Gly | Phe | Gly | Tyr |
|                           |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Val Thr Phe Ala Ser Ala Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu  
50 55 60  
His Phe Leu Gly Asn Arg Ile Leu Glu Val Lys Val Ala Thr Pro Lys  
65 70 75 80  
Glu Glu Met Arg Gln Pro Ala Lys Lys Val Thr Arg Ile Phe Val Ala  
85 90 95  
Arg Ile Pro Ser Ser Val Ser Glu Ser Asp Phe Arg Ser His Phe Glu  
100 105 110  
Arg Tyr Gly Glu Ile Thr Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser  
115 120 125  
Lys Gln His Arg Arg Ile Gly Phe Ile Thr Phe Ser Ala Asp Ser  
130 135 140  
Val Glu Asp Leu Met Glu Asp Thr His Asp Leu Gly Gly Thr Thr Val  
145 150 155 160  
Ala Val Asp Arg Ala Thr Pro Lys Glu Asp Asp His Pro Pro Arg Pro  
165 170 175  
Pro Pro Val Ala Arg Met Ser Arg Pro Pro Val Ala Ile Ala Gly Gly  
180 185 190  
Phe Gly Ala Pro Gly Gly Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala  
195 200 205  
Ala Thr Arg Tyr Ala Ala Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro  
210 215 220  
Ala Thr Phe Tyr Gly Arg Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn  
225 230 235 240  
Lys Ile Phe Val Gly Arg Leu Pro Gln Glu Ala Ser Val Asp Asp Leu  
245 250 255  
Arg Asp Tyr Phe Gly Arg Phe Gly His Ile Gln Asp Ala Tyr Ile Pro  
260 265 270  
Lys Asp Pro Lys Arg Ser Gly His Arg Gly Phe Gly Phe Val Thr Phe  
275 280 285  
Ala Glu Asn Gly Val Ala Asp Arg Val Ala Arg Arg Ser His Glu Ile  
290 295 300  
Cys Gly Gln Glu Val Ala Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala  
305 310 315 320  
Gly Pro Ser Ala Gly Ala Ser Ser Met Leu Ser Ser Ser Arg Pro Glu  
325 330 335  
Tyr Phe Gly Gly Tyr Gly Gly Pro Met Arg Ala Phe Gly Arg Met Tyr  
340 345 350  
Gly Gly Met Ser Leu Asp Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg  
355 360 365  
Pro Ser Arg Pro Asp Arg Arg Tyr Arg Pro Tyr  
370 375

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..357

(D) OTHER INFORMATION: / Ceres Seq. ID 1567935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Met Ser Lys Phe Gly Asp Leu Glu Asp Cys Ile Val Met Lys Asp Arg  
1 5 10 15  
Ser Thr Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr Phe Ala Ser Ala  
20 25 30  
Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu His Phe Leu Gly Asn Arg  
35 40 45  
Ile Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu Met Arg Gln Pro



[illegible]

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..345  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Arg | Ser | Thr | Gly | Arg | Ser | Arg | Gly | Phe | Gly | Tyr | Val | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ala | Ser | Ala | Glu | Asp | Ala | Lys | Asn | Ala | Leu | Lys | Gly | Glu | His | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Asn | Arg | Ile | Leu | Glu | Val | Lys | Val | Ala | Thr | Pro | Lys | Glu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Arg | Gln | Pro | Ala | Lys | Lys | Val | Thr | Arg | Ile | Phe | Val | Ala | Arg | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Ser | Val | Ser | Glu | Ser | Asp | Phe | Arg | Ser | His | Phe | Glu | Arg | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Gly Glu Ile Thr Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser Lys Gln  
85 90 95  
His Arg Arg Ile Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser Val Glu  
100 105 110  
Asp Leu Met Glu Asp Thr His Asp Leu Gly Gly Thr Thr Val Ala Val  
115 120 125  
Asp Arg Ala Thr Pro Lys Glu Asp Asp His Pro Pro Arg Pro Pro Pro  
130 135 140  
Val Ala Arg Met Ser Arg Pro Pro Val Ala Ile Ala Gly Gly Phe Gly  
145 150 155 160  
Ala Pro Gly Gly Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala Ala Thr  
165 170 175  
Arg Tyr Ala Ala Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro Ala Thr  
180 185 190  
Phe Tyr Gly Arg Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn Lys Ile  
195 200 205  
Phe Val Gly Arg Leu Pro Gln Glu Ala Ser Val Asp Asp Leu Arg Asp  
210 215 220  
Tyr Phe Gly Arg Phe Gly His Ile Gln Asp Ala Tyr Ile Pro Lys Asp  
225 230 235 240  
Pro Lys Arg Ser Gly His Arg Gly Phe Gly Phe Val Thr Phe Ala Glu  
245 250 255  
Asn Gly Val Ala Asp Arg Val Ala Arg Arg Ser His Glu Ile Cys Gly  
260 265 270  
Gln Glu Val Ala Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala Gly Pro  
275 280 285  
Ser Ala Gly Ala Ser Ser Met Leu Ser Ser Ser Arg Pro Glu Tyr Phe  
290 295 300  
Gly Gly Tyr Gly Gly Pro Met Arg Ala Phe Gly Arg Met Tyr Gly Gly  
305 310 315 320  
Met Ser Leu Asp Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg Pro Ser  
325 330 335  
Arg Pro Asp Arg Arg Tyr Arg Pro Tyr  
340 345

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attttttcttg agagatccaa aaaaagtatc agaaagaaga agaagacgac tccaaaaaWc | 60  |
| gatgccgtat tacaccaacg acgacaatga cgtcgcacgat ttcaccgaat acgatccgat | 120 |
| gccttatagt ggaggctacg acatcaccgt gacatacggc cgttcaattc caccgtccga  | 180 |
| cgagacttgt taccctctct cctctctctc cggcgcagcc tttgagtatc agcgacctaa  | 240 |
| tttctcttct aacaacgatt cttctgctta tgacgaccaaa gctcttaaaa ccgagtacag | 300 |
| tagctatgca cgacccggac ccgttggtatc tggatctgat tttggccgga aacctaatc  | 360 |
| tggatatgga gggagaacgg aggttgagta tggccggaaa actgaatcgg agcatggatc  | 420 |
| tggctatggt gggagaattg agagcgatta cgtgaagcct agctatggcg gtcacgagga  | 480 |
| tgatggtgac gatggtcaca aaaaacatag tggttaaggat ggataagaag aaagatggta | 540 |
| gagtaagaag aaggagaagg agaagaagaa atagcagtac aaggagcatc atgatgatga  | 600 |
| agatgatgag tttaagaaga agaagaagaa agactataat gatgatgatg agaagaagaa  | 660 |
| tgattatgat gagaagaaga agaagaagaa agactataat gatgatgatg agaagaagaa  | 720 |
| gaagaagcat tataatgatg atgatgatga gaagaagaag aagcattaca atgatgatga  | 780 |
| tgatgagaag aagaagaaga aggagtatca tgatgatgag gataagaaga agaagaagca  | 840 |
| ctatgataat gatgatgatg agaagaagaa gaagaaggat catcgtgatg atgatgatga  | 900 |

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| gaagaagaag | aagaaggata | accaccacaa  | gggacatgac | taaaaaaggt  | ttatgatttg | 960  |
| ggatttgcac | tcttatgact | aaataagtaa  | caacaactta | agcacacttc  | tgctctctac | 1020 |
| gtttatgtca | attgttggtt | tgtttttgct  | tcgtgttttt | gctgctaaact | tcaatgagat | 1080 |
| cttcataagt | catatgtaat | atgttttagtg | tacgtgtttt | ctagtgatgt  | cgtttggtct | 1140 |

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Phe | Leu | Arg | Asp | Pro | Lys | Lys | Val | Ser | Glu | Arg | Arg | Arg | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gln | Lys | Xaa | Met | Pro | Tyr | Tyr | Thr | Asn | Asp | Asp | Asn | Asp | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Phe | Thr | Glu | Tyr | Asp | Pro | Met | Pro | Tyr | Ser | Gly | Gly | Tyr | Asp | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Val | Thr | Tyr | Gly | Arg | Ser | Ile | Pro | Pro | Ser | Asp | Glu | Thr | Cys | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Ser | Ser | Leu | Ser | Gly | Asp | Ala | Phe | Glu | Tyr | Gln | Arg | Pro | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Ser | Ser | Asn | Asn | Asp | Ser | Ser | Ala | Tyr | Asp | Asp | Gln | Ala | Leu | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Glu | Tyr | Ser | Ser | Tyr | Ala | Arg | Pro | Gly | Pro | Val | Gly | Ser | Gly | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Phe | Gly | Arg | Lys | Pro | Asn | Ser | Gly | Tyr | Gly | Gly | Arg | Thr | Glu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Tyr | Gly | Arg | Lys | Thr | Glu | Ser | Glu | His | Gly | Ser | Gly | Tyr | Gly | Gly |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Ile | Glu | Ser | Asp | Tyr | Val | Lys | Pro | Ser | Tyr | Gly | Gly | His | Glu | Asp |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Gly | Asp | Asp | Gly | His | Lys | Lys | His | Ser | Gly | Lys | Asp | Tyr | Asp | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Asp | Glu | Lys | Ser | Lys | Lys | Lys | Glu | Lys | Glu | Lys | Lys | Lys | Asp | Lys |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Lys | Lys | Asp | Gly | Asn | Asn | Ser | Glu | Asp | Asp | Glu | Phe | Lys | Lys | Lys | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 210 |

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Tyr | Tyr | Thr | Asn | Asp | Asp | Asn | Asp | Val | Asp | Asp | Phe | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Asp | Pro | Met | Pro | Tyr | Ser | Gly | Gly | Tyr | Asp | Ile | Thr | Val | Thr | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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(2) INFORMATION FOR SEQ ID NO:776:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..171
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567944
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:
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(2) INFORMATION FOR SEQ ID NO:777:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1257

(D) OTHER INFORMATION: / Ceres Seq. ID 1567945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| agtataaaga  | cgacaaagta | aaccaaiaaaa | aaaagagttc  | tcctacaatt  | ttcctaaatt  | 60   |
| cttggatttg  | agatttcact | ttttccgatt  | tgaacaatg   | atgataactc  | gcggtggagc  | 120  |
| caaggcggcg  | aaatcgctgt | taatggcggc  | tggaccacgt  | ttgttctoga  | cggtccgtac  | 180  |
| ggtttcgtct  | cacgaggctt | tatcagcaag  | ccatattttg  | aagcctgggtg | ttacatctgc  | 240  |
| ttggatatgg  | actagagctc | cgacgattgg  | aggtatgaga  | ttcgctagca  | cgatcactct  | 300  |
| gggagagaaa  | actccgatga | aggaggagga  | cgcgaaatcag | aagaaaacag  | agaacgaatc  | 360  |
| caccgggtgga | gacgccgccc | gaggtaataa  | caagggagat  | aaaggaatcg  | cgagctattg  | 420  |
| gggtgttgaa  | cctaataaga | ttactaaaga  | agatggttct  | gaatggaagt  | ggaactgttt  | 480  |
| caggccatgg  | gagacgtata | aagctgatat  | agatagatct  | gaagaagcat  | catgttccaa  | 540  |
| cgacgtttct  | tgatagaata | gcttattgga  | ctgttaaatac | tcttcgttgg  | cctaccgatt  | 600  |
| tgttcttcca  | gaggagatat | ggatgtcgag  | ctatgatgct  | tgaaactgta  | gcagcagtag  | 660  |
| ctggaatggg  | tggaggaatg | ttactacact  | gcaaatcgct  | tcgacgtttt  | gagcaaagtg  | 720  |
| gaggatggat  | taaggctctt | cttgaggaag  | cagagaatga  | gagaatgcat  | cttatgacat  | 780  |
| tcatggaagt  | cgcgaaaccg | aaatggtagc  | agagagcgct  | cgtgatcact  | gtgcaaggag  | 840  |
| tcttcttcaa  | cgcttatttc | cttgggttact | taatctctcc  | caagtttgct  | catcgtagtg  | 900  |
| ttgggtacct  | tgaagaagaa | gcgatccatt  | cttataactga | gtttctcaag  | gaacttgaca  | 960  |
| aaggtaacat  | tgagaatggt | cctgctccgg  | ctattgctat  | tgattactgg  | aggcttccctg | 1020 |
| ctgatgcgac  | Acttcgtgat | gttgtgatgg  | ttgttcgtgc  | tgacgaggct  | catcacctgtg | 1080 |
| atgtaaacca  | ttttgcatct | gatattcact  | accaaggtcg  | tgaactaaag  | gaagctccag  | 1140 |
| ctccaattgg  | gtatcattga | ttcgattaaa  | agaagagctt  | tttctcaagt  | ttaaaacttt  | 1200 |
| gttctaaaga  | atttaagtgc | tttgacttgt  | atatacataa  | tcacctctgc  | ttaagct     |      |

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1567946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Leu | Glu | Thr | Val | Ala | Ala | Val | Pro | Gly | Met | Val | Gly | Gly | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | His | Cys | Lys | Ser | Leu | Arg | Arg | Phe | Glu | Gln | Ser | Gly | Gly | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Lys | Ala | Leu | Leu | Glu | Glu | Ala | Glu | Asn | Glu | Arg | Met | His | Leu | Met |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Thr | Phe | Met | Glu | Val | Ala | Lys | Pro | Lys | Trp | Tyr | Glu | Arg | Ala | Leu | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Thr | Val | Gln | Gly | Val | Phe | Phe | Asn | Ala | Tyr | Phe | Leu | Gly | Tyr | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Ser | Pro | Lys | Phe | Ala | His | Arg | Met | Val | Gly | Tyr | Leu | Glu | Glu | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ile | His | Ser | Tyr | Thr | Glu | Phe | Leu | Lys | Glu | Leu | Asp | Lys | Gly | Asn |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ile | Glu | Asn | Val | Pro | Ala | Pro | Ala | Ile | Ala | Ile | Asp | Tyr | Trp | Arg | Leu |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Pro | Ala | Asp | Ala | Thr | Leu | Arg | Asp | Val | Val | Met | Val | Val | Arg | Ala | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Glu | Ala | His | His | Arg | Asp | Val | Asn | His | Phe | Ala | Ser | Asp | Ile | His | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Gly | Arg | Glu | Leu | Lys | Glu | Ala | Pro | Ala | Pro | Ile | Gly | Tyr | His |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:779:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 174 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..174  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567947  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

Met Leu Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Gly Met Leu  
1                  5                  10                  15  
Leu His Cys Lys Ser Leu Arg Arg Phe Glu Gln Ser Gly Gly Trp Ile  
                  20                  25                  30  
Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met Thr  
                  35                  40                  45  
Phe Met Glu Val Ala Lys Pro Lys Trp Tyr Glu Arg Ala Leu Val Ile  
                  50                  55                  60  
Thr Val Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Gly Tyr Leu Ile  
65                  70                  75                  80  
Ser Pro Lys Phe Ala His Arg Met Val Gly Tyr Leu Glu Glu Glu Ala  
                  85                  90                  95  
Ile His Ser Tyr Thr Glu Phe Leu Lys Glu Leu Asp Lys Gly Asn Ile  
                  100                  105                  110  
Glu Asn Val Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu Pro  
                  115                  120                  125  
Ala Asp Ala Thr Leu Arg Asp Val Val Met Val Val Arg Ala Asp Glu  
130                  135                  140  
Ala His His Arg Asp Val Asn His Phe Ala Ser Asp Ile His Tyr Gln  
145                  150                  155                  160  
Gly Arg Glu Leu Lys Glu Ala Pro Ala Pro Ile Gly Tyr His  
                  165                  170

(2) INFORMATION FOR SEQ ID NO:780:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 164 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..164  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567948  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

Met Val Gly Gly Met Leu Leu His Cys Lys Ser Leu Arg Arg Phe Glu  
1                  5                  10                  15  
Gln Ser Gly Gly Trp Ile Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu  
                  20                  25                  30  
Arg Met His Leu Met Thr Phe Met Glu Val Ala Lys Pro Lys Trp Tyr  
                  35                  40                  45  
Glu Arg Ala Leu Val Ile Thr Val Gln Gly Val Phe Phe Asn Ala Tyr  
50                  55                  60  
Phe Leu Gly Tyr Leu Ile Ser Pro Lys Phe Ala His Arg Met Val Gly  
65                  70                  75                  80  
Tyr Leu Glu Glu Glu Ala Ile His Ser Tyr Thr Glu Phe Leu Lys Glu  
                  85                  90                  95  
Leu Asp Lys Gly Asn Ile Glu Asn Val Pro Ala Pro Ala Ile Ala Ile  
                  100                  105                  110  
Asp Tyr Trp Arg Leu Pro Ala Asp Ala Thr Leu Arg Asp Val Val Met  
115                  120                  125

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Arg | Ala | Asp | Glu | Ala | His | His | Arg | Asp | Val | Asn | His | Phe | Ala |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Asp | Ile | His | Tyr | Gln | Gly | Arg | Glu | Leu | Lys | Glu | Ala | Pro | Ala | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Gly | Tyr | His |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1969
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| aacagctggc | catgctatgc  | atgtgttcat  | caatggccaa  | ttatctggat | ctgcgtatgg  | 60   |
| tagtttagac | tctcctaaac  | taacttttcg  | gaaaggtgtg  | aatctaagag | ctggtttcaa  | 120  |
| caaaattgcg | atactaagca  | tcgctgttgg  | tctcccgaat  | gtgggtccac | attttgagac  | 180  |
| atggaatgct | ggagtttttg  | gtccagtttc  | attgaatggt  | ctcaatggcg | gacgaaaaga  | 240  |
| tctatcatgg | cagaaatgga  | cttataaggt  | tggtcttaaa  | ggagagtctc | tgagtcttca  | 300  |
| ttcacttagt | gggagctcat  | cggttgagtg  | ggcagaaggt  | gcatttggtg | cacagaaaca  | 360  |
| accacttact | tggtacaaga  | cgactttctc  | tgctccagct  | ggaaattcgc | cattggctgt  | 420  |
| agacatggga | agcatgggaa  | aaggtcaaat  | atggataaat  | gggcagagct | tgggacgtca  | 480  |
| ctggcctgca | tataaagcag  | ttggttcttg  | cagcgagtgt  | tcttatactg | gaacattcag  | 540  |
| agaggacaag | tgcttaagaa  | actgtggaga  | ggcttctcaa  | agatggtacc | atgtcccaag  | 600  |
| gtcgtggcta | aaaccaagtg  | gcaatctatt  | ggttgctctt  | gaggagtggg | gaggagaccc  | 660  |
| gaacggaatc | tcgttgggtc  | gaagagaagt  | ggacagtgtg  | tgtgcagata | tctatgaatg  | 720  |
| gcaatcaacg | ctggtgaact  | accaattgca  | tgcttctgga  | aaagttaata | aaccattgca  | 780  |
| toccaaagtg | catttgcaat  | gcgggGcccg  | gacaaaagat  | caccaccgtg | aagtttgcta  | 840  |
| gtttcgggac | acctgaaggg  | acttgtggta  | gttaccgtca  | aggaagctgt | catgcccac   | 900  |
| actcctatga | cgctttcaac  | aaactatgtg  | ttgggcagaa  | ctggtgttct | gtaactgtag  | 960  |
| caccggagat | gtttgggtgga | gatccgtgtc  | caaagtgtat  | gaagaaactc | gcggtggaag  | 1020 |
| ccgtttgtgc | ttaaatgaaa  | gcagacgcag  | cagcaatcaa  | aagactgtaa | aggtgggttac | 1080 |
| ttacgcattc | ttacagggtt  | ctgatggtat  | tagtatgttt  | tatgaagaca | acagaagaag  | 1140 |
| ttggtatttt | tctagctcct  | tatttttatca | cggtggaagt  | tgtacaaagg | gacgcaaac   | 1200 |
| gccgttcaac | aatttgcaga  | gttgtgattt  | atatgtaaat  | aagcttgga  | agggtttggt  | 1260 |
| attgtaacc  | aagaaagaag  | atgaagaaga  | agaagcacat  | tgagactgga | gaatctaagt  | 1320 |
| ccatgtgtag | attctttctt  | ttcttcttct  | ttttcttttag | aaacaacaca | aaccccaaaa  | 1380 |
| acttaaaaaa | taactctaca  | gagatggctg  | ttggaatcct  | tgaggttagt | ctgatcagtg  | 1440 |
| gcaaaggctc | caagcgtctc  | gattttcttg  | gtaagataga  | tccatagtgt | gagatccaat  | 1500 |
| acaaagggca | aaccgcgcaa  | agcagcgttg  | ctaaagaaga  | tgagggtaga | aatccgacat  | 1560 |
| ggaatgataa | attgaaatgg  | agagcagagt  | ttcctggctc  | cggcgccgac | tacaaactca  | 1620 |
| tcgtcaaagt | catggatcat  | gatactttct  | cctctgacga  | tttcattggc | gaagccacgg  | 1680 |
| tacatgtgaa | agagctattg  | gaaatgggag  | tggagaaggg  | aacggcggag | ctaaggccaa  | 1740 |
| ccaagtacaa | cattgttgac  | tcgatctctc  | cctttgttgg  | cgagcttctc | attggagttt  | 1800 |
| cttactctct | tttgcaagac  | aggggaatgg  | atggagaaca  | gtttggagga | tggaagcata  | 1860 |
| gccaaagtga | ttagtttggt  | ttcttaaaac  | tgctgatttt  | atcttcttct | tctatcttta  | 1920 |
| gtgtcaacat | cattaagata  | ttcataagta  | caaaaaatta  | tttaaattg  |             |      |

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279

00000000-00000000

(D) OTHER INFORMATION: / Ceres Seq. ID 1567958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Thr Ala Gly His Ala Met His Val Phe Ile Asn Gly Gln Leu Ser Gly  
1 5 10 15  
Ser Ala Tyr Gly Ser Leu Asp Ser Pro Lys Leu Thr Phe Arg Lys Gly  
20 25 30  
Val Asn Leu Arg Ala Gly Phe Asn Lys Ile Ala Ile Leu Ser Ile Ala  
35 40 45  
Val Gly Leu Pro Asn Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly  
50 55 60  
Val Leu Gly Pro Val Ser Leu Asn Gly Leu Asn Gly Gly Arg Lys Asp  
65 70 75 80  
Leu Ser Trp Gln Lys Trp Thr Tyr Lys Val Gly Leu Lys Gly Glu Ser  
85 90 95  
Leu Ser Leu His Ser Leu Ser Gly Ser Ser Ser Val Glu Trp Ala Glu  
100 105 110  
Gly Ala Phe Val Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Thr Thr  
115 120 125  
Phe Ser Ala Pro Ala Gly Asn Ser Pro Leu Ala Val Asp Met Gly Ser  
130 135 140  
Met Gly Lys Gly Gln Ile Trp Ile Asn Gly Gln Ser Leu Gly Arg His  
145 150 155 160  
Trp Pro Ala Tyr Lys Ala Val Gly Ser Cys Ser Glu Cys Ser Tyr Thr  
165 170 175  
Gly Thr Phe Arg Glu Asp Lys Cys Leu Arg Asn Cys Gly Glu Ala Ser  
180 185 190  
Gln Arg Trp Tyr His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn  
195 200 205  
Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asp Pro Asn Gly Ile Ser  
210 215 220  
Leu Val Arg Arg Glu Val Asp Ser Val Cys Ala Asp Ile Tyr Glu Trp  
225 230 235 240  
Gln Ser Thr Leu Val Asn Tyr Gln Leu His Ala Ser Gly Lys Val Asn  
245 250 255  
Lys Pro Leu His Pro Lys Val His Leu Gln Cys Gly Ala Arg Thr Lys  
260 265 270  
Asp His His Arg Glu Val Cys  
275

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1567959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met His Val Phe Ile Asn Gly Gln Leu Ser Gly Ser Ala Tyr Gly Ser  
1 5 10 15  
Leu Asp Ser Pro Lys Leu Thr Phe Arg Lys Gly Val Asn Leu Arg Ala  
20 25 30  
Gly Phe Asn Lys Ile Ala Ile Leu Ser Ile Ala Val Gly Leu Pro Asn  
35 40 45  
Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro Val  
50 55 60  
Ser Leu Asn Gly Leu Asn Gly Gly Arg Lys Asp Leu Ser Trp Gln Lys  
65 70 75 80  
Trp Thr Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser Leu His Ser



85 90 95  
Leu Ser Gly Ser Ser Val Glu Trp Ala Glu Gly Ala Phe Val Ala  
100 105 110  
Gln Lys Gln Pro Leu Thr Trp Tyr Lys Thr Thr Phe Ser Ala Pro Ala  
115 120 125  
Gly Asn Ser Pro Leu Ala Val Asp Met Gly Ser Met Gly Lys Gly Gln  
130 135 140  
Ile Trp Ile Asn Gly Gln Ser Leu Gly Arg His Trp Pro Ala Tyr Lys  
145 150 155 160  
Ala Val Gly Ser Cys Ser Glu Cys Ser Tyr Thr Gly Thr Phe Arg Glu  
165 170 175  
Asp Lys Cys Leu Arg Asn Cys Gly Glu Ala Ser Gln Arg Trp Tyr His  
180 185 190  
Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn Leu Leu Val Val Phe  
195 200 205  
Glu Glu Trp Gly Gly Asp Pro Asn Gly Ile Ser Leu Val Arg Arg Glu  
210 215 220  
Val Asp Ser Val Cys Ala Asp Ile Tyr Glu Trp Gln Ser Thr Leu Val  
225 230 235 240  
Asn Tyr Gln Leu His Ala Ser Gly Lys Val Asn Lys Pro Leu His Pro  
245 250 255  
Lys Val His Leu Gln Cys Gly Ala Arg Thr Lys Asp His His Arg Glu  
260 265 270  
Val Cys

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1567960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

Met Lys Lys Lys Lys His Ile Glu Thr Gly Glu Ser Lys Ser Met Cys  
1 5 10 15  
Arg Phe Phe Phe Phe Phe Phe Phe Phe Phe Arg Asn Asn Thr Asn Pro  
20 25 30  
Lys Asn Leu Lys Asn Asn Ser Thr Glu Met Ala Val Gly Ile Leu Glu  
35 40 45  
Val Ser Leu Ile Ser Gly Lys Gly Leu Lys Arg Ser Asp Phe Leu Gly  
50 55 60  
Lys Ile Asp Pro Tyr Val Glu Ile Gln Tyr Lys Gly Gln Thr Arg Lys  
65 70 75 80  
Ser Ser Val Ala Lys Glu Asp Gly Gly Arg Asn Pro Thr Trp Asn Asp  
85 90 95  
Lys Leu Lys Trp Arg Ala Glu Phe Pro Gly Ser Gly Ala Asp Tyr Lys  
100 105 110  
Leu Ile Val Lys Val Met Asp His Asp Thr Phe Ser Ser Asp Asp Phe  
115 120 125  
Ile Gly Glu Ala Thr Val His Val Lys Glu Leu Leu Glu Met Gly Val  
130 135 140  
Glu Lys Gly Thr Ala Glu Leu Arg Pro Thr Lys Tyr Asn Ile Val Asp  
145 150 155 160  
Ser Asp Leu Ser Phe Val Gly Glu Leu Leu Ile Gly Val Ser Tyr Ser  
165 170 175  
Leu Leu Gln Asp Arg Gly Met Asp Gly Glu Gln Phe Gly Gly Trp Lys  
180 185 190

His Ser Gln Val Asp  
195

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1858
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| cttcttaaac | tcgtttttta  | ctctccatct  | ctaaaaagac | catcaacgct | cttctcttta | 60   |
| ttgcagcaga | aacagaaccc  | agttcaataa  | agcttttttg | taagaaaatt | tgaaaggaaa | 120  |
| agatatttga | aaactcgtag  | agagaaagtg  | gcacagaatc | tgaaattctg | acacttttta | 180  |
| ccacgaataa | tgattctctt  | ttgaaaaaca  | tgactcaatg | ttttctttat | ctttttctct | 240  |
| gaattgaggt | ttgtttgtac  | ttaaagtatg  | ctcctttatc | taccgttgac | tgattctact | 300  |
| cttttattct | caacttttct  | ctgatttgct  | cgtgtgttta | cttcaattcc | tcagttcttg | 360  |
| tgtagaaagt | tgagtttcat  | gtgatcaaaa  | ttggggcttt | actactttta | agagaatgag | 420  |
| tgacaaagac | gagtttgccg  | caaagaagaa  | ggatttggtc | aatacgccag | tggatttgta | 480  |
| tcctccggag | aatccaatgt  | tgggtccttc  | tcgatgatg  | gattcattca | gagaaactct | 540  |
| ttggcatgat | ggtggtttca  | atgtccacac  | agatgcagac | acttccttta | gaggtataaa | 600  |
| taatattgat | atacctcttg  | aaatgggttg  | gaatatggct | cagttccctg | cagattcagg | 660  |
| attcattgag | cgtgctgcaa  | agttttcttt  | ttttggKatg | tggtgaaatg | atgatgaacc | 720  |
| aacaacaatc | atctcttgga  | gttcocagatt | caactggctt | gtttcttcaa | gatacacaga | 780  |
| ttcctagtgg | atccaaacta  | gataatggtc  | ctcttactga | tgcatctaag | ttagtgaag  | 840  |
| agagatcgat | taataatgta  | tcagaggatt  | ctcaatctag | tggaggtaat | ggtcatgatg | 900  |
| atgctaagtg | tgggcaaaca  | tcttccaagg  | ggttttagta | taagaagagg | aaaagaattg | 960  |
| ggaaggattg | tgaagaagaa  | gaagataaaa  | agcaaaaagg | tgagcaaagt | ccaacttcaa | 1020 |
| atgcgaacaa | gacaaacagt  | gagaagcaac  | cttctgattc | tttaaaggat | gggtatatct | 1080 |
| acatgagggc | acgaagaggc  | caggctacta  | atagtcacag | tcttgctgaa | agagtaagaa | 1140 |
| gagaaaaaat | cagtgaaggg  | atgaagttct  | tgcaagatct | tgtgccagg  | tgcgacaagg | 1200 |
| tgactggtaa | ggcagttatg  | ctcgatgaaa  | tcattaacta | tgtgcaatca | cttcaatgcc | 1260 |
| aaatcgagtt | tttatcgatg  | aaactttcgg  | ctgtgaatcc | tgtgctcgat | tttaacctcg | 1320 |
| aaagcctcct | tgcaaaagat  | gctcttcaat  | catctgcacc | gacatttccc | cacaacatgt | 1380 |
| cgatgcttta | tctctctgta  | tcgtatctct  | ctcaaacagg | attcatgcaa | cogaacattt | 1440 |
| cctcaattgt | gctattgagt  | ggaggattaa  | aacggcagga | aacacatgga | tatgaaagtg | 1500 |
| atcaccacaa | tcttgctcac  | aagaaccatg  | aaaccggcac | tgacactgat | catgaagata | 1560 |
| caacagctga | catgaagggtg | gagccgtaga  | tgtttcttct | tcactttgta | ctcagcttta | 1620 |
| gctgctgata | tagtgcgccg  | cggtcgagaa  | ttttattaac | ttcgaacaga | agagtgaaaa | 1680 |
| cgaaacagag | gaggaagcag  | attttgtctt  | tgaaatattg | acagctcccg | gagaaagagt | 1740 |
| cgagagtaag | aatcaacaat  | gttgtgtaat  | gaatagctac | tgtctgcttc | ttttgtagct | 1800 |
| attgtctgct | tcttttttgt  | acatataaat  | ccatgcaagg | gaagaggaat | gttaatcc   |      |

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Val | Val | Ser | Met | Ser | Thr | Gln | Met | Gln | Thr | Leu | Pro | Leu | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ile | Ile | Ile | Leu | Ile | Tyr | Leu | Leu | Lys | Trp | Val | Gly | Ile | Trp | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |

Ser Ser Leu Gln Ile Gln Asp Ser Leu Ser Val Leu Gln Ser Phe Leu  
35 40 45  
Phe Leu Xaa Cys Gly Glu Met Met Met Asn Gln Gln Ser Ser Leu  
50 55 60  
Gly Val Pro Asp Ser Thr Gly Leu Phe Leu Gln Asp Thr Gln Ile Pro  
65 70 75 80  
Ser Gly Ser Lys Leu Asp Asn Gly Pro Leu Thr Asp Ala Ser Lys Leu  
85 90 95  
Val Lys Glu Arg Ser Ile Asn Asn Val Ser Glu Asp Ser Gln Ser Ser  
100 105 110  
Gly Gly Asn Gly His Asp Asp Ala Lys Cys Gly Gln Thr Ser Ser Lys  
115 120 125  
Gly Phe Ser Ser Lys Lys Arg Lys Arg Ile Gly Lys Asp Cys Glu Glu  
130 135 140  
Glu Glu Asp Lys Lys Gln Lys Asp Glu Gln Ser Pro Thr Ser Asn Ala  
145 150 155 160  
Asn Lys Thr Asn Ser Glu Lys Gln Pro Ser Asp Ser Leu Lys Asp Gly  
165 170 175  
Tyr Ile His Met Arg Ala Arg Arg Gly Gln Ala Thr Asn Ser His Ser  
180 185 190  
Leu Ala Glu Arg Val Arg Arg Glu Lys Ile Ser Glu Arg Met Lys Phe  
195 200 205  
Leu Gln Asp Leu Val Pro Gly Cys Asp Lys Val Thr Gly Lys Ala Val  
210 215 220  
Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Cys Gln Ile  
225 230 235 240  
Glu Phe Leu Ser Met Lys Leu Ser Ala Val Asn Pro Val Leu Asp Phe  
245 250 255  
Asn Leu Glu Ser Leu Leu Ala Lys Asp Ala Leu Gln Ser Ser Ala Pro  
260 265 270  
Thr Phe Pro His Asn Met Ser Met Leu Tyr Pro Pro Val Ser Tyr Leu  
275 280 285  
Ser Gln Thr Gly Phe Met Gln Pro Asn Ile Ser Ser Met Leu Leu Leu  
290 295 300  
Ser Gly Gly Leu Lys Arg Gln Glu Thr His Gly Tyr Glu Ser Asp His  
305 310 315 320  
His Asn Leu Val His Lys Asn His Glu Thr Gly Thr Ala Pro Asp His  
325 330 335  
Glu Asp Thr Thr Ala Asp Met Lys Val Glu Pro  
340 345

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1567966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

Met Val Val Ser Met Ser Thr Gln Met Gln Thr Leu Pro Leu Glu Val  
1 5 10 15  
Ile Ile Ile Leu Ile Tyr Leu Leu Lys Trp Val Gly Ile Trp Leu Ser  
20 25 30  
Ser Leu Gln Ile Gln Asp Ser Leu Ser Val Leu Gln Ser Phe Leu Phe  
35 40 45  
Leu Xaa Cys Gly Glu Met Met Met Asn Gln Gln Gln Ser Ser Leu Gly  
50 55 60  
Val Pro Asp Ser Thr Gly Leu Phe Leu Gln Asp Thr Gln Ile Pro Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Gly | Ser | Lys | Leu | Asp | Asn | Gly | Pro | Leu | Thr | Asp | Ala | Ser | Lys | Leu | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Glu | Arg | Ser | Ile | Asn | Asn | Val | Ser | Glu | Asp | Ser | Gln | Ser | Ser | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Asn | Gly | His | Asp | Asp | Ala | Lys | Cys | Gly | Gln | Thr | Ser | Ser | Lys | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ser | Ser | Lys | Lys | Arg | Lys | Arg | Ile | Gly | Lys | Asp | Cys | Glu | Glu | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Glu | Asp | Lys | Lys | Gln | Lys | Asp | Glu | Gln | Ser | Pro | Thr | Ser | Asn | Ala | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Thr | Asn | Ser | Glu | Lys | Gln | Pro | Ser | Asp | Ser | Leu | Lys | Asp | Gly | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | His | Met | Arg | Ala | Arg | Arg | Gly | Gln | Ala | Thr | Asn | Ser | His | Ser | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Glu | Arg | Val | Arg | Arg | Glu | Lys | Ile | Ser | Glu | Arg | Met | Lys | Phe | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Asp | Leu | Val | Pro | Gly | Cys | Asp | Lys | Val | Thr | Gly | Lys | Ala | Val | Met |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Asp | Glu | Ile | Ile | Asn | Tyr | Val | Gln | Ser | Leu | Gln | Cys | Gln | Ile | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Leu | Ser | Met | Lys | Leu | Ser | Ala | Val | Asn | Pro | Val | Leu | Asp | Phe | Asn |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Glu | Ser | Leu | Leu | Ala | Lys | Asp | Ala | Leu | Gln | Ser | Ser | Ala | Pro | Thr |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Phe | Pro | His | Asn | Met | Ser | Met | Leu | Tyr | Pro | Pro | Val | Ser | Tyr | Leu | Ser |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Thr | Gly | Phe | Met | Gln | Pro | Asn | Ile | Ser | Ser | Met | Leu | Leu | Leu | Ser |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Gly | Gly | Leu | Lys | Arg | Gln | Glu | Thr | His | Gly | Tyr | Glu | Ser | Asp | His | His |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Asn | Leu | Val | His | Lys | Asn | His | Glu | Thr | Gly | Thr | Ala | Pro | Asp | His | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Thr | Thr | Ala | Asp | Met | Lys | Val | Glu | Pro |     |     |     |     |     |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1567967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Gln | Met | Gln | Thr | Leu | Pro | Leu | Glu | Val | Ile | Ile | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Tyr | Leu | Leu | Lys | Trp | Val | Gly | Ile | Trp | Leu | Ser | Ser | Leu | Gln | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Asp | Ser | Leu | Ser | Val | Leu | Gln | Ser | Phe | Leu | Phe | Leu | Xaa | Cys | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Glu | Met | Met | Met | Asn | Gln | Gln | Gln | Ser | Ser | Leu | Gly | Val | Pro | Asp | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gly | Leu | Phe | Leu | Gln | Asp | Thr | Gln | Ile | Pro | Ser | Gly | Ser | Lys | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Asn | Gly | Pro | Leu | Thr | Asp | Ala | Ser | Lys | Leu | Val | Lys | Glu | Arg | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Asn | Asn | Val | Ser | Glu | Asp | Ser | Gln | Ser | Ser | Gly | Gly | Asn | Gly | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Asp Asp Ala Lys Cys Gly Gln Thr Ser Ser Lys Gly Phe Ser Ser Lys  
115 120 125  
Lys Arg Lys Arg Ile Gly Lys Asp Cys Glu Glu Glu Asp Lys Lys  
130 135 140  
Gln Lys Asp Glu Gln Ser Pro Thr Ser Asn Ala Asn Lys Thr Asn Ser  
145 150 155 160  
Glu Lys Gln Pro Ser Asp Ser Leu Lys Asp Gly Tyr Ile His Met Arg  
165 170 175  
Ala Arg Arg Gly Gln Ala Thr Asn Ser His Ser Leu Ala Glu Arg Val  
180 185 190  
Arg Arg Glu Lys Ile Ser Glu Arg Met Lys Phe Leu Gln Asp Leu Val  
195 200 205  
Pro Gly Cys Asp Lys Val Thr Gly Lys Ala Val Met Leu Asp Glu Ile  
210 215 220  
Ile Asn Tyr Val Gln Ser Leu Gln Cys Gln Ile Glu Phe Leu Ser Met  
225 230 235 240  
Lys Leu Ser Ala Val Asn Pro Val Leu Asp Phe Asn Leu Glu Ser Leu  
245 250 255  
Leu Ala Lys Asp Ala Leu Gln Ser Ser Ala Pro Thr Phe Pro His Asn  
260 265 270  
Met Ser Met Leu Tyr Pro Pro Val Ser Tyr Leu Ser Gln Thr Gly Phe  
275 280 285  
Met Gln Pro Asn Ile Ser Ser Met Leu Leu Leu Ser Gly Gly Leu Lys  
290 295 300  
Arg Gln Glu Thr His Gly Tyr Glu Ser Asp His His Asn Leu Val His  
305 310 315 320  
Lys Asn His Glu Thr Gly Thr Ala Pro Asp His Glu Asp Thr Thr Ala  
325 330 335  
Asp Met Lys Val Glu Pro  
340

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..522
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aaccctagct tgggtccacgc tcagagcatt ttggccattt gggccactca agttatcttg  | 60  |
| atgggagctg ttgaaggcta cagagtcgca ggaaatgggc cattgggaga ggccgaggac   | 120 |
| ttgctttacc ccggtggcag cttcgaccca ttgggtcttg ctaccgaccc agaggctttc   | 180 |
| gcggaagtga aggtgaagga gctcaagaac ggaagattgg ctatgttctc tatgtttgga   | 240 |
| ttcttcgttc aagccattgt cactggtaag ggaccgatag agaacccttg tgaccatttg   | 300 |
| gccgatccag tcaacaacaa cgcattgggccc ttcgcaacca actttgttcc cggaaagtga | 360 |
| gccaagtgtt atcagtttgt attttgcttt tctttcagtc ttttgaattc gaggtagaga   | 420 |
| catgaggaga aagagaaggt tgGtatgtga tggtttgaga ctttcagatg taaattkgca   | 480 |
| agactttgta tgatttgtca ttaatcaaac tcatttttct ct                      |     |

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

00000000-00000000

(D) OTHER INFORMATION: / Ceres Seq. ID 1567976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala Ile Trp Ala Thr  
1 5 10 15  
Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg Val Ala Gly Asn  
20 25 30  
Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro Gly Gly Ser Phe  
35 40 45  
Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe Ala Glu Leu Lys  
50 55 60  
Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe Ser Met Phe Gly  
65 70 75 80  
Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro Ile Glu Asn Leu  
85 90 95  
Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala Trp Ala Phe Ala  
100 105 110  
Thr Asn Phe Val Pro Gly Lys  
115

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1567977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

Met Gly Ala Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly  
1 5 10 15  
Glu Ala Glu Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly  
20 25 30  
Leu Ala Thr Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu  
35 40 45  
Lys Asn Gly Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln  
50 55 60  
Ala Ile Val Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu  
65 70 75 80  
Ala Asp Pro Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val  
85 90 95  
Pro Gly Lys

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..852

(D) OTHER INFORMATION: / Ceres Seq. ID 1567993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ctttggaggt cagggaaagg aaaaatcacg ttctacctcg atcctgaggt agattttaca | 60  |
| caggagaaat ctgatactca ggaaaattca gggaaaagag gagacgtatt gttccttcca | 120 |
| caaaggcctt atatggttct gggatctttg cgtcaGcaat tgctttatcc tacctggagt | 180 |
| gcaactgtgg aggagacgac acctggtggc agtaatatg acggttcacc acctctgctg  | 240 |
| attagagagg acggaaatga aaagccgaca acagatgatc tgatgcggac tctagagaag | 300 |

(2) INFORMATION FOR SEQ ID NO:793:

(A) LENGTH: 227 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1567994

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1567995

|            |     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Val | Leu        | Gly        | Ser<br>5   | Leu        | Arg        | Gln        | Gln        | Leu<br>10  | Leu        | Tyr        | Pro        | Thr        | Trp<br>15  | Ser        |
| Ala        | Thr | Val        | Glu        | Glu        | Thr        | Thr        | Pro        | Gly<br>25  | Gly        | Ser        | Asn        | Ile        | Asp<br>30  | Gly        | Ser        |
| Pro        | Pro | Leu        | Leu        | Ile        | Arg        | Glu        | Asp<br>40  | Gly        | Asn        | Glu        | Lys        | Pro<br>45  | Thr        | Thr        | Asp        |
| Asp        | Leu | Met        | Arg        | Thr        | Leu        | Glu        | Lys<br>55  | Val        | Cys        | Leu        | Gly<br>60  | His        | Ile        | Ala        | Asp        |
| Arg<br>65  | Phe | Gly        | Gly        | Leu        | Asp<br>70  | Ser        | Ile        | His        | Glu        | Trp<br>75  | Ser        | Ser        | Val        | Leu        | Ser<br>80  |
| Leu        | Gly | Glu        | Gln        | Gln        | Arg<br>85  | Leu        | Ala        | Phe        | Ala<br>90  | Arg        | Leu        | Leu        | Leu        | Ser<br>95  | Gln        |
| Pro        | Lys | Leu        | Ala<br>100 | Leu        | Leu        | Asp        | Glu        | Ser<br>105 | Thr        | Ser        | Ala        | Leu        | Asp<br>110 | Glu        | Ala        |
| Asn        | Glu | Ala<br>115 | Phe        | Leu        | Tyr        | Gln        | Gln<br>120 | Ile        | Gln        | Ser        | Ala        | Gly<br>125 | Ile        | Thr        | Tyr        |
| Ile<br>130 | Ser | Ile        | Gly        | His        | Arg        | Arg<br>135 | Thr        | Leu        | Thr        | Lys        | Phe<br>140 | His        | Asn        | Lys        | Ile        |
| Leu<br>145 | Gln | Ile        | Ser        | Thr        | Ala<br>150 | Asp        | Pro        | Lys        | Ser        | Asn<br>155 | Glu        | Arg        | Asn        | Trp        | Arg<br>160 |
| Ile        | Glu | Asp        | Val        | Asp<br>165 | Ala        | Gln        | Asp        | Ser        | Leu<br>170 | Tyr        | Gly        | Arg        | Leu        | Asn<br>175 | Gln        |
| Lys        | Glu | Val        | Pro<br>180 | Ser        | Gly        | Ser        |            |            |            |            |            |            |            |            |            |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1567996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

[illegible]

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1336 base pairs

(B) TYPE: nucleic acid



- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1336  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567997  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

```
caacatatgg ccaagaccca ctttgattgc ttggaaaatt atattttgct atggagcatt 60
tgaagctatt cttcagctgc ttctgcctgg taaaagagtt gaggggtccaa tatctccagc 120
cggaaaccca ccagtttaca aggccaatgg tctggctgct tactttgtga cactagcaac 180
ctatcttggg ctttggtggg ttggaatcct caacctgca attgtctatg atcacttggg 240
tgaaatatct tcggcactaa tattcggaag cttcatatct tgtgttttgt tgtacataaa 300
aggccatggt gcaccttcac caagtgactc tggttcatgt ggtaacctaa taattgactt 360
ctattggggc atggagttgt accctcgaat tggtaagagc tttgacatca aggtgtttac 420
taattgcaga ttcggaatga tgtcttgggc agttcttgca gtcacgtact gcataaaaca 480
gtatgaaata aatggcaaag tatctgattc aatgctgggt aacaccatcc tgatgctggg 540
gtatgtcaca aaattcttct ggtgggaagc tggttattgg aacaccatgg acattgcaca 600
tgacogagct ggattctata tatgctgggg ttgtctagtg tgggtgcctt ctgtctacac 660
ttctccaggc atgtaccttg tgaaccaccc cgctgaactc ggaactcagt tggcaatata 720
cattctcggt gcaggaattc tgtgcattta cataaactat gactgtgata gacaaaggca 780
agagttcagg aggacaaacg ggaatgtttt ggtttgggga agagccccgt caaagattgt 840
ggcgctgtat actacaacat ctggtgaaac taaaactagt cttctcttaa cgtctggatg 900
gtggggattg gctcgctcatt tccattatgt tcctgagatc ttaagtgcct tcttctggac 960
Cgtaccggct ctcttcgata acttcttggc atacttctac gtcataattc tcacccttct 1020
tctctttgat cgagccaaga gagacgatga ccgatgccga tcaaagtatg ggaaatattg 1080
gaagctgtat tgtgagaaag tcaaatacag gatcattccg ggaatttatt gattgtaacg 1140
aagtctgttg ttctcatttt ctacttatta cgtaattcga aacgttggaa tcatcaaaaag 1200
accgtgccaa aacaaaaatg caaattgatg cgatagacat tcttttgctg atttgtatgc 1260
tataggtttt caaatctcta gCtacgctta tgtatttccc tagattatca aagttagcct 1320
gccgttttct aatttt
```

(2) INFORMATION FOR SEQ ID NO:797:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 376 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..376  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567998  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

```
Asn Ile Trp Pro Arg Pro Thr Leu Ile Ala Trp Lys Ile Ile Phe Cys
1 5 10 15
Tyr Gly Ala Phe Glu Ala Ile Leu Gln Leu Leu Leu Pro Gly Lys Arg
20 25 30
Val Glu Gly Pro Ile Ser Pro Ala Gly Asn Arg Pro Val Tyr Lys Ala
35 40 45
Asn Gly Leu Ala Ala Tyr Phe Val Thr Leu Ala Thr Tyr Leu Gly Leu
50 55 60
Trp Trp Phe Gly Ile Phe Asn Pro Ala Ile Val Tyr Asp His Leu Gly
65 70 75 80
Glu Ile Phe Ser Ala Leu Ile Phe Gly Ser Phe Ile Phe Cys Val Leu
85 90 95
Leu Tyr Ile Lys Gly His Val Ala Pro Ser Ser Ser Asp Ser Gly Ser
100 105 110
Cys Gly Asn Leu Ile Ile Asp Phe Tyr Trp Gly Met Glu Leu Tyr Pro
115 120 125
Arg Ile Gly Lys Ser Phe Asp Ile Lys Val Phe Thr Asn Cys Arg Phe
130 135 140
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Tyr | Pro | Arg | Ile | Gly | Lys | Ser | Phe | Asp | Ile | Lys | Val | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asn | Cys | Arg | Phe | Gly | Met | Met | Ser | Trp | Ala | Val | Leu | Ala | Val | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Cys | Ile | Lys | Gln | Tyr | Glu | Ile | Asn | Gly | Lys | Val | Ser | Asp | Ser | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Asn | Thr | Ile | Leu | Met | Leu | Val | Tyr | Val | Thr | Lys | Phe | Phe | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Glu | Ala | Gly | Tyr | Trp | Asn | Thr | Met | Asp | Ile | Ala | His | Asp | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Phe | Tyr | Ile | Cys | Trp | Gly | Cys | Leu | Val | Trp | Val | Pro | Ser | Val | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Ser | Pro | Gly | Met | Tyr | Leu | Val | Asn | His | Pro | Val | Glu | Leu | Gly | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Leu | Ala | Ile | Tyr | Ile | Leu | Val | Ala | Gly | Ile | Leu | Cys | Ile | Tyr | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Tyr | Asp | Cys | Asp | Arg | Gln | Arg | Gln | Glu | Phe | Arg | Arg | Thr | Asn | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Cys | Leu | Val | Trp | Gly | Arg | Ala | Pro | Ser | Lys | Ile | Val | Ala | Ser | Tyr |

(2) INFORMATION FOR SEQ ID NO:799:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

[illegible]

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 564 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..564

(D) OTHER INFORMATION: / Ceres Seq. ID 1568007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

```
attaaattcg tagcgttcaa tgctggccct aggatctgtc tgggtaagga tctggcgtat 60
ctacaaatga aatcaattgc atcggcggtt ttgCtccgcc accggttgac ggtggtgacg 120
gggcataagg tggaacagaa gatgtcgtta actttattca tgaagtacgg tcttttagtt 180
aacgtccacg aacgggattt aacggcaatc gcggcggatc tacgagagtg taaatctaac 240
gtcgtcaatg acgggggttg taacggcggt tcaagttagg tagggtaggt gaatcaatcg 300
catctatcat ttactgtcta ttagagagtg gcactcgctt tttgggcgcg tgttaaatac 360
gccgttcttt ggccaactca gcaaggcacg ccagttgtc gtcggttggt tggctgcata 420
attcaataga ggtaattttg caaagtgcgt ttgttctgtt cctttttttt tactcatatg 480
ccttggtaat tcagacagta aaatttgatt tcattatttt gtaagcatct ctcaatttga 540
tttaataaat cttattctaa aggc
```

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1568008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

```
Ile Lys Phe Val Ala Phe Asn Ala Gly Pro Arg Ile Cys Leu Gly Lys
1 5 10 15
Asp Leu Ala Tyr Leu Gln Met Lys Ser Ile Ala Ser Ala Val Leu Leu
20 25 30
Arg His Arg Leu Thr Val Val Thr Gly His Lys Val Glu Gln Lys Met
35 40 45
Ser Leu Thr Leu Phe Met Lys Tyr Gly Leu Leu Val Asn Val His Glu
50 55 60
Arg Asp Leu Thr Ala Ile Ala Ala Asp Leu Arg Glu Cys Lys Ser Asn
65 70 75 80
Val Val Asn Asp Gly Val Gly Asn Gly Val Ser Ser
85 90
```

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1568009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```
Met Lys Ser Ile Ala Ser Ala Val Leu Leu Arg His Arg Leu Thr Val
1 5 10 15
Val Thr Gly His Lys Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met
20 25 30
Lys Tyr Gly Leu Leu Val Asn Val His Glu Arg Asp Leu Thr Ala Ile
35 40 45
Ala Ala Asp Leu Arg Glu Cys Lys Ser Asn Val Val Asn Asp Gly Val
50 55 60
Gly Asn Gly Val Ser Ser
```

65

70

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| ctataaatag  | aacaccatgg  | aaaggaaaag | agacacacac  | aaataaagaa | aacgaaaaca | 60   |
| ctttttatact | tatatgtcag  | ccatggctcc | gactttgcaa  | ggccagtgga | tcaaggtggg | 120  |
| gcagaaagga  | ggaacgggac  | caggacctag | aagttcacac  | ggcatagccg | cggtcggaga | 180  |
| caagctctac  | agtttcggcg  | gcgagttaac | accaaacaaa  | cacatcgaca | aagacctcta | 240  |
| cgtctttgac  | ttcaacactc  | aaacttggtc | aatcgctcaa  | cccaaaggag | acgccccaac | 300  |
| tgtatcctgc  | ttaggcgtgc  | gcatgggtgc | cgtgggaact  | aagatctata | tctttggagg | 360  |
| ccgcgatgag  | aaccgcaact  | tcgaaaactt | tcgctcctac  | gatacgggtg | catccgagtg | 420  |
| gacattcctg  | acgaagcttg  | atgaggtggg | aggaccgcag  | gctcgtactt | tccattcgat | 480  |
| ggcttcggat  | gaaaaccatg  | tgtatgtatt | cggtgggggtg | agcaaaggcg | gtactatgaa | 540  |
| tactcccacg  | cggttcagga  | caatcgaggc | gtataacatt  | gctggggaaa | tgggctcagc | 600  |
| taccggatcc  | aggagataac  | ttcgagaaaa | gaggaggagc  | gggattcgct | gtggtacaag | 660  |
| ggaagatttg  | ggtggtttat  | gggtttgcga | cctcgattgt  | gcccgagggc | aaagatgact | 720  |
| atgagtctaa  | tgctgtgcaa  | ttctatgata | cggcttccaa  | aaagtggacc | gaagtagaga | 780  |
| ctacaggagc  | gaaaccttcc  | gcaaggagcg | tgtttgccca  | tgcggtagtg | ggaaagtata | 840  |
| taataatatt  | tgcagggtgag | gtatggcctg | atctcaatgg  | gcattatggt | cccGggacgc | 900  |
| tgtccaatga  | gggatatgcg  | ttggacaccg | agacactggt  | gtgggaaaag | ttgggagaag | 960  |
| aaggtgcacc  | agccatacca  | cgaggttgga | ctgcctatac  | tgctgccact | gtcgatggaa | 1020 |
| agaatggcct  | cctcatgcat  | ggcggaaagc | ttccgaccaa  | cgagcgaact | gatgatctct | 1080 |
| acttctatgc  | ggtcaattca  | gcttaatgcg | tgtcaagatt  | tgtgttgtgt | gtgtggctcg | 1140 |
| ttaatatatta | ttactatcca  | ataaggagcc | ctaattggtt  | gctgtattat | tacaaattat | 1200 |
| ctgtgtgtgg  | gactcgtoga  | gcttttttac | tctaattgag  | cctactcatg | gttgtgtgag | 1260 |
| tggttcctca  | agtatcattg  | tccaataagg | agccaattta  | tttatggctg | gctgttttat | 1320 |
| tacaaattat  | gtgtatgtgt  | taataattaa | agattgaatt  | atct       |            |      |

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Thr | Leu | Gln | Gly | Gln | Trp | Ile | Lys | Val | Gly | Gln | Lys | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Thr | Gly | Pro | Gly | Pro | Arg | Ser | Ser | His | Gly | Ile | Ala | Ala | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Lys | Leu | Tyr | Ser | Phe | Gly | Gly | Glu | Leu | Thr | Pro | Asn | Lys | His | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Lys | Asp | Leu | Tyr | Val | Phe | Asp | Phe | Asn | Thr | Gln | Thr | Trp | Ser | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Gln | Pro | Lys | Gly | Asp | Ala | Pro | Thr | Val | Ser | Cys | Leu | Gly | Val | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Val | Ala | Val | Gly | Thr | Lys | Ile | Tyr | Ile | Phe | Gly | Gly | Arg | Asp | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Arg | Asn | Phe | Glu | Asn | Phe | Arg | Ser | Tyr | Asp | Thr | Val | Thr | Ser | Glu |

100 105 110  
Trp Thr Phe Leu Thr Lys Leu Asp Glu Val Gly Gly Pro Glu Ala Arg  
115 120 125  
Thr Phe His Ser Met Ala Ser Asp Glu Asn His Val Tyr Val Phe Gly  
130 135 140  
Gly Val Ser Lys Gly Gly Thr Met Asn Thr Pro Thr Arg Phe Arg Thr  
145 150 155 160  
Ile Glu Ala Tyr Asn Ile Ala Gly Glu Met Gly Ser Ala Thr Gly Ser  
165 170 175  
Arg Arg

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

Met Val Ala Val Gly Thr Lys Ile Tyr Ile Phe Gly Gly Arg Asp Glu  
1 5 10 15  
Asn Arg Asn Phe Glu Asn Phe Arg Ser Tyr Asp Thr Val Thr Ser Glu  
20 25 30  
Trp Thr Phe Leu Thr Lys Leu Asp Glu Val Gly Gly Pro Glu Ala Arg  
35 40 45  
Thr Phe His Ser Met Ala Ser Asp Glu Asn His Val Tyr Val Phe Gly  
50 55 60  
Gly Val Ser Lys Gly Gly Thr Met Asn Thr Pro Thr Arg Phe Arg Thr  
65 70 75 80  
Ile Glu Ala Tyr Asn Ile Ala Gly Glu Met Gly Ser Ala Thr Gly Ser  
85 90 95  
Arg Arg

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

Met Gly Ile Met Val Pro Gly Arg Cys Pro Met Arg Asp Met Arg Trp  
1 5 10 15  
Thr Pro Arg His Trp Cys Gly Lys Ser Trp Glu Lys Lys Val His Gln  
20 25 30  
Pro Tyr His Glu Val Gly Leu Pro Ile Leu Leu Pro Leu Ser Met Glu  
35 40 45  
Arg Met Ala Ser Ser Cys Met Ala Glu Ser Phe Arg Pro Thr Ser Glu  
50 55 60  
Leu Met Ile Ser Thr Ser Met Arg Ser Ile Gln Leu Asn Ala Cys Gln  
65 70 75 80  
Asp Leu Cys Cys Val Cys Gly Ser Leu Ile Phe Ile Thr Ile Gln  
85 90 95

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| aatcgaaaaa | acctcggcta | gatctcacat  | ttataatctc | tcactctctc | tctttctctg | 60   |
| gtaaataaat | aagtgtgaag | atgggtggctg | tgaggcgaag | gagaacacaa | gcgtcaaacc | 120  |
| ctagatccga | accaccgcaa | cacatgtcgg  | atcatgattc | cgattccgat | tgggatacag | 180  |
| tctgcgaaga | atgcagttcc | ggtaaacaac  | cagcaaagct | gcttctttgc | gacaaatgcg | 240  |
| ataaagggkt | Ctcatctttt | ctgtctcaga  | cogatcctcg | tttcagttcc | caaaggctct | 300  |
| tggttctgcc | cttcttggtc | caaacatcag  | atccctaaat | ctttccctct | tattcagact | 360  |
| aaaattatag | atttcttccg | gattaagcgg  | tctccagatt | catctcaaat | ctcaagttct | 420  |
| tcagatagta | ttgggaagaa | acggaaaaag  | actagcttgg | tgatgtcaaa | gaagaagaga | 480  |
| aggcttcttc | catacaatcc | tagcaatgat  | cctcaaagga | ggctagagca | aatggcgtct | 540  |
| ctggccactg | cgttgagagc | ttccaacacc  | aagttcagca | atgagcttac | ttatgtatct | 600  |
| ggaaaggctc | caagatctgc | aaaccaagct  | gcttttgaga | aaggaggcat | gcaggttcta | 660  |
| tctaaagaag | gcgtagagac | cttagccttg  | tgcaagaaaa | tgatggacct | cggtgaatgc | 720  |
| ccgccactta | tggtcgtctt | cgatccttat  | gaagggttca | cagtagaggc | ggacagggtt | 780  |
| ataaaagact | ggacaattat | cacagagtat  | ggtggagatg | ttgattatct | gagcaataga | 840  |
| gaagatgact | atgatggaga | cagtatgatg  | actctacttc | atgcctctga | tccttcgcga | 900  |
| tgtctcgtaa | tttgccctga | cagacgcagt  | aacatcgccc | ggttcatcag | tggcatcaac | 960  |
| aatcactcac | cagaaggag  | gaagaagcag  | aacctgaagt | gtgtgagggt | caacatcaac | 1020 |
| ggagaagcta | gggttcttct | cgtagctaat  | agagacatat | cgaaagggga | aagattgtat | 1080 |
| tatgattaca | acggatatga | acatgagtat  | ccaactgaac | attttgt    |            |      |

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..324
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Pro | Ile | Pro | Ile | Gly | Ile | Gln | Ser | Ala | Lys | Asn | Ala | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Asn | Asn | Gln | Gln | Ser | Cys | Phe | Phe | Ala | Thr | Asn | Ala | Ile | Lys | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | His | Leu | Phe | Cys | Leu | Arg | Pro | Ile | Leu | Val | Ser | Val | Pro | Lys | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Trp | Phe | Cys | Pro | Ser | Cys | Ser | Lys | His | Gln | Ile | Pro | Lys | Ser | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Ile | Gln | Thr | Lys | Ile | Ile | Asp | Phe | Phe | Arg | Ile | Lys | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Asp | Ser | Ser | Gln | Ile | Ser | Ser | Ser | Ser | Asp | Ser | Ile | Gly | Lys | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Lys | Lys | Thr | Ser | Leu | Val | Met | Ser | Lys | Lys | Lys | Arg | Arg | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Tyr | Asn | Pro | Ser | Asn | Asp | Pro | Gln | Arg | Arg | Leu | Glu | Gln | Met | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ser | Leu | Ala | Thr | Ala | Leu | Arg | Ala | Ser | Asn | Thr | Lys | Phe | Ser | Asn | Glu |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |     | 140 |     |

Leu Thr Tyr Val Ser Gly Lys Ala Pro Arg Ser Ala Asn Gln Ala Ala  
145 150 155 160  
Phe Glu Lys Gly Gly Met Gln Val Leu Ser Lys Glu Gly Val Glu Thr  
165 170 175  
Leu Ala Leu Cys Lys Lys Met Met Asp Leu Gly Glu Cys Pro Pro Leu  
180 185 190  
Met Val Val Phe Asp Pro Tyr Glu Gly Phe Thr Val Glu Ala Asp Arg  
195 200 205  
Phe Ile Lys Asp Trp Thr Ile Ile Thr Glu Tyr Val Gly Asp Val Asp  
210 215 220  
Tyr Leu Ser Asn Arg Glu Asp Asp Tyr Asp Gly Asp Ser Met Met Thr  
225 230 235 240  
Leu Leu His Ala Ser Asp Pro Ser Arg Cys Leu Val Ile Cys Pro Asp  
245 250 255  
Arg Arg Ser Asn Ile Ala Arg Phe Ile Ser Gly Ile Asn Asn His Ser  
260 265 270  
Pro Glu Gly Arg Lys Lys Gln Asn Leu Lys Cys Val Arg Phe Asn Ile  
275 280 285  
Asn Gly Glu Ala Arg Val Leu Leu Val Ala Asn Arg Asp Ile Ser Lys  
290 295 300  
Gly Glu Arg Leu Tyr Tyr Asp Tyr Asn Gly Tyr Glu His Glu Tyr Pro  
305 310 315 320  
Thr Glu His Phe

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1568039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

Met Ser Lys Lys Lys Arg Arg Leu Leu Pro Tyr Asn Pro Ser Asn Asp  
1 5 10 15  
Pro Gln Arg Arg Leu Glu Gln Met Ala Ser Leu Ala Thr Ala Leu Arg  
20 25 30  
Ala Ser Asn Thr Lys Phe Ser Asn Glu Leu Thr Tyr Val Ser Gly Lys  
35 40 45  
Ala Pro Arg Ser Ala Asn Gln Ala Ala Phe Glu Lys Gly Gly Met Gln  
50 55 60  
Val Leu Ser Lys Glu Gly Val Glu Thr Leu Ala Leu Cys Lys Lys Met  
65 70 75 80  
Met Asp Leu Gly Glu Cys Pro Pro Leu Met Val Val Phe Asp Pro Tyr  
85 90 95  
Glu Gly Phe Thr Val Glu Ala Asp Arg Phe Ile Lys Asp Trp Thr Ile  
100 105 110  
Ile Thr Glu Tyr Val Gly Asp Val Asp Tyr Leu Ser Asn Arg Glu Asp  
115 120 125  
Asp Tyr Asp Gly Asp Ser Met Met Thr Leu Leu His Ala Ser Asp Pro  
130 135 140  
Ser Arg Cys Leu Val Ile Cys Pro Asp Arg Arg Ser Asn Ile Ala Arg  
145 150 155 160  
Phe Ile Ser Gly Ile Asn Asn His Ser Pro Glu Gly Arg Lys Lys Gln  
165 170 175  
Asn Leu Lys Cys Val Arg Phe Asn Ile Asn Gly Glu Ala Arg Val Leu  
180 185 190  
Leu Val Ala Asn Arg Asp Ile Ser Lys Gly Glu Arg Leu Tyr Tyr Asp



195 200 205  
Tyr Asn Gly Tyr Glu His Glu Tyr Pro Thr Glu His Phe  
210 215 220

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

Met Ala Ser Leu Ala Thr Ala Leu Arg Ala Ser Asn Thr Lys Phe Ser  
1 5 10 15  
Asn Glu Leu Thr Tyr Val Ser Gly Lys Ala Pro Arg Ser Ala Asn Gln  
20 25 30  
Ala Ala Phe Glu Lys Gly Gly Met Gln Val Leu Ser Lys Glu Gly Val  
35 40 45  
Glu Thr Leu Ala Leu Cys Lys Lys Met Met Asp Leu Gly Glu Cys Pro  
50 55 60  
Pro Leu Met Val Val Phe Asp Pro Tyr Glu Gly Phe Thr Val Glu Ala  
65 70 75 80  
Asp Arg Phe Ile Lys Asp Trp Thr Ile Ile Thr Glu Tyr Val Gly Asp  
85 90 95  
Val Asp Tyr Leu Ser Asn Arg Glu Asp Asp Tyr Asp Gly Asp Ser Met  
100 105 110  
Met Thr Leu Leu His Ala Ser Asp Pro Ser Arg Cys Leu Val Ile Cys  
115 120 125  
Pro Asp Arg Arg Ser Asn Ile Ala Arg Phe Ile Ser Gly Ile Asn Asn  
130 135 140  
His Ser Pro Glu Gly Arg Lys Lys Gln Asn Leu Lys Cys Val Arg Phe  
145 150 155 160  
Asn Ile Asn Gly Glu Ala Arg Val Leu Leu Val Ala Asn Arg Asp Ile  
165 170 175  
Ser Lys Gly Glu Arg Leu Tyr Tyr Asp Tyr Asn Gly Tyr Glu His Glu  
180 185 190  
Tyr Pro Thr Glu His Phe  
195

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

acactgttta tctgattcgt ctctctgat aatcaagagt agtagtgagg ttctctggaa 60  
aatattcgat ttttaaaaga ctctgatgat gacattaaac tcactatctc cagctgaatc 120  
caaagctatt tctttcttgg atacctccag gttcaatcca atccctaaac tctcaggtgg 180  
gttttagtttg aggaggagga atcaaggagg aggttttggg aaaggtgtta agtggttcagt 240  
gaaagtgcag cagcaacaac aacctcctcc agcatggcct gggagagctg tccctgagggc 300  
gcctcgtcaa tcttgggatg gaccaaacc catctctatc gttggatcta ctggttctat 360  
tggcactcag acattggata ttgtggctga gaatcctgac aaattcagag ttgtggctct 420  
agctgctggt tcgaatgtta ctctacttgc tgatcaggta aggagattta agcctgcatt 480

(2) INFORMATION FOR SEQ ID NO:812:

(A) LENGTH: 328 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1568046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Thr | Leu | Asn | Ser | Leu | Ser | Pro | Ala | Glu | Ser | Lys | Ala | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Asp | Thr | Ser | Arg | Phe | Asn | Pro | Ile | Pro | Lys | Leu | Ser | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Leu | Arg | Arg | Arg | Asn | Gln | Gly | Arg | Gly | Phe | Gly | Lys | Gly | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Cys | Ser | Val | Lys | Val | Gln | Gln | Gln | Gln | Gln | Pro | Pro | Pro | Ala | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gly | Arg | Ala | Val | Pro | Glu | Ala | Pro | Arg | Gln | Ser | Trp | Asp | Gly | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Pro | Ile | Ser | Ile | Val | Gly | Ser | Thr | Gly | Ser | Ile | Gly | Thr | Gln | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | Ile | Val | Ala | Glu | Asn | Pro | Asp | Lys | Phe | Arg | Val | Val | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ala | Gly | Ser | Asn | Val | Thr | Leu | Leu | Ala | Asp | Gln | Val | Arg | Arg | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Pro | Ala | Leu | Val | Ala | Val | Arg | Asn | Glu | Ser | Leu | Ile | Asn | Glu | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Glu | Ala | Leu | Ala | Asp | Leu | Asp | Tyr | Lys | Leu | Glu | Ile | Ile | Pro | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Gln | Gly | Val | Ile | Glu | Val | Ala | Arg | His | Pro | Glu | Ala | Val | Thr | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Thr | Gly | Ile | Val | Gly | Cys | Ala | Gly | Leu | Lys | Pro | Thr | Val | Ala | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Glu | Ala | Gly | Lys | Asp | Ile | Ala | Leu | Ala | Asn | Lys | Glu | Thr | Leu | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Gly | Gly | Pro | Phe | Val | Leu | Pro | Leu | Ala | Asn | Lys | His | Asn | Val | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEO ID NO:813:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1568047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

[illegible]

275 280 285  
Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala His  
290 295 300  
Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Asp Cys His Ser Ser Ala  
305 310 315 320  
Lys Tyr His Thr Phe His Asp  
325

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ccccaccct caaagatctc tcaagaatg gcttcgcgg ctgttgcac gatggttctt 60  
gaccctaaag catcacggc cttgatggat ctatccaccg cagacgaaga agatctctat 120  
ggccgcctca aatcgcttga acgacaacta gagttcacccg atatccaaga agaatatgtg 180  
aaagacgagc aaaagaatct caaacgagag ctgttacgag cacaagaaga ggtcaaacga 240  
attcaatccg tgccttttgt gataggctcag ttcattggaga tgatagatca gaacaacggc 300  
atcgctggat ctactactgg ctccaattac taagtcagaa ttctcagcac aatcaataga 360  
gaactcttaa agccttctgc ttccgctcgt cttcacccgc actccaacgc ccttgttgat 420  
gttttgccctc cggaggctga ttctagcatc tcccttctca gccaatctga gaagcctgac 480  
gtctcctaca atgatattgg aggatgcgat attcagaaac aggaaattcg tgaggctgtt 540  
gaattgcctc ttaccaccca cgagctttac aaacagattg gtattgacct acctcgtgga 600  
gtcttgctct atggacctcc tggtagctga aagactatgt tggctaaggc tgttgccaat 660  
cacacaactg ctgccttcat tagggttgtt ggatccgagt ttgtgcaaaa gtatctcggc 720  
gagggacctc gtatggttcg tgatgtcttc cgtcttgcca aggaaaatgc tccagctatc 780  
atcttcattg atgaggtaga tgccatcgct actgctaggt ttgatgctca aacaggagcc 840  
gatagggaag ttcagcgat tctcatggag cttcttaatc agatggatgg atttgaccag 900  
accgtgaatg tcaaggatcat aatggcaaca aacagggcag acactctaga tccgtctctc 960  
ttacgtcctg gaagacttga tcgtaagatt gagttcccc ttcttgatag acgtcaaaa 1020  
aggcttggtt tccaggatag cacctccaaa atgaacctta gcgatgaggt tgacttgga 1080  
gactatgttt cacggcctga taaattagc gctgctgaga tagcagcaat ttgccaggaa 1140  
gctggtatgc atgcggtgcg aaagaacaga tatgtgatac tacctaagga tttcgagaag 1200  
ggctaccgcg caaatgttaa gaagccagac acggactttg agttttacaa gtgaagagaa 1260  
agcagaagtg gaaccagatt atggctgttg ttaaaattcc agtgtgtttt gagaattatt 1320  
aaggacatgg aatcaaattt gcagttaaat taagaactaa gttgcatNct cctaatttct 1380  
gtaactcgag ttacatttg tttttagct atcagctttt tacagttc

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

Met Leu Ala Lys Ala Val Ala Asn His Thr Thr Ala Ala Phe Ile Arg  
1 5 10 15  
Val Val Gly Ser Glu Phe Val Gln Lys Tyr Leu Gly Glu Gly Pro Arg  
20 25 30  
Met Val Arg Asp Val Phe Arg Leu Ala Lys Glu Asn Ala Pro Ala Ile  
35 40 45

Ile Phe Ile Asp Glu Val Asp Ala Ile Ala Thr Ala Arg Phe Asp Ala  
50 55 60  
Gln Thr Gly Ala Asp Arg Glu Val Gln Arg Ile Leu Met Glu Leu Leu  
65 70 75 80  
Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val Lys Val Ile Met  
85 90 95  
Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu Leu Arg Pro Gly  
100 105 110  
Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp Arg Arg Gln Lys  
115 120 125  
Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn Leu Ser Asp Glu  
130 135 140  
Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys Ile Ser Ala Ala  
145 150 155 160  
Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His Ala Val Arg Lys  
165 170 175  
Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys Gly Tyr Arg Ala  
180 185 190  
Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr Lys  
195 200 205

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1568060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

Met Val Arg Asp Val Phe Arg Leu Ala Lys Glu Asn Ala Pro Ala Ile  
1 5 10 15  
Ile Phe Ile Asp Glu Val Asp Ala Ile Ala Thr Ala Arg Phe Asp Ala  
20 25 30  
Gln Thr Gly Ala Asp Arg Glu Val Gln Arg Ile Leu Met Glu Leu Leu  
35 40 45  
Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val Lys Val Ile Met  
50 55 60  
Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu Leu Arg Pro Gly  
65 70 75 80  
Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp Arg Arg Gln Lys  
85 90 95  
Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn Leu Ser Asp Glu  
100 105 110  
Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys Ile Ser Ala Ala  
115 120 125  
Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His Ala Val Arg Lys  
130 135 140  
Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys Gly Tyr Arg Ala  
145 150 155 160  
Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr Lys  
165 170

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1568061

| SEQUENCE DESCRIPTION: 121-130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met                           | Glu | Leu | Leu | Asn | Gln | Met | Asp | Gly | Phe | Asp | Gln | Thr | Val | Asn | Val |  |
| 1                             |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys                           | Val | Ile | Met | Ala | Thr | Asn | Arg | Ala | Asp | Thr | Leu | Asp | Pro | Ala | Leu |  |
|                               |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu                           | Arg | Pro | Gly | Arg | Leu | Asp | Arg | Lys | Ile | Glu | Phe | Pro | Leu | Pro | Asp |  |
|                               |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg                           | Arg | Gln | Lys | Arg | Leu | Val | Phe | Gln | Val | Cys | Thr | Ser | Lys | Met | Asn |  |
|                               | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu                           | Ser | Asp | Glu | Val | Asp | Leu | Glu | Asp | Tyr | Val | Ser | Arg | Pro | Asp | Lys |  |
| 65                            |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ile                           | Ser | Ala | Ala | Glu | Ile | Ala | Ala | Ile | Cys | Gln | Glu | Ala | Gly | Met | His |  |
|                               |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala                           | Val | Arg | Lys | Asn | Arg | Tyr | Val | Ile | Leu | Pro | Lys | Asp | Phe | Glu | Lys |  |
|                               |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly                           | Tyr | Arg | Ala | Asn | Val | Lys | Lys | Pro | Asp | Thr | Asp | Phe | Glu | Phe | Tyr |  |
|                               |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:818:

(A) LENGTH: 883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..883

(D) OTHER INFORMATION: / Ceres Seq. ID 1568087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aaaaacaaaag | aggaacttga  | gaattttatg | cttgagacaa | aatggcgaaa | gatacgtacg | 60  |
| aggaagagtg  | cgactacttg  | tttaaggcgg | tgttgatcgg | agactcagcc | gtcggaaaat | 120 |
| caaacctott  | gtctagattt  | tctaaagacg | agttccggtt | tgactctaaa | ccaaccatcg | 180 |
| gagtagagtt  | tgcttacogg  | aatgttcacg | tcggagataa | aatcatcaag | gctcagattt | 240 |
| gggacaccgc  | cggccaaгаа  | agattttcag | caatcacaag | ttcgtactac | cgtggagcat | 300 |
| taggggcatt  | actgatttac  | gacatcacta | gacgaacaac | tttcgacaac | atcaagaaat | 360 |
| ggcttttcga  | gcttagagac  | ttcgccaatc | ccgaaaccgt | cgttgctctc | gtcggaaaac | 420 |
| aatcttgatct | ccgacaatct  | agagaagttg | aagaagacga | gggtaagact | ctagcagaat | 480 |
| cagaaggtct  | ctacttcctc  | gagacttcgg | ctttagagaa | tgtaaacgtc | gaagaagcgt | 540 |
| ttctagtgat  | gatcggacgg  | atacatgagg | ttgttactca | gaggatagct | tcggaaaaca | 600 |
| aatccaacgg  | tgctgcgacg  | cctcacatta | acggtaatgg | gaacggtacg | gtccttccgg | 660 |
| ttggtaaaга  | aattgtgaat  | atacacgaag | tacttgctac | tcaaccctta | ttaagctcat | 720 |
| cttccaactg  | ttgttttaag  | taaataatta | atgtattttt | ttcgtttatt | gttttggaat | 780 |
| actttgatga  | tgttttttatt | tgctgtgKA  | ttcgtgaaaa | tttgccttg  | gttgagtaca | 840 |
| tgaatttaaa  | tcatacaatt  | atatocaaat | aaatatgaaa | atc        |            |     |

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1568088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

Met Ala Glu Asp Thr Tyr Glu Glu Glu Cys Asp Tyr Leu Phe Lys Ala  
1 5 10 15  
Val Leu Ile Gly Asp Ser Ala Val Gly Lys Ser Asn Leu Leu Ser Arg  
20 25 30  
Phe Ser Lys Asp Glu Phe Arg Phe Asp Ser Lys Pro Thr Ile Gly Val  
35 40 45  
Glu Phe Ala Tyr Arg Asn Val His Val Gly Asp Lys Ile Ile Lys Ala  
50 55 60  
Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Ala Ile Thr Ser  
65 70 75 80  
Ser Tyr Tyr Arg Gly Ala Leu Gly Ala Leu Ile Tyr Asp Ile Thr  
85 90 95  
Arg Arg Thr Thr Phe Asp Asn Ile Lys Lys Trp Leu Phe Glu Leu Arg  
100 105 110  
Asp Phe Ala Asn Pro Glu Thr Val Val Val Leu Val Gly Asn Lys Ser  
115 120 125  
Asp Leu Arg Gln Ser Arg Glu Val Glu Glu Asp Glu Gly Lys Thr Leu  
130 135 140  
Ala Glu Ser Glu Gly Leu Tyr Phe Leu Glu Thr Ser Ala Leu Glu Asn  
145 150 155 160  
Val Asn Val Glu Glu Ala Phe Leu Val Met Ile Gly Arg Ile His Glu  
165 170 175  
Val Val Thr Gln Arg Ile Ala Ser Glu Asn Lys Ser Asn Gly Ala Ala  
180 185 190  
Thr Pro His Ile Asn Gly Asn Gly Asn Gly Thr Val Leu Pro Val Gly  
195 200 205  
Lys Glu Ile Val Asn Ile His Glu Val Thr Ala Thr Gln Pro Leu Leu  
210 215 220  
Ser Ser Ser Ser Asn Cys Cys Phe Lys  
225 230

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| aaaggatttta | acgtaGttgt | ggtgagagag | tatgatccaa | agagagactt | aacgagtgtg | 60   |
| gaagagcttg  | aggaaaactg | tgaagtcgga | tctttattag | tggatctcat | gggtgaccct | 120  |
| cttgcccga   | tccgacaatc | tccttctttc | cacatgctgg | tggcagagat | cggtaatgag | 180  |
| atagtcgga   | tgatcagagg | aacgatcaaa | atggtgacac | gtggtgtaaa | tgcattacgt | 240  |
| caagccgacg  | acgtttcgcc | ggaaataaac | accaccaaac | ttgccttcgt | ctccggcctt | 300  |
| agagtctctc  | cgttttacag | gaggatggga | attggactga | aactggtgca | aagacttgaa | 360  |
| gagtggtttc  | tacgaaacga | cgccgtttac | tcctacgtgc | aaactgaaaa | cgacaacata | 420  |
| gcttcggtca  | aactcttcac | cgagaaaagt | ggttactcca | aattccgtac | accaactttc | 480  |
| ttggtcaacc  | cggtcttcaa | ccaccgagtc | actgtctctc | gacgagtcaa | aatcatcaaa | 540  |
| ctcgctccct  | ccgacgctga | gtcactctac | cgcaaccgat | tctcaaccac | cgagtttttc | 600  |
| ccttcggaca  | tcaactcaat | cctcaccaac | aaactctccc | tcggcactta | tctggctgtg | 660  |
| ccacgtggag  | gagacaacgt | ttccgggtcg | ttaccggacc | agaccgggtc | atgggcccgt | 720  |
| ataagtattt  | ggaacagtaa | agatgtttac | agacttcaag | tcaaaggagc | gtcgcgtctt | 780  |
| aaacgcattg  | tagctaagtc | aacgcgcgtt | ttcgacggag | cgtttccgtt | tttgaaaatc | 840  |
| ccgtcgtttc  | ccaatctttt | caagtcgttc | gcatgacatt | ttatgtacgg | tatcggtggc | 900  |
| gaagggccac  | gagcggcgga | gatggtggag | gocgtttgct | cacacgcaca | taacttagct | 960  |
| agaaaaagcg  | gttggtgccg | cgtggctgct | gaggtggcga | gctgtgagcc | gctcagagtt | 1020 |
| gggattccac  | attggaaggt | gctctcgccg | gaggatttgt | ggtgtttgaa | acgtctccga | 1080 |

tatgacgatg acggcgtaga ctggaccaag tcaccacctg gattgtctat tttcgttgac 1140  
cctagagaaa tataataatt tgtatagaat atattaagag gactctaaca attgcaacca 1200  
aacacacaaa caaaaattac agaattaaat accaaatctc agtctc

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1568090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Gly | Phe | Asn | Val | Val | Val | Val | Arg | Glu | Tyr | Asp | Pro | Lys | Arg | Asp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Thr | Ser | Val | Glu | Glu | Leu | Glu | Glu | Ser | Cys | Glu | Val | Gly | Ser | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Val | Asp | Leu | Met | Gly | Asp | Pro | Leu | Ala | Arg | Ile | Arg | Gln | Ser | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Phe | His | Met | Leu | Val | Ala | Glu | Ile | Gly | Asn | Glu | Ile | Val | Gly | Met |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Arg | Gly | Thr | Ile | Lys | Met | Val | Thr | Arg | Gly | Val | Asn | Ala | Leu | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Gln | Ala | Asp | Asp | Val | Ser | Pro | Glu | Ile | Asn | Thr | Thr | Lys | Leu | Ala | Phe |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Ser | Gly | Leu | Arg | Val | Ser | Pro | Phe | Tyr | Arg | Arg | Met | Gly | Ile | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Lys | Leu | Val | Gln | Arg | Leu | Glu | Trp | Phe | Leu | Arg | Asn | Asp | Ala |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Val | Tyr | Ser | Tyr | Val | Gln | Thr | Glu | Asn | Asp | Asn | Ile | Ala | Ser | Val | Lys |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Phe | Thr | Glu | Lys | Ser | Gly | Tyr | Ser | Lys | Phe | Arg | Thr | Pro | Thr | Phe |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Leu | Val | Asn | Pro | Val | Phe | Asn | His | Arg | Val | Thr | Val | Ser | Arg | Arg | Val |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Lys | Ile | Ile | Lys | Leu | Ala | Pro | Ser | Asp | Ala | Glu | Ser | Leu | Tyr | Arg | Asn |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Arg | Phe | Ser | Thr | Thr | Glu | Phe | Phe | Pro | Ser | Asp | Ile | Asn | Ser | Ile | Leu |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Thr | Asn | Lys | Leu | Ser | Leu | Gly | Thr | Tyr | Leu | Ala | Val | Pro | Arg | Gly | Gly |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Asn | Val | Ser | Gly | Ser | Leu | Pro | Asp | Gln | Thr | Gly | Ser | Trp | Ala | Val |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Ile | Ser | Ile | Trp | Asn | Ser | Lys | Asp | Val | Tyr | Arg | Leu | Gln | Val | Lys | Gly |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Ser | Arg | Leu | Lys | Arg | Met | Leu | Ala | Lys | Ser | Thr | Arg | Val | Phe | Asp |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gly | Ala | Phe | Pro | Phe | Leu | Lys | Ile | Pro | Ser | Phe | Pro | Asn | Leu | Phe | Lys |  |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |
| Ser | Phe | Ala | Met | His | Phe | Met | Tyr | Gly | Ile | Gly | Gly | Glu | Gly | Pro | Arg |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ala | Ala | Glu | Met | Val | Glu | Ala | Leu | Cys | Ser | His | Ala | His | Asn | Leu | Ala |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Arg | Lys | Ser | Gly | Cys | Ala | Val | Val | Ala | Ala | Glu | Val | Ala | Ser | Cys | Glu |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Pro | Leu | Arg | Val | Gly | Ile | Pro | His | Trp | Lys | Val | Leu | Ser | Pro | Glu | Asp |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Leu | Trp | Cys | Leu | Lys | Arg | Leu | Arg | Tyr | Asp | Asp | Asp | Gly | Val | Asp | Trp |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |  |



Thr Lys Ser Pro Pro Gly Leu Ser Ile Phe Val Asp Pro Arg Glu Ile  
370 375 380

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1568091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

Met Gly Asp Pro Leu Ala Arg Ile Arg Gln Ser Pro Ser Phe His Met  
1 5 10 15  
Leu Val Ala Glu Ile Gly Asn Glu Ile Val Gly Met Ile Arg Gly Thr  
20 25 30  
Ile Lys Met Val Thr Arg Gly Val Asn Ala Leu Arg Gln Ala Asp Asp  
35 40 45  
Val Ser Pro Glu Ile Asn Thr Thr Lys Leu Ala Phe Val Ser Gly Leu  
50 55 60  
Arg Val Ser Pro Phe Tyr Arg Arg Met Gly Ile Gly Leu Lys Leu Val  
65 70 75 80  
Gln Arg Leu Glu Glu Trp Phe Leu Arg Asn Asp Ala Val Tyr Ser Tyr  
85 90 95  
Val Gln Thr Glu Asn Asp Asn Ile Ala Ser Val Lys Leu Phe Thr Glu  
100 105 110  
Lys Ser Gly Tyr Ser Lys Phe Arg Thr Pro Thr Phe Leu Val Asn Pro  
115 120 125  
Val Phe Asn His Arg Val Thr Val Ser Arg Arg Val Lys Ile Ile Lys  
130 135 140  
Leu Ala Pro Ser Asp Ala Glu Ser Leu Tyr Arg Asn Arg Phe Ser Thr  
145 150 155 160  
Thr Glu Phe Phe Pro Ser Asp Ile Asn Ser Ile Leu Thr Asn Lys Leu  
165 170 175  
Ser Leu Gly Thr Tyr Leu Ala Val Pro Arg Gly Gly Asp Asn Val Ser  
180 185 190  
Gly Ser Leu Pro Asp Gln Thr Gly Ser Trp Ala Val Ile Ser Ile Trp  
195 200 205  
Asn Ser Lys Asp Val Tyr Arg Leu Gln Val Lys Gly Ala Ser Arg Leu  
210 215 220  
Lys Arg Met Leu Ala Lys Ser Thr Arg Val Phe Asp Gly Ala Phe Pro  
225 230 235 240  
Phe Leu Lys Ile Pro Ser Phe Pro Asn Leu Phe Lys Ser Phe Ala Met  
245 250 255  
His Phe Met Tyr Gly Ile Gly Gly Glu Gly Pro Arg Ala Ala Glu Met  
260 265 270  
Val Glu Ala Leu Cys Ser His Ala His Asn Leu Ala Arg Lys Ser Gly  
275 280 285  
Cys Ala Val Val Ala Ala Glu Val Ala Ser Cys Glu Pro Leu Arg Val  
290 295 300  
Gly Ile Pro His Trp Lys Val Leu Ser Pro Glu Asp Leu Trp Cys Leu  
305 310 315 320  
Lys Arg Leu Arg Tyr Asp Asp Asp Gly Val Asp Trp Thr Lys Ser Pro  
325 330 335  
Pro Gly Leu Ser Ile Phe Val Asp Pro Arg Glu Ile  
340 345

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 333 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..333  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568092  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

Met Leu Val Ala Glu Ile Gly Asn Glu Ile Val Gly Met Ile Arg Gly  
1                  5                  10                  15  
Thr Ile Lys Met Val Thr Arg Gly Val Asn Ala Leu Arg Gln Ala Asp  
                  20                  25                  30  
Asp Val Ser Pro Glu Ile Asn Thr Thr Lys Leu Ala Phe Val Ser Gly  
                  35                  40                  45  
Leu Arg Val Ser Pro Phe Tyr Arg Arg Met Gly Ile Gly Leu Lys Leu  
50                  55                  60  
Val Gln Arg Leu Glu Glu Trp Phe Leu Arg Asn Asp Ala Val Tyr Ser  
65                  70                  75                  80  
Tyr Val Gln Thr Glu Asn Asp Asn Ile Ala Ser Val Lys Leu Phe Thr  
                  85                  90                  95  
Glu Lys Ser Gly Tyr Ser Lys Phe Arg Thr Pro Thr Phe Leu Val Asn  
                  100                 105                 110  
Pro Val Phe Asn His Arg Val Thr Val Ser Arg Arg Val Lys Ile Ile  
                 115                 120                 125  
Lys Leu Ala Pro Ser Asp Ala Glu Ser Leu Tyr Arg Asn Arg Phe Ser  
130                 135                 140  
Thr Thr Glu Phe Phe Pro Ser Asp Ile Asn Ser Ile Leu Thr Asn Lys  
145                 150                 155                 160  
Leu Ser Leu Gly Thr Tyr Leu Ala Val Pro Arg Gly Gly Asp Asn Val  
                 165                 170                 175  
Ser Gly Ser Leu Pro Asp Gln Thr Gly Ser Trp Ala Val Ile Ser Ile  
                 180                 185                 190  
Trp Asn Ser Lys Asp Val Tyr Arg Leu Gln Val Lys Gly Ala Ser Arg  
195                 200                 205  
Leu Lys Arg Met Leu Ala Lys Ser Thr Arg Val Phe Asp Gly Ala Phe  
210                 215                 220  
Pro Phe Leu Lys Ile Pro Ser Phe Pro Asn Leu Phe Lys Ser Phe Ala  
225                 230                 235                 240  
Met His Phe Met Tyr Gly Ile Gly Gly Glu Gly Pro Arg Ala Ala Glu  
                 245                 250                 255  
Met Val Glu Ala Leu Cys Ser His Ala His Asn Leu Ala Arg Lys Ser  
                 260                 265                 270  
Gly Cys Ala Val Val Ala Ala Glu Val Ala Ser Cys Glu Pro Leu Arg  
                 275                 280                 285  
Val Gly Ile Pro His Trp Lys Val Leu Ser Pro Glu Asp Leu Trp Cys  
290                 295                 300  
Leu Lys Arg Leu Arg Tyr Asp Asp Asp Gly Val Asp Trp Thr Lys Ser  
305                 310                 315                 320  
Pro Pro Gly Leu Ser Ile Phe Val Asp Pro Arg Glu Ile  
                 325                 330

- (2) INFORMATION FOR SEQ ID NO:824:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 1183 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

(B) LOCATION: 1..1183

(D) OTHER INFORMATION: / Ceres Seq. ID 1568093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| acatcatctt | cattaatctg  | atcaataaat  | agggttaatc  | aaaagtcag  | aaaccaaac  | 60   |
| agttcaat   | tacgaaaact  | ctcagaaatg  | gagaagtacg  | agaagctaga | gaaggtcgga | 120  |
| gaaggaaat  | acgggaaagt  | ctacaaagcg  | atggagaaag  | gaactggtaa | gcttggtgct | 180  |
| ctgaagaaaa | ctcgtctcga  | gatggacgaa  | gaaggtattc  | caccaactgc | tcttcgtgag | 240  |
| atctcgcttc | tcagatggt   | atcaacatcg  | atctatgttg  | ttcgattact | ctgcgtcgaa | 300  |
| catgttcaat | aaccatcaac  | caaattctca  | tctaccaa    | ccaatctcta | tctcggtttc | 360  |
| gagtatctcg | atactgatct  | taagaaattc  | atcgattcgt  | ataggaaaag | acctaatact | 420  |
| aagcctcttg | agcctttttt  | gattcagaag  | ttgatgtttc  | agctttgtaa | aggtggtgcg | 480  |
| cattgtcata | gtcatggtgt  | gcttcacggt  | gatcttaaac  | cgcgaatact | tcttcgtgtg | 540  |
| aaagataaag | agcttcttaa  | gattgctgat  | ttgggtcttg  | gtcgtgcttt | tactgttctt | 600  |
| cttaagtctt | atacgcgatga | gattgttact  | ctttggtata  | gagctcctga | agttcttctt | 660  |
| ggatctactc | attattcaac  | tgggtgttgac | atgtgggtctg | ttgggtgtat | ctttgctgag | 720  |
| atggttcgga | ggcaagctct  | tttccttggt  | gattctgagt  | ttcagcaatt | gcttcatatc | 780  |
| ttcaggttgc | taggaacacc  | aactgagcag  | caatggcctg  | gtgtttccac | Actgcgtgac | 840  |
| tggcatgttt | accctaagtg  | ggagccgcaa  | gacttaactc  | ttgctgttcc | ttctctttca | 900  |
| cctcaaggag | ttgatcttct  | cacgaaaatg  | ctcaagtaca  | atccagccga | aagaatttca | 960  |
| gcaaaaacag | cacttgatca  | cccatatttt  | gacagccttg  | acaagtctca | gttctgaagt | 1020 |
| tcattgctgt | atctgttgtc  | atcgctcttg  | tgaattttaa  | catttgatct | atctttgttt | 1080 |
| ccgacacatt | agtgtcttat  | gtttggttta  | gagatttgta  | gtctttcaga | agaaactggg | 1140 |
| aaagcttgta | ttctcaagtq  | aatgtaaaac  | acaatgggtg  | ggt        |            |      |

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1568094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Tyr | Glu | Lys | Leu | Glu | Lys | Val | Gly | Glu | Gly | Thr | Tyr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Val | Tyr | Lys | Ala | Met | Glu | Lys | Gly | Thr | Gly | Lys | Leu | Val | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Thr | Arg | Leu | Glu | Met | Asp | Glu | Glu | Gly | Ile | Pro | Pro | Thr | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Arg | Glu | Ile | Ser | Leu | Leu | Gln | Met | Leu | Ser | Thr | Ser | Ile | Tyr | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Arg | Leu | Leu | Cys | Val | Glu | His | Val | His | Gln | Pro | Ser | Thr | Lys | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Ser | Thr | Lys | Ser | Asn | Leu | Tyr | Leu | Val | Phe | Glu | Tyr | Leu | Asp | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Leu | Lys | Lys | Phe | Ile | Asp | Ser | Tyr | Arg | Lys | Gly | Pro | Asn | Pro | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Leu | Glu | Pro | Phe | Leu | Ile | Gln | Lys | Leu | Met | Phe | Gln | Leu | Cys | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Val | Ala | His | Cys | His | Ser | His | Gly | Val | Leu | His | Arg | Asp | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gln | Asn | Leu | Leu | Leu | Val | Lys | Asp | Lys | Glu | Leu | Leu | Lys | Ile | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Leu | Gly | Leu | Gly | Arg | Ala | Phe | Thr | Val | Pro | Leu | Lys | Ser | Tyr | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Glu | Ile | Val | Thr | Leu | Trp | Tyr | Arg | Ala | Pro | Glu | Val | Leu | Leu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Thr | His | Tyr | Ser | Thr | Gly | Val | Asp | Met | Trp | Ser | Val | Gly | Cys | Ile |

195 200 205  
Phe Ala Glu Met Val Arg Arg Gln Ala Leu Phe Pro Gly Asp Ser Glu  
210 215 220  
Phe Gln Gln Leu Leu His Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu  
225 230 235 240  
Gln Gln Trp Pro Gly Val Ser Thr Leu Arg Asp Trp His Val Tyr Pro  
245 250 255  
Lys Trp Glu Pro Gln Asp Leu Thr Leu Ala Val Pro Ser Leu Ser Pro  
260 265 270  
Gln Gly Val Asp Leu Leu Thr Lys Met Leu Lys Tyr Asn Pro Ala Glu  
275 280 285  
Arg Ile Ser Ala Lys Thr Ala Leu Asp His Pro Tyr Phe Asp Ser Leu  
290 295 300  
Asp Lys Ser Gln Phe  
305

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1568095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

Met Glu Lys Gly Thr Gly Lys Leu Val Ala Leu Lys Lys Thr Arg Leu  
1 5 10 15  
Glu Met Asp Glu Gly Ile Pro Pro Thr Ala Leu Arg Glu Ile Ser  
20 25 30  
Leu Leu Gln Met Leu Ser Thr Ser Ile Tyr Val Val Arg Leu Leu Cys  
35 40 45  
Val Glu His Val His Gln Pro Ser Thr Lys Ser Gln Ser Thr Lys Ser  
50 55 60  
Asn Leu Tyr Leu Val Phe Glu Tyr Leu Asp Thr Asp Leu Lys Lys Phe  
65 70 75 80  
Ile Asp Ser Tyr Arg Lys Gly Pro Asn Pro Lys Pro Leu Glu Pro Phe  
85 90 95  
Leu Ile Gln Lys Leu Met Phe Gln Leu Cys Lys Gly Val Ala His Cys  
100 105 110  
His Ser His Gly Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu  
115 120 125  
Leu Val Lys Asp Lys Glu Leu Leu Lys Ile Ala Asp Leu Gly Leu Gly  
130 135 140  
Arg Ala Phe Thr Val Pro Leu Lys Ser Tyr Thr His Glu Ile Val Thr  
145 150 155 160  
Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gly Ser Thr His Tyr Ser  
165 170 175  
Thr Gly Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Val  
180 185 190  
Arg Arg Gln Ala Leu Phe Pro Gly Asp Ser Glu Phe Gln Gln Leu Leu  
195 200 205  
His Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu Gln Gln Trp Pro Gly  
210 215 220  
Val Ser Thr Leu Arg Asp Trp His Val Tyr Pro Lys Trp Glu Pro Gln  
225 230 235 240  
Asp Leu Thr Leu Ala Val Pro Ser Leu Ser Pro Gln Gly Val Asp Leu  
245 250 255  
Leu Thr Lys Met Leu Lys Tyr Asn Pro Ala Glu Arg Ile Ser Ala Lys  
260 265 270

Thr Ala Leu Asp His Pro Tyr Phe Asp Ser Leu Asp Lys Ser Gln Phe  
275 280 285

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

Met Asp Glu Glu Gly Ile Pro Pro Thr Ala Leu Arg Glu Ile Ser Leu  
1 5 10 15  
Leu Gln Met Leu Ser Thr Ser Ile Tyr Val Val Arg Leu Leu Cys Val  
20 25 30  
Glu His Val His Gln Pro Ser Thr Lys Ser Gln Ser Thr Lys Ser Asn  
35 40 45  
Leu Tyr Leu Val Phe Glu Tyr Leu Asp Thr Asp Leu Lys Lys Phe Ile  
50 55 60  
Asp Ser Tyr Arg Lys Gly Pro Asn Pro Lys Pro Leu Glu Pro Phe Leu  
65 70 75 80  
Ile Gln Lys Leu Met Phe Gln Leu Cys Lys Gly Val Ala His Cys His  
85 90 95  
Ser His Gly Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Leu  
100 105 110  
Val Lys Asp Lys Glu Leu Leu Lys Ile Ala Asp Leu Gly Leu Gly Arg  
115 120 125  
Ala Phe Thr Val Pro Leu Lys Ser Tyr Thr His Glu Ile Val Thr Leu  
130 135 140  
Trp Tyr Arg Ala Pro Glu Val Leu Leu Gly Ser Thr His Tyr Ser Thr  
145 150 155 160  
Gly Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Val Arg  
165 170 175  
Arg Gln Ala Leu Phe Pro Gly Asp Ser Glu Phe Gln Gln Leu Leu His  
180 185 190  
Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu Gln Gln Trp Pro Gly Val  
195 200 205  
Ser Thr Leu Arg Asp Trp His Val Tyr Pro Lys Trp Glu Pro Gln Asp  
210 215 220  
Leu Thr Leu Ala Val Pro Ser Leu Ser Pro Gln Gly Val Asp Leu Leu  
225 230 235 240  
Thr Lys Met Leu Lys Tyr Asn Pro Ala Glu Arg Ile Ser Ala Lys Thr  
245 250 255  
Ala Leu Asp His Pro Tyr Phe Asp Ser Leu Asp Lys Ser Gln Phe  
260 265 270

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| ctgtctctct | tcagtgacac | aaacccaaag | aaaagtagtg | agaaacaaaa | tcgaggtaac  | 60   |
| tactagatga | agacgatgac | gcaattaaat | attgcggttg | trgtttagtg | gacgggttctt | 120  |
| attggaatgt | tgagatcatc | ggaggctcaa | cttcaaata  | atttctacgc | gaagagctgt  | 180  |
| ccaaacgcag | agaaaatcat | ttcagatcat | attcaaaatc | atatccacaa | tggtccttct  | 240  |
| cttgacagtc | ctctcatccg | aatgcacttc | catgattgct | tcgttagggg | atgtgacgga  | 300  |
| tcgggtgttg | taaattcaac | atctggtaac | gcagagagag | atgcaccacc | gaatctaaca  | 360  |
| cttagaggat | tcggtttcgt | ggaaaggatt | aaggctcttc | ttgaaaaagt | gtgtcctaag  | 420  |
| actgtttctt | gcgagatat  | cattgctttg | actgctagag | acacagttgt | cgccaccgga  | 480  |
| ggtccttcat | ggagtgttcc | aacgggaaga | agagacggta | ggatctcaaa | tttgaaggag  | 540  |
| gctacgaata | acattccacc | tccaacgagt | aatttcacga | ctttacgacg | acttttcaaa  | 600  |
| aaccaaggcc | ttaatctcaa | ggaccttggt | ctgctctctg | gggctcacac | gattgggtgtc | 660  |
| tcacattggt | cttccatgaa | tactcgtctc | tacaacttct | cgactacagt | caaacaagat  | 720  |
| ccatctctcg | atagccagta | cgcagcta   | ctaaaggcta | acaaatgtaa | gagcctaatac | 780  |
| gacaatagca | ccatcctgga | gatggatccc | ggtagtagca | gaagcttcga | totcagttat  | 840  |
| tataggcttg | tottgaagag | gagaggcttg | ttccaatctg | attctgcctt | gacaacgaac  | 900  |
| tcagcgacgt | tgaaggtgat | caacgacttg | gtcaacgggt | ctgaaaagaa | gtttttcaaa  | 960  |
| gcttttgcta | agtcaatgRg | agaagatggg | gagagttaaw | gtgaCaGact | ggctcagctg  | 1020 |
| gtgtgatcag | gacacgggtg | tctgtcgctg | gaagttagta | agcttggtcg | gaatgtgggtg | 1080 |
| tgttatggtc | attgttggtt | tgtgtgactt | tcggaaaaaa | caaagtgtgt | taatttaatt  | 1140 |
| ttgttggtgt | ttgatttggt | tttatgcacc | caagaatgat | gtgttatggt | tcaattaata  | 1200 |
| ttggaatcat | tt         |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Met | Thr | Gln | Leu | Asn | Ile | Ala | Val | Xaa | Val | Val | Val | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ile | Gly | Met | Leu | Arg | Ser | Ser | Glu | Ala | Gln | Leu | Gln | Met | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Tyr | Ala | Lys | Ser | Cys | Pro | Asn | Ala | Glu | Lys | Ile | Ile | Ser | Asp | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gln | Asn | His | Ile | His | Asn | Gly | Pro | Ser | Leu | Ala | Ala | Pro | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Met | His | Phe | His | Asp | Cys | Phe | Val | Arg | Gly | Cys | Asp | Gly | Ser | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ile | Asn | Ser | Thr | Ser | Gly | Asn | Ala | Glu | Arg | Asp | Ala | Pro | Pro | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Thr | Leu | Arg | Gly | Phe | Gly | Phe | Val | Glu | Arg | Ile | Lys | Ala | Leu | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Glu | Lys | Val | Cys | Pro | Lys | Thr | Val | Ser | Cys | Ala | Asp | Ile | Ile | Ala | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Thr | Ala | Arg | Asp | Thr | Val | Val | Ala | Thr | Gly | Gly | Pro | Ser | Trp | Ser | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Thr | Gly | Arg | Arg | Asp | Gly | Arg | Ile | Ser | Asn | Leu | Lys | Glu | Ala | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asn | Asn | Ile | Pro | Pro | Thr | Ser | Asn | Phe | Thr | Thr | Leu | Arg | Arg | Leu |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |
| Phe | Lys | Asn | Gln | Gly | Leu | Asn | Leu | Lys | Asp | Leu | Val | Leu | Leu | Ser | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Ala | His | Thr | Ile | Gly | Val | Ser | His | Cys | Ser | Ser | Met | Asn | Thr | Arg | Leu |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Tyr | Asn | Phe | Ser | Thr | Thr | Val | Lys | Gln | Asp | Pro | Ser | Leu | Asp | Ser | Gln |

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 210                     | 215                 | 220                 |
| Tyr Ala Ala Asn Leu Lys | Ala Asn Lys Cys Lys | Ser Leu Asn Asp Asn |
| 225                     | 230                 | 235                 |
| Ser Thr Ile Leu Glu Met | Asp Pro Gly Ser Ser | Arg Ser Phe Asp Leu |
| 245                     | 250                 | 255                 |
| Ser Tyr Tyr Arg Leu Val | Leu Lys Arg Arg Gly | Leu Phe Gln Ser Asp |
| 260                     | 265                 | 270                 |
| Ser Ala Leu Thr Thr Asn | Ser Ala Thr Leu Lys | Val Ile Asn Asp Leu |
| 275                     | 280                 | 285                 |
| Val Asn Gly Ser Glu Lys | Lys Phe Phe Lys Ala | Phe Ala Lys Ser Met |
| 290                     | 295                 | 300                 |
| Xaa Glu Asp Gly Glu Ser |                     |                     |
| 305                     | 310                 |                     |

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1568102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Met Thr Gln Leu Asn Ile Ala Val Xaa Val Val Val Thr Val Leu Ile | 1   | 5   | 10  | 15  |
| Gly Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala | 20  | 25  | 30  |     |
| Lys Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn | 35  | 40  | 45  |     |
| His Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His | 50  | 55  | 60  |     |
| Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn | 65  | 70  | 75  | 80  |
| Ser Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu | 85  | 90  | 95  |     |
| Arg Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val | 100 | 105 | 110 |     |
| Cys Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg | 115 | 120 | 125 |     |
| Asp Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly | 130 | 135 | 140 |     |
| Arg Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile | 145 | 150 | 155 | 160 |
| Pro Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn | 165 | 170 | 175 |     |
| Gln Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr | 180 | 185 | 190 |     |
| Ile Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe | 195 | 200 | 205 |     |
| Ser Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala | 210 | 215 | 220 |     |
| Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile | 225 | 230 | 235 | 240 |
| Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr | 245 | 250 | 255 |     |
| Arg Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu | 260 | 265 | 270 |     |
| Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly | 275 | 280 | 285 |     |

Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp  
290 295 300  
Gly Glu Ser  
305

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1568103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala Lys  
1 5 10 15  
Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn His  
20 25 30  
Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His Phe  
35 40 45  
His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn Ser  
50 55 60  
Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu Arg  
65 70 75 80  
Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val Cys  
85 90 95  
Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg Asp  
100 105 110  
Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly Arg  
115 120 125  
Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile Pro  
130 135 140  
Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn Gln  
145 150 155 160  
Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr Ile  
165 170 175  
Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe Ser  
180 185 190  
Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala Asn  
195 200 205  
Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile Leu  
210 215 220  
Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr Arg  
225 230 235 240  
Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu Thr  
245 250 255  
Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly Ser  
260 265 270  
Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp Gly  
275 280 285  
Glu Ser  
290

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1734

(D) OTHER INFORMATION: / Ceres Seq. ID 1568104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| atcaatggct | ctggatgcat  | tcttcttcat | cgtctctcta | tttcttctgt | ttccgtcacc | 60   |
| atccgcgtca | gaatccacta  | ctcagttttg | tagtgcaggg | agagagaatg | gtgtgggac  | 120  |
| ttgtgggggt | tcacgcacga  | ggattttgat | taaaggaggt | actgttgta  | atgcacacca | 180  |
| tcaagaactt | gctgatgttt  | atgtggaaaa | tggtattatt | gtcgctgtgc | agccaaacat | 240  |
| taaggttggg | gatgaagtca  | ctgtcctcga | tgctactgga | aagtttgta  | tgccaggagg | 300  |
| aattgacccc | cacacgcacc  | tcgccatgga | atztatgggt | accgagacta | ttgatgattt | 360  |
| cttcagtggg | caggcagcgg  | cattagctgg | tggaacaact | atgcatatag | actttgttat | 420  |
| acctgtcaat | gggaatctgg  | tggtctggtt | tgaagcctat | gaaaacaaat | ctagagaatc | 480  |
| ttgtatggat | tacggttttc  | atatggcaat | cacaaagtgg | gatgaagggt | tttccaggga | 540  |
| catggagatg | ttgggtcaagg | aaaagggtat | caactctttc | aagtttttcc | tagcgtataa | 600  |
| aggatctctt | atggttaactg | atgacctact | cctagaagga | cttaaaagat | gcaaaccctt | 660  |
| cgggtgcctt | gccatgggtt  | atgctgaaaa | tgagatgca  | gtattcgaag | gacagaaaag | 720  |
| aatgattgar | ctgggcattt  | Acaggtcacg | agggtcatgc | tctttTcaAg | gcctcctgtg | 780  |
| ctcgagggag | aggccactgc  | tagagcaatt | cgtttggctc | gttttattaa | cacgcctctc | 840  |
| tatgttggtt | atgtgatgag  | tggtgatgca | atggacgaga | ttgctaaagc | tcgaaaatca | 900  |
| ggacagaagg | ttattggaga  | gcctgttggt | tctggattaa | tccttgatga | tcattggctt | 960  |
| tggtatcctg | acttcacaat  | tgctgccaa  | tatgtcatga | gtccacctat | cagaccagta | 1020 |
| ggacatggga | aagccctaca  | agatgccctt | tcacacagga | tccttcagct | tgtaggaact | 1080 |
| gatcactgca | ctttcaattc  | tacacaaaaa | gctctaggac | ttgatgattt | ccgcaaaata | 1140 |
| cctaattggt | ttaatggcct  | tgaggaacgg | atgcacttga | tatgggacac | gatggtggag | 1200 |
| tctggccaac | tctcagctac  | tgattatggt | cgaataacca | gcactgagtg | tgctagaatt | 1260 |
| ttcaacatat | atccacggaa  | aggagctatc | cttgctgggt | cggatgcaga | tattatcata | 1320 |
| ttgaatccaa | actcaagcta  | cgagattagc | tcaaagtctc | atcattcaag | atcagacaca | 1380 |
| aacgtctacg | agggcagaag  | aggaaaggga | aaagttgaag | tgacaatagc | aggaggacga | 1440 |
| attgtgtggg | aaaacgagga  | acttaaagtt | gttccaagaa | gtggcaagta | tatagagatg | 1500 |
| cctcctttca | gttacctttt  | cgatgggtat | gagaaatcag | atgctaatta | tctatcttct | 1560 |
| cttcagactc | cagttaagcg  | tgtcagaact | gaagctacgt | aaagtgcagg | tatctatctt | 1620 |
| tcgtgattct | gtaagaacaa  | ttgtacataa | tttgtattaa | aagtattgaa | agagcgatta | 1680 |
| tgaataatgt | gcatgtagtc  | tggttttgag | aaaaataaaa | agattgtaaa | at         |      |

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1568105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Met | Ala | Leu | Asp | Ala | Phe | Phe | Phe | Ile | Val | Ser | Leu | Phe | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Pro | Ser | Pro | Ser | Ala | Ser | Glu | Ser | Thr | Thr | Gln | Phe | Cys | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Arg | Glu | Asn | Gly | Val | Gly | Ser | Cys | Gly | Val | Ser | Ser | Thr | Arg | Ile |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Ile | Lys | Gly | Gly | Thr | Val | Val | Asn | Ala | His | His | Gln | Glu | Leu | Ala |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Asp | Val | Tyr | Val | Glu | Asn | Gly | Ile | Ile | Val | Ala | Val | Gln | Pro | Asn | Ile |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Val | Gly | Asp | Glu | Val | Thr | Val | Leu | Asp | Ala | Thr | Gly | Lys | Phe | Val |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| Met | Pro | Gly | Gly | Ile | Asp | Pro | His | Thr | His | Leu | Ala | Met | Glu | Phe | Met |
|     |     |     |     |     |     |     |     | 100 |     |     |     |     | 110 |     |     |
| Gly | Thr | Glu | Thr | Ile | Asp | Asp | Phe | Phe | Ser | Gly | Gln | Ala | Ala | Ala | Leu |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Asp | Ala | Phe | Phe | Phe | Ile | Val | Ser | Leu | Phe | Leu | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Pro | Ser | Ala | Ser | Glu | Ser | Thr | Thr | Gln | Phe | Cys | Ser | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Glu | Asn | Gly | Val | Gly | Ser | Cys | Gly | Val | Ser | Ser | Thr | Arg | Ile | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Lys | Gly | Gly | Thr | Val | Val | Asn | Ala | His | His | Gln | Glu | Leu | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Tyr | Val | Glu | Asn | Gly | Ile | Ile | Val | Ala | Val | Gln | Pro | Asn | Ile | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Gly | Asp | Glu | Val | Thr | Val | Leu | Asp | Ala | Thr | Gly | Lys | Phe | Val | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Gly | Gly | Ile | Asp | Pro | His | Thr | His | Leu | Ala | Met | Glu | Phe | Met | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Glu | Thr | Ile | Asp | Asp | Phe | Phe | Ser | Gly | Gln | Ala | Ala | Ala | Leu | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Thr | Thr | Met | His | Ile | Asp | Phe | Val | Ile | Pro | Val | Asn | Gly | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Ala | Gly | Phe | Glu | Ala | Tyr | Glu | Asn | Lys | Ser | Arg | Glu | Ser | Cys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Asp | Tyr | Gly | Phe | His | Met | Ala | Ile | Thr | Lys | Trp | Asp | Glu | Gly | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Arg | Asp | Met | Glu | Met | Leu | Val | Lys | Glu | Lys | Gly | Ile | Asn | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Phe | Phe | Leu | Ala | Tyr | Lys | Gly | Ser | Leu | Met | Val | Thr | Asp | Asp | Leu |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Leu | Leu | Glu | Gly | Leu | Lys | Arg | Cys | Lys | Ser | Leu | Gly | Ala | Leu | Ala | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg Met  
225 230 235 240  
Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln Gly  
245 250 255  
Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp Leu  
260 265 270  
Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met  
275 280

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1568107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met Leu Phe Ser Arg Pro Pro Val Leu Glu Gly Glu Ala Thr Ala Arg  
1 5 10 15  
Ala Ile Arg Leu Ala Arg Phe Ile Asn Thr Pro Leu Tyr Val Val His  
20 25 30  
Val Met Ser Val Asp Ala Met Asp Glu Ile Ala Lys Ala Arg Lys Ser  
35 40 45  
Gly Gln Lys Val Ile Gly Glu Pro Val Val Ser Gly Leu Ile Leu Asp  
50 55 60  
Asp His Trp Leu Trp Asp Pro Asp Phe Thr Ile Ala Ser Lys Tyr Val  
65 70 75 80  
Met Ser Pro Pro Ile Arg Pro Val Gly His Gly Lys Ala Leu Gln Asp  
85 90 95  
Ala Leu Ser Thr Gly Ile Leu Gln Leu Val Gly Thr Asp His Cys Thr  
100 105 110  
Phe Asn Ser Thr Gln Lys Ala Leu Gly Leu Asp Asp Phe Arg Lys Ile  
115 120 125  
Pro Asn Gly Val Asn Gly Leu Glu Glu Arg Met His Leu Ile Trp Asp  
130 135 140  
Thr Met Val Glu Ser Gly Gln Leu Ser Ala Thr Asp Tyr Val Arg Ile  
145 150 155 160  
Thr Ser Thr Glu Cys Ala Arg Ile Phe Asn Ile Tyr Pro Arg Lys Gly  
165 170 175  
Ala Ile Leu Ala Gly Ser Asp Ala Asp Ile Ile Ile Leu Asn Pro Asn  
180 185 190  
Ser Ser Tyr Glu Ile Ser Ser Lys Ser His His Ser Arg Ser Asp Thr  
195 200 205  
Asn Val Tyr Glu Gly Arg Arg Gly Lys Gly Lys Val Glu Val Thr Ile  
210 215 220  
Ala Gly Gly Arg Ile Val Trp Glu Asn Glu Glu Leu Lys Val Val Pro  
225 230 235 240  
Arg Ser Gly Lys Tyr Ile Glu Met Pro Pro Phe Ser Tyr Leu Phe Asp  
245 250 255  
Gly Ile Glu Lys Ser Asp Ala Asn Tyr Leu Ser Ser Leu Arg Ala Pro  
260 265 270  
Val Lys Arg Val Arg Thr Glu Ala Thr  
275 280

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 659 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..659  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| ctcttttttct | tcattctttca | tctctcctcc  | cacaaaagag | gacaaaaaac | caaataacga  | 60  |
| gaagtcccat  | ttctctttgt  | tgtcttaggt  | gttaccttca | tcaaccaaac | gcaatggcga  | 120 |
| acgcggcgctc | ggggatggcg  | gtggaggacg  | agtgtaaagt | gaagtttttg | gagctaaaag  | 180 |
| cgaagagaaa  | ctatagggttc | ataatattca  | ggatagatgg | acaacaagtg | gtggtagaaa  | 240 |
| agctgggaag  | cccccaagag  | aactacgacg  | atttcaccaa | ttacctaccg | ccaaatgaat  | 300 |
| gccgctacgc  | cgtttatgac  | ttcgacttca  | ccactgctga | gaatatccag | aagagcaaga  | 360 |
| tcttcttcat  | agcatgggtca | ccggattcat  | ctagagtaag | gatgaagatg | gtgtatgcga  | 420 |
| gctcaaagga  | caggttcaag  | aggggaattgg | atggtattca | ggtggagtta | caagccactg  | 480 |
| acccgagcga  | gatgagtctc  | gacatcatca  | aaagtcgaac | tctctagatc | tccttgcttt  | 540 |
| tctaattata  | tatccataat  | cattgtcatt  | caaacaattt | cctcatctta | tgtaaactttc | 600 |
| gatcttggtt  | tcattcattc  | ttgttcttga  | ctgttttttt | ctatGtttat | ttacatttt   |     |

(2) INFORMATION FOR SEQ ID NO:837:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 174 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..174  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Leu | His | Ser | Ser | Leu | Leu | Pro | Gln | Lys | Arg | Thr | Lys | Asn |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Ile | Thr | Arg | Ser | Pro | Ile | Ser | Leu | Cys | Cys | Leu | Arg | Cys | Tyr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gln | Pro | Asn | Ala | Met | Ala | Asn | Ala | Ala | Ser | Gly | Met | Ala | Val | Glu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Glu | Cys | Lys | Leu | Lys | Phe | Leu | Glu | Leu | Lys | Ala | Lys | Arg | Asn | Tyr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Arg | Phe | Ile | Ile | Phe | Arg | Ile | Asp | Gly | Gln | Gln | Val | Val | Val | Glu | Lys |
|     |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Leu | Gly | Ser | Pro | Gln | Glu | Asn | Tyr | Asp | Asp | Phe | Thr | Asn | Tyr | Leu | Pro |
|     |     |     |     |     |     |     |     | 85  |     |     |     |     |     | 95  |     |
| Pro | Asn | Glu | Cys | Arg | Tyr | Ala | Val | Tyr | Asp | Phe | Asp | Phe | Thr | Thr | Ala |
|     |     |     |     |     |     |     |     | 100 |     |     |     |     |     | 110 |     |
| Glu | Asn | Ile | Gln | Lys | Ser | Lys | Ile | Phe | Phe | Ile | Ala | Trp | Ser | Pro | Asp |
|     |     |     |     |     |     |     |     | 115 |     |     |     |     |     | 125 |     |
| Ser | Ser | Arg | Val | Arg | Met | Lys | Met | Val | Tyr | Ala | Ser | Ser | Lys | Asp | Arg |
|     |     |     |     |     |     |     |     | 130 |     |     |     |     |     | 140 |     |
| Phe | Lys | Arg | Glu | Leu | Asp | Gly | Ile | Gln | Val | Glu | Leu | Gln | Ala | Thr | Asp |
|     |     |     |     |     |     |     |     | 145 |     |     |     |     |     | 155 |     |
| Pro | Ser | Glu | Met | Ser | Leu | Asp | Ile | Ile | Lys | Ser | Arg | Thr | Leu |     |     |
|     |     |     |     |     |     |     |     | 160 |     |     |     |     |     | 170 |     |

(2) INFORMATION FOR SEQ ID NO:838:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1568126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

Met Ala Asn Ala Ala Ser Gly Met Ala Val Glu Asp Glu Cys Lys Leu  
1 5 10 15  
Lys Phe Leu Glu Leu Lys Ala Lys Arg Asn Tyr Arg Phe Ile Ile Phe  
20 25 30  
Arg Ile Asp Gly Gln Gln Val Val Val Glu Lys Leu Gly Ser Pro Gln  
35 40 45  
Glu Asn Tyr Asp Asp Phe Thr Asn Tyr Leu Pro Pro Asn Glu Cys Arg  
50 55 60  
Tyr Ala Val Tyr Asp Phe Asp Phe Thr Thr Ala Glu Asn Ile Gln Lys  
65 70 75 80  
Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro Asp Ser Ser Arg Val Arg  
85 90 95  
Met Lys Met Val Tyr Ala Ser Ser Lys Asp Arg Phe Lys Arg Glu Leu  
100 105 110  
Asp Gly Ile Gln Val Glu Leu Gln Ala Thr Asp Pro Ser Glu Met Ser  
115 120 125  
Leu Asp Ile Ile Lys Ser Arg Thr Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1568127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

Met Ala Val Glu Asp Glu Cys Lys Leu Lys Phe Leu Glu Leu Lys Ala  
1 5 10 15  
Lys Arg Asn Tyr Arg Phe Ile Ile Phe Arg Ile Asp Gly Gln Gln Val  
20 25 30  
Val Val Glu Lys Leu Gly Ser Pro Gln Glu Asn Tyr Asp Asp Phe Thr  
35 40 45  
Asn Tyr Leu Pro Pro Asn Glu Cys Arg Tyr Ala Val Tyr Asp Phe Asp  
50 55 60  
Phe Thr Thr Ala Glu Asn Ile Gln Lys Ser Lys Ile Phe Phe Ile Ala  
65 70 75 80  
Trp Ser Pro Asp Ser Ser Arg Val Arg Met Lys Met Val Tyr Ala Ser  
85 90 95  
Ser Lys Asp Arg Phe Lys Arg Glu Leu Asp Gly Ile Gln Val Glu Leu  
100 105 110  
Gln Ala Thr Asp Pro Ser Glu Met Ser Leu Asp Ile Ile Lys Ser Arg  
115 120 125  
Thr Leu  
130

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1320

(D) OTHER INFORMATION: / Ceres Seq. ID 1568128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

|            |             |             |             |            |            |      |
|------------|-------------|-------------|-------------|------------|------------|------|
| ataagcgggt | tcatattatt  | cttcttcatc  | gattcttgat  | tttgcaagaa | gacaattcaa | 60   |
| gaaagcgatt | tagaagacgg  | aggagttctt  | accggagatc  | ttatacttat | ggatggaatg | 120  |
| tacaatttcc | attcggccgg  | tgattattca  | gataagtcgg  | ttctgatgat | gtcaccggag | 180  |
| agtctcatgt | ttcttccga   | ttaccaagct  | ttgctatgtt  | cctccgccgg | tgaaaatcgt | 240  |
| gtctctgatg | ttttcggatc  | cgacgagcta  | ctctcagtag  | ccgtctccgc | tttgtcgtcg | 300  |
| gaggcggctt | cgatcgctcc  | ggagatccga  | agaaatgatg  | ataacgtttc | tctaactgtc | 360  |
| atcaaagcta | aaatcgcttg  | tcatccttcc  | tatcctcgct  | tacttcaagc | ttacatcgat | 420  |
| tgccaaaaga | aacagggtcgg | agcaccaccc  | gagatagcgt  | gtttactaga | ggagattcaa | 480  |
| cgggagagtg | atgtttataa  | gcaagagggt  | gttcttctt   | cttgcttttg | agctgatcct | 540  |
| gagcttgatg | aatttatgga  | aacgtactgc  | gatatattag  | tgaaatacaa | atcggatcta | 600  |
| gcaagaccgt | ttgacgaggc  | aacgtgtttc  | ttgaacaaga  | ttgagatgca | gctacggaac | 660  |
| ctatgtactg | gtgtcgagtc  | tgccagggga  | gtttctgagg  | atggtgtaat | atcatctgac | 720  |
| gaggaactga | gtggagggtga | tcatgaggta  | gcagaggatg  | ggagacaaag | atgtgaagac | 780  |
| cgggacctca | aagatagggt  | Gctacgcaaa  | tttgggaagcc | gtattagtac | tttaaagctt | 840  |
| gagttctcaa | agaagaagaa  | gaaaggaaag  | ttacctagag  | aagcaagaca | agctcttctc | 900  |
| gattggtgga | atctccatta  | taagtggcct  | taccctactg  | aaggagataa | gatagcatta | 960  |
| gctgatgcaa | cgggggttaga | ccagaaacaa  | atcaacaatt  | ggtttataaa | ccaaaggaaa | 1020 |
| cgtcattgga | agccatcaga  | gaatatgcct  | tttgctatga  | tggatgattc | tagtggatca | 1080 |
| ttctttaccg | aggaatgaat  | ttatttacgg  | tattttat    | acgttactta | aaaagatgga | 1140 |
| tgtataattc | tgcttgcctt  | tgccgacaat  | caaaggaaaa  | aagaaaagaa | agagtgaagc | 1200 |
| atggacgaca | catgaattaa  | tgaattattac | actcactcac  | atgtagtaga | aggaacaagg | 1260 |
| gaacaagtca | aaatgctttg  | taactattat  | tatcggtgaa  | taaaaataac | ttcttttgtc | 1320 |

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1568129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gly | Met | Tyr | Asn | Phe | His | Ser | Ala | Gly | Asp | Tyr | Ser | Asp | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Val | Leu | Met | Met | Ser | Pro | Glu | Ser | Leu | Met | Phe | Pro | Ser | Asp | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Gln | Ala | Leu | Leu | Cys | Ser | Ser | Ala | Gly | Glu | Asn | Arg | Val | Ser | Asp | Val |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Phe | Gly | Ser | Asp | Glu | Leu | Leu | Ser | Val | Ala | Val | Ser | Ala | Leu | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ala | Ala | Ser | Ile | Ala | Pro | Glu | Ile | Arg | Arg | Asn | Asp | Asp | Asn | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Thr | Val | Ile | Lys | Ala | Lys | Ile | Ala | Cys | His | Pro | Ser | Tyr | Pro |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Leu | Leu | Gln | Ala | Tyr | Ile | Asp | Cys | Gln | Lys | Lys | Gln | Val | Gly | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Glu | Ile | Ala | Cys | Leu | Leu | Glu | Glu | Ile | Gln | Arg | Glu | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Tyr | Lys | Gln | Glu | Val | Val | Pro | Ser | Ser | Cys | Phe | Gly | Ala | Asp | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Glu | Leu | Asp | Glu | Phe | Met | Glu | Thr | Tyr | Cys | Asp | Ile | Leu | Val | Lys | Tyr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Lys | Ser | Asp | Leu | Ala | Arg | Pro | Phe | Asp | Glu | Ala | Thr | Cys | Phe | Leu | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Ile | Glu | Met | Gln | Leu | Arg | Asn | Leu | Cys | Thr | Gly | Val | Glu | Ser | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |

Arg Gly Val Ser Glu Asp Gly Val Ile Ser Ser Asp Glu Glu Leu Ser  
195 200 205  
Gly Gly Asp His Glu Val Ala Glu Asp Gly Arg Gln Arg Cys Glu Asp  
210 215 220  
Arg Asp Leu Lys Asp Arg Leu Leu Arg Lys Phe Gly Ser Arg Ile Ser  
225 230 235 240  
Thr Leu Lys Leu Glu Phe Ser Lys Lys Lys Lys Lys Gly Lys Leu Pro  
245 250 255  
Arg Glu Ala Arg Gln Ala Leu Leu Asp Trp Trp Asn Leu His Tyr Lys  
260 265 270  
Trp Pro Tyr Pro Thr Glu Gly Asp Lys Ile Ala Leu Ala Asp Ala Thr  
275 280 285  
Gly Leu Asp Gln Lys Gln Ile Asn Asn Trp Phe Ile Asn Gln Arg Lys  
290 295 300  
Arg His Trp Lys Pro Ser Glu Asn Met Pro Phe Ala Met Met Asp Asp  
305 310 315 320  
Ser Ser Gly Ser Phe Phe Thr Glu Glu  
325

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1568130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met Tyr Asn Phe His Ser Ala Gly Asp Tyr Ser Asp Lys Ser Val Leu  
1 5 10 15  
Met Met Ser Pro Glu Ser Leu Met Phe Pro Ser Asp Tyr Gln Ala Leu  
20 25 30  
Leu Cys Ser Ser Ala Gly Glu Asn Arg Val Ser Asp Val Phe Gly Ser  
35 40 45  
Asp Glu Leu Leu Ser Val Ala Val Ser Ala Leu Ser Ser Glu Ala Ala  
50 55 60  
Ser Ile Ala Pro Glu Ile Arg Arg Asn Asp Asp Asn Val Ser Leu Thr  
65 70 75 80  
Val Ile Lys Ala Lys Ile Ala Cys His Pro Ser Tyr Pro Arg Leu Leu  
85 90 95  
Gln Ala Tyr Ile Asp Cys Gln Lys Lys Gln Val Gly Ala Pro Pro Glu  
100 105 110  
Ile Ala Cys Leu Leu Glu Glu Ile Gln Arg Glu Ser Asp Val Tyr Lys  
115 120 125  
Gln Glu Val Val Pro Ser Ser Cys Phe Gly Ala Asp Pro Glu Leu Asp  
130 135 140  
Glu Phe Met Glu Thr Tyr Cys Asp Ile Leu Val Lys Tyr Lys Ser Asp  
145 150 155 160  
Leu Ala Arg Pro Phe Asp Glu Ala Thr Cys Phe Leu Asn Lys Ile Glu  
165 170 175  
Met Gln Leu Arg Asn Leu Cys Thr Gly Val Glu Ser Ala Arg Gly Val  
180 185 190  
Ser Glu Asp Gly Val Ile Ser Ser Asp Glu Glu Leu Ser Gly Gly Asp  
195 200 205  
His Glu Val Ala Glu Asp Gly Arg Gln Arg Cys Glu Asp Arg Asp Leu  
210 215 220  
Lys Asp Arg Leu Leu Arg Lys Phe Gly Ser Arg Ile Ser Thr Leu Lys  
225 230 235 240  
Leu Glu Phe Ser Lys Lys Lys Lys Lys Gly Lys Leu Pro Arg Glu Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gln | Ala | Leu | Asp | Trp | Trp | Asn | Leu | His | Tyr | Lys | Trp | Pro | Tyr |     |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     |     | 255 |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Pro | Thr | Glu | Gly | Asp | Lys | Ile | Ala | Leu | Ala | Asp | Ala | Thr | Gly | Leu | Asp |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Lys | Gln | Ile | Asn | Asn | Trp | Phe | Ile | Asn | Gln | Arg | Lys | Arg | His | Trp |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Lys | Pro | Ser | Glu | Asn | Met | Pro | Phe | Ala | Met | Met | Asp | Asp | Ser | Ser | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Phe | Phe | Thr | Glu | Glu |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1568131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Ser | Pro | Glu | Ser | Leu | Met | Phe | Pro | Ser | Asp | Tyr | Gln | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Cys | Ser | Ser | Ala | Gly | Glu | Asn | Arg | Val | Ser | Asp | Val | Phe | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Glu | Leu | Leu | Ser | Val | Ala | Val | Ser | Ala | Leu | Ser | Ser | Glu | Ala | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Ala | Pro | Glu | Ile | Arg | Arg | Asn | Asp | Asp | Asn | Val | Ser | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ile | Lys | Ala | Lys | Ile | Ala | Cys | His | Pro | Ser | Tyr | Pro | Arg | Leu | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Ala | Tyr | Ile | Asp | Cys | Gln | Lys | Lys | Gln | Val | Gly | Ala | Pro | Pro | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Cys | Leu | Leu | Glu | Glu | Ile | Gln | Arg | Glu | Ser | Asp | Val | Tyr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Glu | Val | Val | Pro | Ser | Ser | Cys | Phe | Gly | Ala | Asp | Pro | Glu | Leu | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Phe | Met | Glu | Thr | Tyr | Cys | Asp | Ile | Leu | Val | Lys | Tyr | Lys | Ser | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ala | Arg | Pro | Phe | Asp | Glu | Ala | Thr | Cys | Phe | Leu | Asn | Lys | Ile | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Met | Gln | Leu | Arg | Asn | Leu | Cys | Thr | Gly | Val | Glu | Ser | Ala | Arg | Gly | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Glu | Asp | Gly | Val | Ile | Ser | Ser | Asp | Glu | Glu | Leu | Ser | Gly | Gly | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Glu | Val | Ala | Glu | Asp | Gly | Arg | Gln | Arg | Cys | Glu | Asp | Arg | Asp | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Asp | Arg | Leu | Leu | Arg | Lys | Phe | Gly | Ser | Arg | Ile | Ser | Thr | Leu | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Glu | Phe | Ser | Lys | Lys | Lys | Lys | Lys | Gly | Lys | Leu | Pro | Arg | Glu | Ala |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Gln | Ala | Leu | Leu | Asp | Trp | Trp | Asn | Leu | His | Tyr | Lys | Trp | Pro | Tyr |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Thr | Glu | Gly | Asp | Lys | Ile | Ala | Leu | Ala | Asp | Ala | Thr | Gly | Leu | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Lys | Gln | Ile | Asn | Asn | Trp | Phe | Ile | Asn | Gln | Arg | Lys | Arg | His | Trp |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Pro | Ser | Glu | Asn | Met | Pro | Phe | Ala | Met | Met | Asp | Asp | Ser | Ser | Gly |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |



Ser Phe Phe Thr Glu Glu  
305 310

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tctctatggt  | gtagttcttg  | tacagttggc  | tctcttttca  | agaatcgctc  | ccgttgacct  | 60   |
| ccgtgcctct  | ccgatcaact  | tccattctt   | ttaaagtacg  | agagattcat  | caaggaacag  | 120  |
| ctcattaaag  | ccatggcctc  | gaaagagttt  | tctttttcct  | tctgttgtga  | ttgtcattgt  | 180  |
| tgggataatc  | gtggcggtta  | cttatcagtc  | caagttgaaa  | ccacctccgc  | cgaagctatg  | 240  |
| tggctcctcc  | ggtgggtccac | cgatcacagc  | gccgcggata  | aagcttcaag  | atgggaggtg  | 300  |
| tttggcttac  | aaagagcatg  | gacttccaag  | agagaaaagct | aaccgcaaaa  | tcgtcttcat  | 360  |
| ccatggatcc  | gattggtgta  | gacacgatgc  | cgttttcgcc  | actctgcttt  | ctccggattt  | 420  |
| agtagaggaa  | ctaggtgtat  | atatggtttc  | attcgacaga  | ccgggctatt  | gtgagagtga  | 480  |
| tccgcatcca  | agtcgtacac  | cgcgaaagctt | ggtttcggat  | attgaagagc  | tagctgatca  | 540  |
| gttgagtcta  | ggatcgaaat  | tttatgtgct  | cgggtactcg  | atgggaggac  | aagcagcatg  | 600  |
| gggatgtctt  | aaatacattc  | ctcatagggt  | agccggagta  | acactagttg  | ctccagtggg  | 660  |
| taactattat  | tggagaact   | tacctttgaa  | cgtttccact  | gaaggtttta  | actttcaaca  | 720  |
| aaagagagat  | caattggcag  | ttcgtgttgc  | tcactatact  | ccttggctta  | tctattgggtg | 780  |
| gaacacacaa  | aaatGgttcc  | ctggttcgag  | tattgcaaac  | cgagatcaca  | gtctcttggc  | 840  |
| acagccggat  | aaagatatca  | tttcgaagct  | tggttcttcg  | aggaaaccac  | attgggcaga  | 900  |
| ggtaaggcag  | caaggaatac  | atgagagtat  | taaccgtgac  | atgatcgttg  | gttttgggaa  | 960  |
| ctgggaattt  | gatccttttag | acctcgagaa  | tccgtttttg  | aataagggaag | gctctgtgca  | 1020 |
| tttgtggcaa  | ggagatgagg  | acatgttagt  | acctgcgaag  | ctgcagcggt  | accttgetca  | 1080 |
| tcagcttcca  | tgggttccact | atcatgaggt  | tccgagaagt  | ggccacttct  | tccactacac  | 1140 |
| taaagggtgta | gttgatgaca  | ttgtaaagtc  | gctcttaacc  | tccggtgtaa  | gagcatctag  | 1200 |
| agtttgattt  | tgatcatttg  | tagcttccaa  | aaactctgaa  | aaaaatccca  | aaaaaatata  | 1260 |
| cggatacaat  | agagttatgt  | actagttaca  | tttgtcagca  | tcgtagttaa  | tt          |      |

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Arg | Asp | Ser | Ser | Arg | Asn | Ser | Ser | Leu | Lys | Pro | Trp | Pro | Arg |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Lys | Ser | Phe | Leu | Phe | Pro | Ser | Val | Val | Ile | Val | Ile | Val | Gly | Ile | Ile |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Val | Ala | Phe | Thr | Tyr | Gln | Ser | Lys | Leu | Lys | Pro | Pro | Pro | Pro | Lys | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Cys | Gly | Ser | Ser | Gly | Gly | Pro | Pro | Ile | Thr | Ala | Pro | Arg | Ile | Lys | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gln | Asp | Gly | Arg | Tyr | Leu | Ala | Tyr | Lys | Glu | His | Gly | Leu | Pro | Arg | Glu |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | Ala | Asn | Arg | Lys | Ile | Val | Phe | Ile | His | Gly | Ser | Asp | Cys | Cys | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| His | Asp | Ala | Val | Phe | Ala | Thr | Leu | Leu | Ser | Pro | Asp | Leu | Val | Glu | Glu |  |

100 105 110  
Leu Gly Val Tyr Met Val Ser Phe Asp Arg Pro Gly Tyr Cys Glu Ser  
115 120 125  
Asp Pro His Pro Ser Arg Thr Pro Arg Ser Leu Val Ser Asp Ile Glu  
130 135 140  
Glu Leu Ala Asp Gln Leu Ser Leu Gly Ser Lys Phe Tyr Val Leu Gly  
145 150 155 160  
Tyr Ser Met Gly Gly Gln Ala Ala Trp Gly Cys Leu Lys Tyr Ile Pro  
165 170 175  
His Arg Leu Ala Gly Val Thr Leu Val Ala Pro Val Val Asn Tyr Tyr  
180 185 190  
Trp Lys Asn Leu Pro Leu Asn Val Ser Thr Glu Gly Phe Asn Phe Gln  
195 200 205  
Gln Lys Arg Asp Gln Leu Ala Val Arg Val Ala His Tyr Thr Pro Trp  
210 215 220  
Leu Ile Tyr Trp Trp Asn Thr Gln Lys Trp Phe Pro Gly Ser Ser Ile  
225 230 235 240  
Ala Asn Arg Asp His Ser Leu Leu Ala Gln Pro Asp Lys Asp Ile Ile  
245 250 255  
Ser Lys Leu Gly Ser Ser Arg Lys Pro His Trp Ala Glu Val Arg Gln  
260 265 270  
Gln Gly Ile His Glu Ser Ile Asn Arg Asp Met Ile Val Gly Phe Gly  
275 280 285  
Asn Trp Glu Phe Asp Pro Leu Asp Leu Glu Asn Pro Phe Leu Asn Lys  
290 295 300  
Glu Gly Ser Val His Leu Trp Gln Gly Asp Glu Asp Met Leu Val Pro  
305 310 315 320  
Ala Lys Leu Gln Arg Tyr Leu Ala His Gln Leu Pro Trp Val His Tyr  
325 330 335  
His Glu Val Pro Arg Ser Gly His Phe Phe His Tyr Thr Lys Gly Val  
340 345 350  
Val Asp Asp Ile Val Lys Ser Leu Leu Thr Ser Gly Val Arg Ala Ser  
355 360 365  
Arg Val Cys Ile  
370

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1568154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

Met Val Ser Phe Asp Arg Pro Gly Tyr Cys Glu Ser Asp Pro His Pro  
1 5 10 15  
Ser Arg Thr Pro Arg Ser Leu Val Ser Asp Ile Glu Glu Leu Ala Asp  
20 25 30  
Gln Leu Ser Leu Gly Ser Lys Phe Tyr Val Leu Gly Tyr Ser Met Gly  
35 40 45  
Gly Gln Ala Ala Trp Gly Cys Leu Lys Tyr Ile Pro His Arg Leu Ala  
50 55 60  
Gly Val Thr Leu Val Ala Pro Val Val Asn Tyr Tyr Trp Lys Asn Leu  
65 70 75 80  
Pro Leu Asn Val Ser Thr Glu Gly Phe Asn Phe Gln Gln Lys Arg Asp  
85 90 95  
Gln Leu Ala Val Arg Val Ala His Tyr Thr Pro Trp Leu Ile Tyr Trp  
100 105 110

Trp Asn Thr Gln Lys Trp Phe Pro Gly Ser Ser Ile Ala Asn Arg Asp  
115 120 125  
His Ser Leu Leu Ala Gln Pro Asp Lys Asp Ile Ile Ser Lys Leu Gly  
130 135 140  
Ser Ser Arg Lys Pro His Trp Ala Glu Val Arg Gln Gln Gly Ile His  
145 150 155 160  
Glu Ser Ile Asn Arg Asp Met Ile Val Gly Phe Gly Asn Trp Glu Phe  
165 170 175  
Asp Pro Leu Asp Leu Glu Asn Pro Phe Leu Asn Lys Glu Gly Ser Val  
180 185 190  
His Leu Trp Gln Gly Asp Glu Asp Met Leu Val Pro Ala Lys Leu Gln  
195 200 205  
Arg Tyr Leu Ala His Gln Leu Pro Trp Val His Tyr His Glu Val Pro  
210 215 220  
Arg Ser Gly His Phe Phe His Tyr Thr Lys Gly Val Val Asp Asp Ile  
225 230 235 240  
Val Lys Ser Leu Leu Thr Ser Gly Val Arg Ala Ser Arg Val Cys Ile  
245 250 255

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1568155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met Gly Gly Gln Ala Ala Trp Gly Cys Leu Lys Tyr Ile Pro His Arg  
1 5 10 15  
Leu Ala Gly Val Thr Leu Val Ala Pro Val Val Asn Tyr Tyr Trp Lys  
20 25 30  
Asn Leu Pro Leu Asn Val Ser Thr Glu Gly Phe Asn Phe Gln Gln Lys  
35 40 45  
Arg Asp Gln Leu Ala Val Arg Val Ala His Tyr Thr Pro Trp Leu Ile  
50 55 60  
Tyr Trp Trp Asn Thr Gln Lys Trp Phe Pro Gly Ser Ser Ile Ala Asn  
65 70 75 80  
Arg Asp His Ser Leu Leu Ala Gln Pro Asp Lys Asp Ile Ile Ser Lys  
85 90 95  
Leu Gly Ser Ser Arg Lys Pro His Trp Ala Glu Val Arg Gln Gln Gly  
100 105 110  
Ile His Glu Ser Ile Asn Arg Asp Met Ile Val Gly Phe Gly Asn Trp  
115 120 125  
Glu Phe Asp Pro Leu Asp Leu Glu Asn Pro Phe Leu Asn Lys Glu Gly  
130 135 140  
Ser Val His Leu Trp Gln Gly Asp Glu Asp Met Leu Val Pro Ala Lys  
145 150 155 160  
Leu Gln Arg Tyr Leu Ala His Gln Leu Pro Trp Val His Tyr His Glu  
165 170 175  
Val Pro Arg Ser Gly His Phe Phe His Tyr Thr Lys Gly Val Val Asp  
180 185 190  
Asp Ile Val Lys Ser Leu Leu Thr Ser Gly Val Arg Ala Ser Arg Val  
195 200 205  
Cys Ile  
210

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1261 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1261  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568160  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

gaaaacacaaa ttagggtttt taatttccag attgttttgt ttatttgaat aaatctccgc 60  
aagtttcaat taggttgcaa aaatcgaaga aMatttttctt cgattcaaaa aaaatgggaa 120  
aattttgttg cttcacttcc gcttctgagg ttgtgggagg acaatcatca tcacgatcag 180  
gtaaaggaag aagtgatgaa gggatgatca agtatggttt tagtctagtg aaaggaaaaag 240  
ctaaccatcc aatggaagat tatcatgttg ctaactttat caacatccaa gaccatgaat 300  
tgggtctttt tgctatttat gatggtcata tgggtgatag tgtccctgct tacttgcaag 360  
aacgtctctt ctocaatatc ctttaaggagg gagagttttg gggtgatcct cgaaggtcta 420  
ttgcaaaaagc ttatgagaag acggaagcga ttctatcgaa tagttctgac ttgggtcgtg 480  
gtggttctac tgctgtgact gctatattga ttaatgggag aaagttgtgg atagctaattg 540  
ttggtgattc acgagctgtt ctttctcatg gtggcgctat aacgcagatg agtacagatc 600  
atgagcctcg tactgaaagg tcgagtattg aagatagagg tggatttgta tccaatctac 660  
caggtgatgt toctcgggtg aatggtcaat tagctgtgtc tcgtgctttt ggagataagg 720  
gacttaagac acaacttgagt tcagagcctg acataaaaaga agctactgta gatagccaga 780  
cagatgttct tctcttggct agtgatggca tctggaaggt gatgacaaat gaagaggcaa 840  
tgagatagc gagaagagtg aaagatccac agaaagcggc aaaggaatta acagctgaag 900  
cattgagaag agagagtaaa gacgacatat cttgtgtcgt ggtccgattc agatgacaaa 960  
ctctctgaaa ggatacttac ggggagatgg gttccttata taataatttc aatcaaagat 1020  
tcatcaggac aaaaaagctt gttttcactg gattcgactc tgatgattct ggttcggttt 1080  
aggacctgtc taagtttcaa tttgtgatta gctgcttctt gctatagctt atgtgcgttc 1140  
gttggtgtaa ttgtgtgttt taaagacgat aagaaaaatga acaaaaaagg agtggggaat 1200  
gagtttttgt ggtgggtgat ggggggtttt gttattataa ttggttgatt tgttatatYt 1260  
t

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 280 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..280  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568161  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

Met Gly Lys Phe Cys Cys Phe Thr Ser Ala Ser Glu Val Val Gly Gly  
1 5 10 15  
Gln Ser Ser Ser Arg Ser Gly Lys Gly Arg Ser Asp Glu Gly Met Ile  
20 25 30  
Lys Tyr Gly Phe Ser Leu Val Lys Gly Lys Ala Asn His Pro Met Glu  
35 40 45  
Asp Tyr His Val Ala Asn Phe Ile Asn Ile Gln Asp His Glu Leu Gly  
50 55 60  
Leu Phe Ala Ile Tyr Asp Gly His Met Gly Asp Ser Val Pro Ala Tyr  
65 70 75 80  
Leu Gln Lys Arg Leu Phe Ser Asn Ile Leu Lys Glu Gly Glu Phe Trp  
85 90 95  
Val Asp Pro Arg Arg Ser Ile Ala Lys Ala Tyr Glu Lys Thr Glu Ala  
100 105 110  
Ile Leu Ser Asn Ser Ser Asp Leu Gly Arg Gly Gly Ser Thr Ala Val  
115 120 125

Thr Ala Ile Leu Ile Asn Gly Arg Lys Leu Trp Ile Ala Asn Val Gly  
130 135 140  
Asp Ser Arg Ala Val Leu Ser His Gly Gly Ala Ile Thr Gln Met Ser  
145 150 155 160  
Thr Asp His Glu Pro Arg Thr Glu Arg Ser Ser Ile Glu Asp Arg Gly  
165 170 175  
Gly Phe Val Ser Asn Leu Pro Gly Asp Val Pro Arg Val Asn Gly Gln  
180 185 190  
Leu Ala Val Ser Arg Ala Phe Gly Asp Lys Gly Leu Lys Thr His Leu  
195 200 205  
Ser Ser Glu Pro Asp Ile Lys Glu Ala Thr Val Asp Ser Gln Thr Asp  
210 215 220  
Val Leu Leu Leu Ala Ser Asp Gly Ile Trp Lys Val Met Thr Asn Glu  
225 230 235 240  
Glu Ala Met Glu Ile Ala Arg Arg Val Lys Asp Pro Gln Lys Ala Ala  
245 250 255  
Lys Glu Leu Thr Ala Glu Ala Leu Arg Arg Glu Ser Lys Asp Asp Ile  
260 265 270  
Ser Cys Val Val Val Arg Phe Arg  
275 280

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1568162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

Met Ile Lys Tyr Gly Phe Ser Leu Val Lys Gly Lys Ala Asn His Pro  
1 5 10 15  
Met Glu Asp Tyr His Val Ala Asn Phe Ile Asn Ile Gln Asp His Glu  
20 25 30  
Leu Gly Leu Phe Ala Ile Tyr Asp Gly His Met Gly Asp Ser Val Pro  
35 40 45  
Ala Tyr Leu Gln Lys Arg Leu Phe Ser Asn Ile Leu Lys Glu Gly Glu  
50 55 60  
Phe Trp Val Asp Pro Arg Arg Ser Ile Ala Lys Ala Tyr Glu Lys Thr  
65 70 75 80  
Glu Ala Ile Leu Ser Asn Ser Ser Asp Leu Gly Arg Gly Gly Ser Thr  
85 90 95  
Ala Val Thr Ala Ile Leu Ile Asn Gly Arg Lys Leu Trp Ile Ala Asn  
100 105 110  
Val Gly Asp Ser Arg Ala Val Leu Ser His Gly Gly Ala Ile Thr Gln  
115 120 125  
Met Ser Thr Asp His Glu Pro Arg Thr Glu Arg Ser Ser Ile Glu Asp  
130 135 140  
Arg Gly Gly Phe Val Ser Asn Leu Pro Gly Asp Val Pro Arg Val Asn  
145 150 155 160  
Gly Gln Leu Ala Val Ser Arg Ala Phe Gly Asp Lys Gly Leu Lys Thr  
165 170 175  
His Leu Ser Ser Glu Pro Asp Ile Lys Glu Ala Thr Val Asp Ser Gln  
180 185 190  
Thr Asp Val Leu Leu Leu Ala Ser Asp Gly Ile Trp Lys Val Met Thr  
195 200 205  
Asn Glu Glu Ala Met Glu Ile Ala Arg Arg Val Lys Asp Pro Gln Lys  
210 215 220  
Ala Ala Lys Glu Leu Thr Ala Glu Ala Leu Arg Arg Glu Ser Lys Asp

(2) INFORMATION FOR SEO ID NO:851:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1568163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

(2) INFORMATION FOR SEO ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1128

(D) OTHER INFORMATION: / Ceres Seq. ID 1568176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acacatacaa | gactctcctc | acagaacgat | ttagatttta | tcgggaaaaa | gttcagtcag | 60  |
| tgacactaat | gttcgaatcg | aacatggttc | ttcaaacact | atcttcttct | tctcctccaa | 120 |
| ttcaccgtct | ctatcttcac | cattctcaga | ttctcccttc | ttctgggtca | cccagcaaga | 180 |
| tttctcttca | gatacatgga | aggactttgg | ccattcgatc | ttttcatgat | tatgtctttg | 240 |

cagaaatttc tgctagaggt ttaccgggctt tgaacaaagc ttccttgaag aagctaccaa 300  
tcaaaggatc taccttttctg ctggggcaga gcttggtgat ggttttctgct caccacacagt 360  
tggcagcagc agcagaaatc ataaagcctg aaccgattta cgAagttgga gagttatttg 420  
aaccttagtat tcagctttct tacttgctgt tactactggg gttgcttgga gttggtactt 480  
tctatgtgat ccgtcaagta cttgtacgca gagaactaga cctctccgct aaagaattgc 540  
aggagcaagt aaggagcgga gatgcaagtg caacagagct ctttgagctt ggtgcagtga 600  
tgttgaggaa gttttatcct gcagccaaca agtttttgca acaagctatc cagaaatggg 660  
acggtgatga tcaagatctt gctcaggtct ataacgctct tggagtgagt tatgtacgag 720  
aggataaact tgacaaagga attgctcagt ttgaaatggc ggtgaagctg caaccgggtt 780  
atgtaacagc ttggaacaac cttgggggatg cttatgagaa gaagaaggag ttgccttttg 840  
cattgaatgc gtttgaagaa gttttgttgt ttgatccaaa caataagggtg gctcggccty 900  
ggcgagatgc gttgaaggat cgcgtgaagc tttataaagg tgttggtggct gttaagtcta 960  
agaaacgggtg acggctcaaa caagatgcaa actctgaacc aagaaccgtt ggtctctctc 1020  
ccccttggtg attttttttg tttgtaata tgtatggaga ttttggttta atatgaaaa 1080  
gaaactttgt tgttttttgt aaccaataaa atcagatggt taaaactt

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1568177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Tyr | Lys | Thr | Leu | Leu | Thr | Glu | Arg | Phe | Arg | Phe | Asn | Arg | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gln | Ser | Val | Thr | Leu | Met | Phe | Glu | Ser | Asn | Met | Val | Leu | Gln | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Ser | Ser | Ser | Ser | Pro | Pro | Ile | His | Arg | Leu | Tyr | Leu | His | His | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ile | Leu | Pro | Ser | Ser | Gly | Ser | Pro | Ser | Lys | Ile | Ser | Leu | Gln | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Gly | Arg | Thr | Leu | Ala | Ile | Arg | Ser | Phe | His | Asp | Tyr | Val | Phe | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ile | Ser | Ala | Arg | Gly | Leu | Pro | Ala | Leu | Asn | Lys | Ala | Ser | Leu | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Pro | Ile | Lys | Gly | Ser | Thr | Phe | Leu | Leu | Gly | Gln | Ser | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Val | Ser | Ala | His | Pro | Gln | Leu | Ala | Ala | Ala | Ala | Glu | Ile | Ile | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Glu | Pro | Ile | Tyr | Glu | Val | Gly | Glu | Leu | Phe | Glu | Leu | Ser | Ile | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Tyr | Leu | Leu | Leu | Leu | Gly | Leu | Leu | Gly | Val | Gly | Thr | Phe |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Tyr | Val | Ile | Arg | Gln | Val | Leu | Val | Arg | Arg | Glu | Leu | Asp | Leu | Ser | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Glu | Leu | Gln | Glu | Gln | Val | Arg | Ser | Gly | Asp | Ala | Ser | Ala | Thr | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Phe | Glu | Leu | Gly | Ala | Val | Met | Leu | Arg | Lys | Phe | Tyr | Pro | Ala | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Lys | Phe | Leu | Gln | Gln | Ala | Ile | Gln | Lys | Trp | Asp | Gly | Asp | Asp | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Leu | Ala | Gln | Val | Tyr | Asn | Ala | Leu | Gly | Val | Ser | Tyr | Val | Arg | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Lys | Leu | Asp | Lys | Gly | Ile | Ala | Gln | Phe | Glu | Met | Ala | Val | Lys | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Pro | Gly | Tyr | Val | Thr | Ala | Trp | Asn | Asn | Leu | Gly | Asp | Ala | Tyr | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |

Lys Lys Lys Glu Leu Pro Leu Ala Leu Asn Ala Phe Glu Glu Val Leu  
275 280 285  
Leu Phe Asp Pro Asn Asn Lys Val Ala Arg Pro Xaa Arg Asp Ala Leu  
290 295 300  
Lys Asp Arg Val Lys Leu Tyr Lys Gly Val Val Ala Val Lys Ser Lys  
305 310 315 320  
Lys Arg

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1568178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met Phe Glu Ser Asn Met Val Leu Gln Thr Leu Ser Ser Ser Ser Pro  
1 5 10 15  
Pro Ile His Arg Leu Tyr Leu His His Ser Gln Ile Leu Pro Ser Ser  
20 25 30  
Gly Ser Pro Ser Lys Ile Ser Leu Gln Ile His Gly Arg Thr Leu Ala  
35 40 45  
Ile Arg Ser Phe His Asp Tyr Val Phe Ala Glu Ile Ser Ala Arg Gly  
50 55 60  
Leu Pro Ala Leu Asn Lys Ala Ser Leu Lys Lys Leu Pro Ile Lys Gly  
65 70 75 80  
Ser Thr Phe Leu Leu Gly Gln Ser Leu Leu Met Val Ser Ala His Pro  
85 90 95  
Gln Leu Ala Ala Ala Ala Glu Ile Ile Lys Pro Glu Pro Ile Tyr Glu  
100 105 110  
Val Gly Glu Leu Phe Glu Leu Ser Ile Gln Leu Ser Tyr Leu Leu Leu  
115 120 125  
Leu Leu Gly Leu Leu Gly Val Gly Thr Phe Tyr Val Ile Arg Gln Val  
130 135 140  
Leu Val Arg Arg Glu Leu Asp Leu Ser Ala Lys Glu Leu Gln Glu Gln  
145 150 155 160  
Val Arg Ser Gly Asp Ala Ser Ala Thr Glu Leu Phe Glu Leu Gly Ala  
165 170 175  
Val Met Leu Arg Lys Phe Tyr Pro Ala Ala Asn Lys Phe Leu Gln Gln  
180 185 190  
Ala Ile Gln Lys Trp Asp Gly Asp Asp Gln Asp Leu Ala Gln Val Tyr  
195 200 205  
Asn Ala Leu Gly Val Ser Tyr Val Arg Glu Asp Lys Leu Asp Lys Gly  
210 215 220  
Ile Ala Gln Phe Glu Met Ala Val Lys Leu Gln Pro Gly Tyr Val Thr  
225 230 235 240  
Ala Trp Asn Asn Leu Gly Asp Ala Tyr Glu Lys Lys Lys Glu Leu Pro  
245 250 255  
Leu Ala Leu Asn Ala Phe Glu Glu Val Leu Leu Phe Asp Pro Asn Asn  
260 265 270  
Lys Val Ala Arg Pro Xaa Arg Asp Ala Leu Lys Asp Arg Val Lys Leu  
275 280 285  
Tyr Lys Gly Val Val Ala Val Lys Ser Lys Lys Arg  
290 295 300

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

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- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..295  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568179  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

Met Val Leu Gln Thr Leu Ser Ser Ser Ser Pro Pro Ile His Arg Leu  
1 5 10 15  
Tyr Leu His His Ser Gln Ile Leu Pro Ser Ser Gly Ser Pro Ser Lys  
20 25 30  
Ile Ser Leu Gln Ile His Gly Arg Thr Leu Ala Ile Arg Ser Phe His  
35 40 45  
Asp Tyr Val Phe Ala Glu Ile Ser Ala Arg Gly Leu Pro Ala Leu Asn  
50 55 60  
Lys Ala Ser Leu Lys Lys Leu Pro Ile Lys Gly Ser Thr Phe Leu Leu  
65 70 75 80  
Gly Gln Ser Leu Leu Met Val Ser Ala His Pro Gln Leu Ala Ala Ala  
85 90 95  
Ala Glu Ile Ile Lys Pro Glu Pro Ile Tyr Glu Val Gly Glu Leu Phe  
100 105 110  
Glu Leu Ser Ile Gln Leu Ser Tyr Leu Leu Leu Leu Leu Gly Leu Leu  
115 120 125  
Gly Val Gly Thr Phe Tyr Val Ile Arg Gln Val Leu Val Arg Arg Glu  
130 135 140  
Leu Asp Leu Ser Ala Lys Glu Leu Gln Glu Gln Val Arg Ser Gly Asp  
145 150 155 160  
Ala Ser Ala Thr Glu Leu Phe Glu Leu Gly Ala Val Met Leu Arg Lys  
165 170 175  
Phe Tyr Pro Ala Ala Asn Lys Phe Leu Gln Gln Ala Ile Gln Lys Trp  
180 185 190  
Asp Gly Asp Asp Gln Asp Leu Ala Gln Val Tyr Asn Ala Leu Gly Val  
195 200 205  
Ser Tyr Val Arg Glu Asp Lys Leu Asp Lys Gly Ile Ala Gln Phe Glu  
210 215 220  
Met Ala Val Lys Leu Gln Pro Gly Tyr Val Thr Ala Trp Asn Asn Leu  
225 230 235 240  
Gly Asp Ala Tyr Glu Lys Lys Lys Glu Leu Pro Leu Ala Leu Asn Ala  
245 250 255  
Phe Glu Glu Val Leu Leu Phe Asp Pro Asn Asn Lys Val Ala Arg Pro  
260 265 270  
Xaa Arg Asp Ala Leu Lys Asp Arg Val Lys Leu Tyr Lys Gly Val Val  
275 280 285  
Ala Val Lys Ser Lys Lys Arg  
290 295

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1525 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1525  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

gaatcgctgt tacctcatgt gatgctcgta tcattcccag ggcaagggtca cataagccct 60  
cttcttcgtc tcggaaagat cattgcctct aaaggcttaa tcgtcacctt tgtaaccaca 120

```

gaggaaccat tgggcaagaa gatgogtcaa gccacaata ttcaagacgg tgtgctcaaa 180
ccggtcgggc taggttttct ccggttcgag ttcttcgagg atggatttgt ctacaaagaa 240
gactttgatt tggtacaaaa atcacttgaa gtttcgggaa aacgagagat caagaatctt 300
gtcaagaaat atgagaagca accagtgaaga tgtctcataa ataatgcctt tgttccatgg 360
gtttgtgaca tagccgagga gcttcaaate ccatcagctg ttctttgggt ccagtcttgt 420
gcttgctcgc cgccttatta ctattaccac caccagttag ttaagtttcc gaccgaaacc 480
gagccggaaa taaccgttga cgtccctttc aagccattaa aattgaagca tgacgagSat 540
ccctagcttt cttcaccctt cctctccgct gtcctctata ggaggtacca ttttagagca 600
gatcaagcga cttcacaagc ctttctctgt tctcatcgaa acttttcaag aacttgaaaa 660
agataccatt gaccacatgt ccagctctg ccctcaagtc aacttcaacc ccatcggctc 720
gctttttact atggctaaaa ccataaggtc tgacatcaag ggagacatct ccaagccaga 780
tagtgactgc atagagtggc ttcactcgag agaaccatcc tccgttggtt acatctcttt 840
tgggactttg gctttcttga agcaaaacca gatcgacgag attgctcaeg gcattctcaa 900
ctccgggttg tctgtcttat gggttttgcg tcctccctta gaaggcttag ccatagaacc 960
acatgtcttg cctctagagc ttgaagagaa agggaagatt gtggaatggg gtcaacaaga 1020
gaaAgytttg gctcatcctg cgggttgcttg cttcttaagt cactgtggat ggaactcaac 1080
catggaggct ttaacttcag gagttcccg tatttgtttc ccgcagtggg gagatcaggt 1140
gacaaatgcg gtgtacctga ttggtgtttt caagacagga ttgagactca gccgtggagc 1200
ttctgatgag aggattgttc caagggagga ggttgctgag cgactgcttg aggccaccgt 1260
tgagagagaag gcggtggagc tgagagaaaa cgctcggagg tggaggagg aggcggaagc 1320
tgccgtggct tacggtggaa catcggaag gaattttcaa gagtttggtt acaagttggt 1380
tgatgtcaag acaatgacaa acattaataa tgtcgtgtaa gtcgtaataa tcatattgat 1440
acttggttatt accggattac gatttttaat tgtttaatat gtactaaatt gtatgcatcg 1500
atataaagtg aacaatttta tgtttg

```

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

```

Met Thr Xaa Ile Pro Ser Phe Leu His Pro Ser Ser Pro Leu Ser Ser
1 5 10 15
Ile Gly Gly Thr Ile Leu Glu Gln Ile Lys Arg Leu His Lys Pro Phe
20 25 30
Ser Val Leu Ile Glu Thr Phe Gln Glu Leu Glu Lys Asp Thr Ile Asp
35 40 45
His Met Ser Gln Leu Cys Pro Gln Val Asn Phe Asn Pro Ile Gly Pro
50 55 60
Leu Phe Thr Met Ala Lys Thr Ile Arg Ser Asp Ile Lys Gly Asp Ile
65 70 75 80
Ser Lys Pro Asp Ser Asp Cys Ile Glu Trp Leu His Ser Arg Glu Pro
85 90 95
Ser Ser Val Val Tyr Ile Ser Phe Gly Thr Leu Ala Phe Leu Lys Gln
100 105 110
Asn Gln Ile Asp Glu Ile Ala His Gly Ile Leu Asn Ser Gly Leu Ser
115 120 125
Cys Leu Trp Val Leu Arg Pro Pro Leu Glu Gly Leu Ala Ile Glu Pro
130 135 140
His Val Leu Pro Leu Glu Glu Lys Gly Lys Ile Val Glu Trp
145 150 155 160
Cys Gln Gln Glu Lys Xaa Leu Ala His Pro Ala Val Ala Cys Phe Leu
165 170 175
Ser His Cys Gly Trp Asn Ser Thr Met Glu Ala Leu Thr Ser Gly Val
180 185 190
Pro Val Ile Cys Phe Pro Gln Trp Gly Asp Gln Val Thr Asn Ala Val

```

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(2) INFORMATION FOR SEO ID NO:858:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1568182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..229  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568183  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

Met Ala Lys Thr Ile Arg Ser Asp Ile Lys Gly Asp Ile Ser Lys Pro  
1 5 10 15  
Asp Ser Asp Cys Ile Glu Trp Leu His Ser Arg Glu Pro Ser Ser Val  
20 25 30  
Val Tyr Ile Ser Phe Gly Thr Leu Ala Phe Leu Lys Gln Asn Gln Ile  
35 40 45  
Asp Glu Ile Ala His Gly Ile Leu Asn Ser Gly Leu Ser Cys Leu Trp  
50 55 60  
Val Leu Arg Pro Pro Leu Glu Gly Leu Ala Ile Glu Pro His Val Leu  
65 70 75 80  
Pro Leu Glu Leu Glu Glu Lys Gly Lys Ile Val Glu Trp Cys Gln Gln  
85 90 95  
Glu Lys Xaa Leu Ala His Pro Ala Val Ala Cys Phe Leu Ser His Cys  
100 105 110  
Gly Trp Asn Ser Thr Met Glu Ala Leu Thr Ser Gly Val Pro Val Ile  
115 120 125  
Cys Phe Pro Gln Trp Gly Asp Gln Val Thr Asn Ala Val Tyr Leu Ile  
130 135 140  
Gly Val Phe Lys Thr Gly Leu Arg Leu Ser Arg Gly Ala Ser Asp Glu  
145 150 155 160  
Arg Ile Val Pro Arg Glu Glu Val Ala Glu Arg Leu Leu Glu Ala Thr  
165 170 175  
Val Gly Glu Lys Ala Val Glu Leu Arg Glu Asn Ala Arg Arg Trp Lys  
180 185 190  
Glu Glu Ala Glu Ser Ala Val Ala Tyr Gly Gly Thr Ser Glu Arg Asn  
195 200 205  
Phe Gln Glu Phe Val Asp Lys Leu Val Asp Val Lys Thr Met Thr Asn  
210 215 220  
Ile Asn Asn Val Val  
225

(2) INFORMATION FOR SEQ ID NO:860:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1295 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1295  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568184  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

aaaacaaaaa aacacagcct ttgttctgtt tctctgcgat ttcttcgatt ttcctcttct 60  
tcgttttgat tttcagattt gtttaactcg gtcgttgctg tgacttcaaa tttcttaaaa 120  
gagagagaga gagagagagg agatagttca gaaaatctgt cagacttggg atcttttctcg 180  
gcaatgcgac gcttggttcg cgcgaaatcc ctctcccgag aggatacaac ctttttgtca 240  
ttctcttctt cttcgggtgac gcgtttcttc aaggctcttc ctctccgttc agatccaaga 300  
gatgtccgct aattctcatc ctcttaattc caaaaacgtc ctctgtaatg cagccgccgg 360  
tgccgccgcc ggggttggtt cggtctacgt tgtgtgtcct cttgatgtta taaaaacgag 420  
gtttcagggt catgggctgc ctaagctcgg tgatgcaaac atcaaaggta gtctaattgt 480  
tggcagtctt gagcagatct tcaagagaga agggatgcgt ggcttatacc gcggtctttc 540  
ccctactgtc atggctcttc tctccaattg ggccatttat tttacaatgt atgaccagct 600  
caagagcttt ctttggttcaa atgatcacia actcagcgtt ggagctaacg tattggctgc 660

```
ttcgggagct ggagctgcaa ctaccattgc cacaaatcct ctttgggtcg tcaagactag 720
acttcagaca caaggaatga gagtgggtat agtgccatac aaaagcacat tttctgcttt 780
aaggagaata gcttatgagg aggggaattcg cggattgtac agtgggtcttg tccctgcact 840
agctgggtatc agtcatgttg ccattcagtt tcccacatat gagatgatca aagtgtactt 900
ggccaagaaa ggtgataaat cagtcgataa cctcaatgct cgtgatgtag cagttgcctc 960
ttcgattgca aagatatattg catccacatt aacttaccgc cagcaggtag tacgagctag 1020
gcttcaagag caagggcacc acagtgagaa acgttactca ggagtaagag attgcatcaa 1080
gaaagtgttt gagaaagatg ggttccctgg tttttacaga gGCTgcgcca cgaatctact 1140
gagaacaact cctgcagcag ttataacttt cactagcttc gaaatggtgc atcgtttcct 1200
cgtcactcat ataccttctg agcaaagctc tatactttaa atccggtttt ttttttttga 1260
tgatgatgac gattaaaagt tattttttaca caggt
```

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1568185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

```
Met Ser Ala Asn Ser His Pro Pro Asn Ser Lys Asn Val Leu Cys Asn
1 5 10 15
Ala Ala Ala Gly Ala Ala Ala Gly Val Val Ala Ala Thr Phe Val Cys
20 25 30
Pro Leu Asp Val Ile Lys Thr Arg Phe Gln Val His Gly Leu Pro Lys
35 40 45
Leu Gly Asp Ala Asn Ile Lys Gly Ser Leu Ile Val Gly Ser Leu Glu
50 55 60
Gln Ile Phe Lys Arg Glu Gly Met Arg Gly Leu Tyr Arg Gly Leu Ser
65 70 75 80
Pro Thr Val Met Ala Leu Leu Ser Asn Trp Ala Ile Tyr Phe Thr Met
85 90 95
Tyr Asp Gln Leu Lys Ser Phe Leu Cys Ser Asn Asp His Lys Leu Ser
100 105 110
Val Gly Ala Asn Val Leu Ala Ala Ser Gly Ala Gly Ala Ala Thr Thr
115 120 125
Ile Ala Thr Asn Pro Leu Trp Val Val Lys Thr Arg Leu Gln Thr Gln
130 135 140
Gly Met Arg Val Gly Ile Val Pro Tyr Lys Ser Thr Phe Ser Ala Leu
145 150 155 160
Arg Arg Ile Ala Tyr Glu Glu Gly Ile Arg Gly Leu Tyr Ser Gly Leu
165 170 175
Val Pro Ala Leu Ala Gly Ile Ser His Val Ala Ile Gln Phe Pro Thr
180 185 190
Tyr Glu Met Ile Lys Val Tyr Leu Ala Lys Lys Gly Asp Lys Ser Val
195 200 205
Asp Asn Leu Asn Ala Arg Asp Val Ala Val Ala Ser Ser Ile Ala Lys
210 215 220
Ile Phe Ala Ser Thr Leu Thr Tyr Pro His Glu Val Val Arg Ala Arg
225 230 235 240
Leu Gln Glu Gln Gly His His Ser Glu Lys Arg Tyr Ser Gly Val Arg
245 250 255
Asp Cys Ile Lys Lys Val Phe Glu Lys Asp Gly Phe Pro Gly Phe Tyr
260 265 270
Arg Gly Cys Ala Thr Asn Leu Leu Arg Thr Thr Pro Ala Ala Val Ile
275 280 285
Thr Phe Thr Ser Phe Glu Met Val His Arg Phe Leu Val Thr His Ile
290 295 300
```

Pro Ser Glu Gln Ser Ser Ile Leu  
305 310

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Met Arg Gly Leu Tyr Arg Gly Leu Ser Pro Thr Val Met Ala Leu Leu  
1 5 10 15  
Ser Asn Trp Ala Ile Tyr Phe Thr Met Tyr Asp Gln Leu Lys Ser Phe  
20 25 30  
Leu Cys Ser Asn Asp His Lys Leu Ser Val Gly Ala Asn Val Leu Ala  
35 40 45  
Ala Ser Gly Ala Gly Ala Ala Thr Thr Ile Ala Thr Asn Pro Leu Trp  
50 55 60  
Val Val Lys Thr Arg Leu Gln Thr Gln Gly Met Arg Val Gly Ile Val  
65 70 75 80  
Pro Tyr Lys Ser Thr Phe Ser Ala Leu Arg Arg Ile Ala Tyr Glu Glu  
85 90 95  
Gly Ile Arg Gly Leu Tyr Ser Gly Leu Val Pro Ala Leu Ala Gly Ile  
100 105 110  
Ser His Val Ala Ile Gln Phe Pro Thr Tyr Glu Met Ile Lys Val Tyr  
115 120 125  
Leu Ala Lys Lys Gly Asp Lys Ser Val Asp Asn Leu Asn Ala Arg Asp  
130 135 140  
Val Ala Val Ala Ser Ser Ile Ala Lys Ile Phe Ala Ser Thr Leu Thr  
145 150 155 160  
Tyr Pro His Glu Val Val Arg Ala Arg Leu Gln Glu Gln Gly His His  
165 170 175  
Ser Glu Lys Arg Tyr Ser Gly Val Arg Asp Cys Ile Lys Lys Val Phe  
180 185 190  
Glu Lys Asp Gly Phe Pro Gly Phe Tyr Arg Gly Cys Ala Thr Asn Leu  
195 200 205  
Leu Arg Thr Thr Pro Ala Ala Val Ile Thr Phe Thr Ser Phe Glu Met  
210 215 220  
Val His Arg Phe Leu Val Thr His Ile Pro Ser Glu Gln Ser Ser Ile  
225 230 235 240  
Leu

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

Met Ala Leu Leu Ser Asn Trp Ala Ile Tyr Phe Thr Met Tyr Asp Gln  
1 5 10 15  
Leu Lys Ser Phe Leu Cys Ser Asn Asp His Lys Leu Ser Val Gly Ala

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Asn Val Leu Ala Ala Ser Gly Ala Gly Ala Ala Thr Thr Ile Ala Thr |     |     |
| 35                                                              | 40  | 45  |
| Asn Pro Leu Trp Val Val Lys Thr Arg Leu Gln Thr Gln Gly Met Arg |     |     |
| 50                                                              | 55  | 60  |
| Val Gly Ile Val Pro Tyr Lys Ser Thr Phe Ser Ala Leu Arg Arg Ile |     |     |
| 65                                                              | 70  | 75  |
| Ala Tyr Glu Glu Gly Ile Arg Gly Leu Tyr Ser Gly Leu Val Pro Ala |     |     |
| 85                                                              | 90  | 95  |
| Leu Ala Gly Ile Ser His Val Ala Ile Gln Phe Pro Thr Tyr Glu Met |     |     |
| 100                                                             | 105 | 110 |
| Ile Lys Val Tyr Leu Ala Lys Lys Gly Asp Lys Ser Val Asp Asn Leu |     |     |
| 115                                                             | 120 | 125 |
| Asn Ala Arg Asp Val Ala Val Ala Ser Ser Ile Ala Lys Ile Phe Ala |     |     |
| 130                                                             | 135 | 140 |
| Ser Thr Leu Thr Tyr Pro His Glu Val Val Arg Ala Arg Leu Gln Glu |     |     |
| 145                                                             | 150 | 155 |
| Gln Gly His His Ser Glu Lys Arg Tyr Ser Gly Val Arg Asp Cys Ile |     |     |
| 165                                                             | 170 | 175 |
| Lys Lys Val Phe Glu Lys Asp Gly Phe Pro Gly Phe Tyr Arg Gly Cys |     |     |
| 180                                                             | 185 | 190 |
| Ala Thr Asn Leu Leu Arg Thr Thr Pro Ala Ala Val Ile Thr Phe Thr |     |     |
| 195                                                             | 200 | 205 |
| Ser Phe Glu Met Val His Arg Phe Leu Val Thr His Ile Pro Ser Glu |     |     |
| 210                                                             | 215 | 220 |
| Gln Ser Ser Ile Leu                                             |     |     |
| 225                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

|              |             |             |             |             |             |      |
|--------------|-------------|-------------|-------------|-------------|-------------|------|
| aaagtgttggga | tattttattga | accgagtgggt | ttcttttcggt | gactcgccca  | ccatggaagc  | 60   |
| tgaaagtacc   | caagatatca  | tcacgtcgg   | agctggaatc  | tccggccttg  | ccactgcact  | 120  |
| tgggtccac    | aggcttggga  | tcagaagcat  | agtgtctgga  | tcttctgagc  | agctgagagc  | 180  |
| aacaggattt   | gcactttcat  | tatattttaa  | tgcttgggaag | gccatggaag  | ctctcggtat  | 240  |
| ttctcagcat   | attcgcagtc  | tcggtgatcg  | ctttcaagga  | tgggtgggtca | gacccatttc  | 300  |
| tgcaggagat   | cctcctaaag  | aaatgttatt  | tccagaatct  | gaagaatatg  | aggttcgcag  | 360  |
| catacagagg   | aagctcttgt  | tagacgctct  | agcgggacgaa | ttgcctcaag  | ggaccatacg  | 420  |
| gttctcatct   | aagcttggtc  | acatcgaatt  | gtccggacac  | tacaagatgg  | ttcatctctc  | 480  |
| cgacgggact   | atacttaaaa  | ccaagggttt  | ggtagggtgt  | gatggagtga  | agtcagtgggt | 540  |
| tggttaagtgg  | ctaggcttca  | agaatccggt  | taaaacttcc  | cgtgtagcaa  | tccgcgggat  | 600  |
| cgctcatttc   | cagacaggcc  | acgaattagg  | gagaagggttc | tttcagtttt  | atggcaacgg  | 660  |
| tggtcgttcc   | ggtttcatct  | catgtgacca  | aaacactgtc  | tactggttcc  | taaccacac   | 720  |
| ctctactgat   | ttagataaga  | aaaatcatca  | gaagatcaaa  | cagtttgtgc  | tgaccaagat  | 780  |
| caaagacttg   | cctgacaaca  | tcaagagtat  | cctggagacc  | actgatcttg  | atagtttggt  | 840  |
| gatgaatcca   | ctcatgtatc  | gacctccctg  | ggaacttctt  | tgggcaaaca  | ttgcaaaaga  | 900  |
| caacgtatgt   | gttgacgggg  | atgcacttca  | cccaatgact  | cctgatattg  | gacaagggtg  | 960  |
| ttgctcggcg   | atggaggacg  | gagttatcct  | cgctcgttgt  | ctcgggtgaag | caatgaaagc  | 1020 |
| taagaatatg   | aaaggtgaaa  | cagaagatga  | gaacgagagt  | tataggcgga  | ttgaagatgg  | 1080 |
| tttgaagaag   | tatgcaggat  | cgaggaaatg  | gagaagcatt  | gatcttataa  | ctacatcata  | 1140 |
| tacagttaggt  | ttcatacagc  | agagcagagg  | caagtggatg  | accctgttta  | gagacaagtt  | 1200 |
| catgtcctct   | ttcctttctt  | ggttgcKgtA  | gYtgaaaaag  | tctcatttca  | actgtggaag  | 1260 |
| acttagccat   | gaatgattct  | caatgagcaa  | gcacaatggt  | ag          |             |      |

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1568189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Phe | Gly | Tyr | Leu | Asn | Arg | Val | Val | Ser | Phe | Val | Asp | Ser | Pro |     |
| 1   |     |     |     | 5   |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Thr | Met | Glu | Ala | Glu | Ser | Thr | Gln | Asp | Ile | Ile | Ile | Val | Gly | Ala | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Ser | Gly | Leu | Ala | Thr | Ala | Leu | Gly | Leu | His | Arg | Leu | Gly | Ile | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Val | Leu | Glu | Ser | Ser | Glu | Gln | Leu | Arg | Ala | Thr | Gly | Phe | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Leu | Tyr | Phe | Asn | Ala | Trp | Lys | Ala | Met | Glu | Ala | Leu | Gly | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Gln | His | Ile | Arg | Ser | Leu | Gly | Asp | Arg | Phe | Gln | Gly | Trp | Val | Val |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Pro | Ile | Ser | Ala | Gly | Asp | Pro | Pro | Lys | Glu | Met | Leu | Phe | Pro | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Glu | Glu | Tyr | Glu | Val | Arg | Cys | Ile | Gln | Arg | Lys | Leu | Leu | Leu | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Leu | Ala | Gly | Glu | Leu | Pro | Gln | Gly | Thr | Ile | Arg | Phe | Ser | Ser | Lys |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Val | His | Ile | Glu | Leu | Ser | Gly | His | Tyr | Lys | Met | Val | His | Leu | Ser |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Asp | Gly | Thr | Ile | Leu | Lys | Thr | Lys | Val | Leu | Val | Gly | Cys | Asp | Gly | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Ser | Val | Val | Gly | Lys | Trp | Leu | Gly | Phe | Lys | Asn | Pro | Val | Lys | Thr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Arg | Val | Ala | Ile | Arg | Gly | Ile | Ala | His | Phe | Gln | Thr | Gly | His | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gly | Arg | Arg | Phe | Phe | Gln | Phe | Tyr | Gly | Asn | Gly | Val | Arg | Ser | Gly |
|     |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Phe | Ile | Ser | Cys | Asp | Gln | Asn | Thr | Val | Tyr | Trp | Phe | Leu | Thr | His | Thr |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Ser | Thr | Asp | Leu | Asp | Lys | Lys | Asn | His | Gln | Lys | Ile | Lys | Gln | Phe | Val |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Thr | Lys | Ile | Lys | Asp | Leu | Pro | Asp | Asn | Ile | Lys | Ser | Ile | Leu | Glu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Thr | Thr | Asp | Leu | Asp | Ser | Leu | Val | Met | Asn | Pro | Leu | Met | Tyr | Arg | Pro |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Trp | Glu | Leu | Leu | Trp | Ala | Asn | Ile | Ala | Lys | Asp | Asn | Val | Cys | Val |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Ala | Gly | Asp | Ala | Leu | His | Pro | Met | Thr | Pro | Asp | Ile | Gly | Gln | Gly | Gly |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |
| Cys | Ser | Ala | Met | Glu | Asp | Gly | Val | Ile | Leu | Ala | Arg | Cys | Leu | Gly | Glu |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ala | Met | Lys | Ala | Lys | Asn | Met | Lys | Gly | Glu | Thr | Glu | Asp | Glu | Asn | Glu |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Ser | Tyr | Arg | Arg | Ile | Glu | Asp | Gly | Leu | Lys | Lys | Tyr | Ala | Gly | Ser | Arg |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Trp | Arg | Ser | Ile | Asp | Leu | Ile | Thr | Thr | Ser | Tyr | Thr | Val | Gly | Phe |
|     |     |     | 370 |     |     |     | 375 |     |     |     | 380 |     |     |     |     |
| Ile | Gln | Gln | Ser | Arg | Gly | Lys | Trp | Met | Thr | Leu | Phe | Arg | Asp | Lys | Phe |



(2) INFORMATION FOR SEQ ID NO:866:

(A) LENGTH: 392 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Glu | Ser | Thr | Gln | Asp | Ile | Ile | Val | Gly | Ala | Gly | Ile |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Gly | Leu | Ala | Thr | Ala | Leu | Gly | Leu | His | Arg | Leu | Gly | Ile | Arg | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Val | Leu | Glu | Ser | Ser | Glu | Gln | Leu | Arg | Ala | Thr | Gly | Phe | Ala | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Leu | Tyr | Phe | Asn | Ala | Trp | Lys | Ala | Met | Glu | Ala | Leu | Gly | Ile | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gln | His | Ile | Arg | Ser | Leu | Gly | Asp | Arg | Phe | Gln | Gly | Trp | Val | Val | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Ile | Ser | Ala | Gly | Asp | Pro | Pro | Lys | Glu | Met | Leu | Phe | Pro | Glu | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Tyr | Glu | Val | Arg | Cys | Ile | Gln | Arg | Lys | Leu | Leu | Leu | Asp | Ala |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Ala | Gly | Glu | Leu | Pro | Gln | Gly | Thr | Ile | Arg | Phe | Ser | Ser | Lys | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Val | His | Ile | Glu | Leu | Ser | Gly | His | Tyr | Lys | Met | Val | His | Leu | Ser | Asp |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Gly | Thr | Ile | Leu | Lys | Thr | Lys | Val | Leu | Val | Gly | Cys | Asp | Gly | Val | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Val | Val | Gly | Lys | Trp | Leu | Gly | Phe | Lys | Asn | Pro | Val | Lys | Thr | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Arg | Val | Ala | Ile | Arg | Gly | Ile | Ala | His | Phe | Gln | Thr | Gly | His | Glu | Leu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Arg | Arg | Phe | Phe | Gln | Phe | Tyr | Gly | Asn | Gly | Val | Arg | Ser | Gly | Phe |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ile | Ser | Cys | Asp | Gln | Asn | Thr | Val | Tyr | Trp | Phe | Leu | Thr | His | Thr | Ser |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Thr | Asp | Leu | Asp | Lys | Lys | Asn | His | Gln | Lys | Ile | Lys | Gln | Phe | Val | Leu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Thr | Lys | Ile | Lys | Asp | Leu | Pro | Asp | Asn | Ile | Lys | Ser | Ile | Leu | Glu | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Thr | Asp | Leu | Asp | Ser | Leu | Val | Met | Asn | Pro | Leu | Met | Tyr | Arg | Pro | Pro |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| Trp | Glu | Leu | Leu | Trp | Ala | Asn | Ile | Ala | Lys | Asp | Asn | Val | Cys | Val | Ala |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Gly | Asp | Ala | Leu | His | Pro | Met | Thr | Pro | Asp | Ile | Gly | Gln | Gly | Gly | Cys |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ser | Ala | Met | Glu | Asp | Gly | Val | Ile | Leu | Ala | Arg | Cys | Leu | Gly | Glu | Ala |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Met | Lys | Ala | Lys | Asn | Met | Lys | Gly | Glu | Thr | Glu | Asp | Glu | Asn | Glu | Ser |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Tyr | Arg | Arg | Ile | Glu | Asp | Gly | Leu | Lys | Lys | Tyr | Ala | Gly | Ser | Arg | Lys |
|     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |
| Trp | Arg | Ser | Ile | Asp | Leu | Ile | Thr |     |     |     |     |     |     |     |     |

Gln Gln Ser Arg Gly Lys Trp Met Thr Leu Phe Arg Asp Lys Phe Met  
370 375 380  
Ser Ser Phe Leu Ser Trp Leu Xaa  
385 390

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1568191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

Met Glu Ala Leu Gly Ile Ser Gln His Ile Arg Ser Leu Gly Asp Arg  
1 5 10 15  
Phe Gln Gly Trp Val Val Arg Pro Ile Ser Ala Gly Asp Pro Pro Lys  
20 25 30  
Glu Met Leu Phe Pro Glu Ser Glu Tyr Glu Val Arg Cys Ile Gln  
35 40 45  
Arg Lys Leu Leu Leu Asp Ala Leu Ala Gly Glu Leu Pro Gln Gly Thr  
50 55 60  
Ile Arg Phe Ser Ser Lys Leu Val His Ile Glu Leu Ser Gly His Tyr  
65 70 75 80  
Lys Met Val His Leu Ser Asp Gly Thr Ile Leu Lys Thr Lys Val Leu  
85 90 95  
Val Gly Cys Asp Gly Val Lys Ser Val Val Gly Lys Trp Leu Gly Phe  
100 105 110  
Lys Asn Pro Val Lys Thr Ser Arg Val Ala Ile Arg Gly Ile Ala His  
115 120 125  
Phe Gln Thr Gly His Glu Leu Gly Arg Arg Phe Phe Gln Phe Tyr Gly  
130 135 140  
Asn Gly Val Arg Ser Gly Phe Ile Ser Cys Asp Gln Asn Thr Val Tyr  
145 150 155 160  
Trp Phe Leu Thr His Thr Ser Thr Asp Leu Asp Lys Lys Asn His Gln  
165 170 175  
Lys Ile Lys Gln Phe Val Leu Thr Lys Ile Lys Asp Leu Pro Asp Asn  
180 185 190  
Ile Lys Ser Ile Leu Glu Thr Thr Asp Leu Asp Ser Leu Val Met Asn  
195 200 205  
Pro Leu Met Tyr Arg Pro Pro Trp Glu Leu Leu Trp Ala Asn Ile Ala  
210 215 220  
Lys Asp Asn Val Cys Val Ala Gly Asp Ala Leu His Pro Met Thr Pro  
225 230 235 240  
Asp Ile Gly Gln Gly Gly Cys Ser Ala Met Glu Asp Gly Val Ile Leu  
245 250 255  
Ala Arg Cys Leu Gly Glu Ala Met Lys Ala Lys Asn Met Lys Gly Glu  
260 265 270  
Thr Glu Asp Glu Asn Glu Ser Tyr Arg Arg Ile Glu Asp Gly Leu Lys  
275 280 285  
Lys Tyr Ala Gly Ser Arg Lys Trp Arg Ser Ile Asp Leu Ile Thr Thr  
290 295 300  
Ser Tyr Thr Val Gly Phe Ile Gln Gln Ser Arg Gly Lys Trp Met Thr  
305 310 315 320  
Leu Phe Arg Asp Lys Phe Met Ser Ser Phe Leu Ser Trp Leu Xaa  
325 330 335

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1364 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1364  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```
cwywyactct ctctttctcc ttagcttccct cttcaagggt tttttgaaaa gctgcaaatt 60
tccatagcca tggacactgc taaatggcct caggagtttg ttgtgaagcc aatgaacgag 120
atcgtgacaa acacatgcct aaaacaacag tcgaatcctc cttctcctgc tactcctgtg 180
gaaaggaagg caagaccgga gaaagaccag gctttgaact gtccaagatg caactcctta 240
aacaccaagt tctgttacta caacaactac agcctgacgc agcccaggta cttttgtaaa 300
gactgcagga ggtattggac cgcaGgtggt tccctcagga acatccccgt cgggtggcggc 360
gtccgcaaga acaagagatc ttcttccaat tcctcttccct cttcaccctc ttctgtcttct 420
tcttcaaaga aacctctttt tgccaacaac aacacgccta cgcctcctct tcctcatctt 480
aacctaaga ttggtgaagc agccgctact aaagttcaag acttgacgtt ttctcaaggg 540
tttgggaaacg cccacgaggt taaagatctc aacttggcgt tttctcaagg gtttgggatc 600
ggtcaccatc atcacagtag tatcccagag tttctgcaag tagtaccag cagcagtatg 660
aagaacaacc cactggtctc aacttctctg gctttggagc ttttagggat ctctagtctc 720
tctgcttccct ctaactcaag ccctgctttc atgtcttata caaatgttca tgattcatcg 780
gtctacacag catccggggt ttggtctgagt taccacaggt ttcaagagtt catgagacca 840
gctttgggat tctctcttga ttggtggggat cctctacgtc aagaagaggg gtccagtggc 900
actaataatg gaaggccgtt gctgccattt gagagcctcc tcaaacttcc agtttcatca 960
tcaagacca atagtgggtg gaatggcaat ctgaaagaga ttaatgatga gcgtagtgat 1020
catgaacatg agaaagaaga aggagaagct gaccaatctg ttgggttttg gagtggcatg 1080
ttaagtgctg gtgcttctgc tgotgcatct ggtggtggtt catggcaata attatagtca 1140
tggaaccatc ccatgagagt ttttagaaca aatgattaca tttttcatcc atgttttaaa 1200
aagatgagag ggtaactat ataactctggg tacttactat tttagtcctt ttcctttggt 1260
ttccttctcc ttttctaaaa attattatta actttgttg gttggggatg gatactgtat 1320
gtatttagac tctcttttaa atcaatctca gttgttagtt acct
```

(2) INFORMATION FOR SEQ ID NO:869:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 353 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..353  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

```
Met Asp Thr Ala Lys Trp Pro Gln Glu Phe Val Val Lys Pro Met Asn
1 5 10 15
Glu Ile Val Thr Asn Thr Cys Leu Lys Gln Gln Ser Asn Pro Pro Ser
20 25 30
Pro Ala Thr Pro Val Glu Arg Lys Ala Arg Pro Glu Lys Asp Gln Ala
35 40 45
Leu Asn Cys Pro Arg Cys Asn Ser Leu Asn Thr Lys Phe Cys Tyr Tyr
50 55 60
Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Asp Cys Arg
65 70 75 80
Arg Tyr Trp Thr Ala Gly Gly Ser Leu Arg Asn Ile Pro Val Gly Gly
85 90 95
Gly Val Arg Lys Asn Lys Arg Ser Ser Ser Asn Ser Ser Ser Ser
100 105 110
Pro Ser Ser Ser Ser Ser Ser Lys Lys Pro Leu Phe Ala Asn Asn Asn
115 120 125
Thr Pro Thr Pro Pro Leu Pro His Leu Asn Pro Lys Ile Gly Glu Ala
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Ala Ala Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe Gly Asn |     |     |
| 145                                                             | 150 | 155 |
| Ala His Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly Phe Gly |     | 160 |
|                                                                 | 165 | 170 |
| Ile Gly His His His His Ser Ser Ile Pro Glu Phe Leu Gln Val Val |     | 175 |
|                                                                 | 180 | 185 |
| Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser Ser Ala |     | 190 |
|                                                                 | 195 | 200 |
| Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn Ser Arg |     | 205 |
|                                                                 | 210 | 215 |
| Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val Tyr Thr |     | 220 |
| 225                                                             | 230 | 235 |
| Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe Met Arg |     | 240 |
|                                                                 | 245 | 250 |
| Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg Gln Glu |     | 255 |
|                                                                 | 260 | 265 |
| Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro Phe Glu |     | 270 |
|                                                                 | 275 | 280 |
| Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser Gly Gly |     | 285 |
|                                                                 | 290 | 295 |
| Asn Gly Asn Leu Lys Glu Ile Asn Asp Glu Arg Ser Asp His Glu His |     | 300 |
| 305                                                             | 310 | 315 |
| Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp Ser Gly |     | 320 |
|                                                                 | 325 | 330 |
| Met Leu Ser Ala Gly Ala Ser Ala Ala Ala Ser Gly Gly Gly Ser Trp |     | 335 |
|                                                                 | 340 | 345 |
|                                                                 |     | 350 |
| Gln                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Asn Glu Ile Val Thr Asn Thr Cys Leu Lys Gln Gln Ser Asn Pro |     |
| 1                                                               | 5   |
| Pro Ser Pro Ala Thr Pro Val Glu Arg Lys Ala Arg Pro Glu Lys Asp |     |
|                                                                 | 10  |
|                                                                 | 15  |
| Gln Ala Leu Asn Cys Pro Arg Cys Asn Ser Leu Asn Thr Lys Phe Cys |     |
|                                                                 | 20  |
|                                                                 | 25  |
| Tyr Tyr Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Asp |     |
|                                                                 | 30  |
|                                                                 | 35  |
|                                                                 | 40  |
| Cys Arg Arg Tyr Trp Thr Ala Gly Gly Ser Leu Arg Asn Ile Pro Val |     |
|                                                                 | 45  |
|                                                                 | 50  |
|                                                                 | 55  |
| Gly Gly Gly Val Arg Lys Asn Lys Arg Ser Ser Ser Asn Ser Ser Ser |     |
|                                                                 | 60  |
|                                                                 | 65  |
|                                                                 | 70  |
|                                                                 | 75  |
| Ser Ser Pro Ser Ser Ser Ser Ser Lys Lys Pro Leu Phe Ala Asn     |     |
|                                                                 | 80  |
|                                                                 | 85  |
|                                                                 | 90  |
|                                                                 | 95  |
| Asn Asn Thr Pro Thr Pro Pro Leu Pro His Leu Asn Pro Lys Ile Gly |     |
|                                                                 | 100 |
|                                                                 | 105 |
|                                                                 | 110 |
| Glu Ala Ala Ala Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe |     |
|                                                                 | 115 |
|                                                                 | 120 |
|                                                                 | 125 |
| Gly Asn Ala His Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly |     |
|                                                                 | 130 |
|                                                                 | 135 |
|                                                                 | 140 |
| 145                                                             | 150 |
|                                                                 | 155 |
|                                                                 | 160 |

Phe Gly Ile Gly His His His Ser Ser Ile Pro Glu Phe Leu Gln  
165 170 175  
Val Val Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser  
180 185 190  
Ser Ala Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn  
195 200 205  
Ser Arg Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val  
210 215 220  
Tyr Thr Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe  
225 230 235 240  
Met Arg Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg  
245 250 255  
Gln Glu Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro  
260 265 270  
Phe Glu Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser  
275 280 285  
Gly Gly Asn Gly Asn Leu Lys Glu Ile Asn Asp Glu Arg Ser Asp His  
290 295 300  
Glu His Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp  
305 310 315 320  
Ser Gly Met Leu Ser Ala Gly Ala Ser Ala Ala Ser Gly Gly Gly  
325 330 335  
Ser Trp Gln

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| atctaacttt  | tccagataat | atattcaaaa | ttttacagag | aggaagaaga  | agttcccgac  | 60   |
| acttgtgaga  | gactataaaa | ctatacgatc | tcctcctctc | gctctcttca  | gatcacaaag  | 120  |
| ttttcgtttt  | tagggtttct | tcatacgatc | cggtttgtga | tcttcttctt  | catcaatggc  | 180  |
| gtctagtgat  | aaacaaacaa | gccccaaagg | tcacacctca | ccgtctcctc  | tccgtaattc  | 240  |
| caagttttgt  | cagtcaaata | tgagaatttt | gatctcagga | ggagctggat  | tcattggctc  | 300  |
| tcaccttggt  | gataagctga | tggaaaacga | aaagaatgag | gtgattgttg  | ctgataacta  | 360  |
| tttcaccggt  | tcaaaggaca | atctcaagaa | gtggattggt | catccgagat  | ttgaGgctta  | 420  |
| tccgtcatga  | tgtcacagag | Ccacttctga | tcgaggttga | tcagattttac | catcttgcac  | 480  |
| gtcctgcttc  | tcctatcttc | tacaagtaca | accctgtgaa | gacaatcaag  | accaatgtca  | 540  |
| ttggcacact  | gaacatgcta | ggtcttgcca | agcgtgttgg | agcaaggatt  | ttgcttacct  | 600  |
| caacctcgga  | ggtatatgga | gatcctotta | tccatcccca | gcccgaagac  | tattggggaa  | 660  |
| atgtcaaccc  | aattggtggt | aggagctggt | atgatgaagg | caagcgtggt  | gctgagacct  | 720  |
| tgatgtttga  | ctaccacagg | cagcatggaa | ttgaaatccg | cattgccaga  | atcttcaaca  | 780  |
| cttatgggtcc | acgcatgaac | attgatgatg | gacgtgttgt | aagcaacttc  | attgctcaag  | 840  |
| cactccgtgg  | tgaggcattg | actgttcaga | aaccagggac | acagactcgc  | agtttctggt  | 900  |
| atgtatctga  | catggttgat | ggacttatgc | gcctcatgga | aggagatgac  | actggtccca  | 960  |
| tcaacatcgg  | taacccaggt | gagttttaca | tggtggagtt | ggctgagaca  | gtgaaagagc  | 1020 |
| tgattaaccc  | gagcatagag | ataaagatgg | ttgagaacac | accggatgat  | ccaagacaga  | 1080 |
| ggaagccaTg  | acatacaaaa | ggctaTaaga | agttttggga | tgggaaccaa  | aggtgaagct  | 1140 |
| tcgtgaaggc  | ctgcccctta | tggagaaga  | cttcaggcta | aggctcggag  | tccacaagaa  | 1200 |
| ctaaaactcc  | atcaccgatg | atcacacgca | aacgtgaatg | cactacataa  | cccagttcta  | 1260 |
| cacttttcat  | attccttggt | gcaagtgggt | tgtttcataa | aatatgtttc  | tactttccac  | 1320 |
| agtcagaaat  | tattcctaga | gaaaaataaa | gattatgaac | gaatgctttt  | tatatattaag | 1380 |
| gaagataaaa  | attacttt   |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 178 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..178  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568200  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Leu | Ala | Lys | Arg | Val | Gly | Ala | Arg | Ile | Leu | Leu | Thr | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Ser | Glu | Val | Tyr | Gly | Asp | Pro | Leu | Ile | His | Pro | Gln | Pro | Glu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Tyr | Trp | Gly | Asn | Val | Asn | Pro | Ile | Gly | Val | Arg | Ser | Cys | Tyr | Asp | Glu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Gly | Lys | Arg | Val | Ala | Glu | Thr | Leu | Met | Phe | Asp | Tyr | His | Arg | Gln | His |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Gly | Ile | Glu | Ile | Arg | Ile | Ala | Arg | Ile | Phe | Asn | Thr | Tyr | Gly | Pro | Arg |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Met | Asn | Ile | Asp | Asp | Gly | Arg | Val | Val | Ser | Asn | Phe | Ile | Ala | Gln | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Arg | Gly | Glu | Ala | Leu | Thr | Val | Gln | Lys | Pro | Gly | Thr | Gln | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ser | Phe | Cys | Tyr | Val | Ser | Asp | Met | Val | Asp | Gly | Leu | Met | Arg | Leu | Met |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Glu | Gly | Asp | Asp | Thr | Gly | Pro | Ile | Asn | Ile | Gly | Asn | Pro | Gly | Glu | Phe |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Thr | Met | Val | Glu | Leu | Ala | Glu | Thr | Val | Lys | Glu | Leu | Ile | Asn | Pro | Ser |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |
| Ile | Glu | Ile | Lys | Met | Val | Glu | Asn | Thr | Pro | Asp | Asp | Pro | Arg | Gln | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 122 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..122  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568201  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Asp | Tyr | His | Arg | Gln | His | Gly | Ile | Glu | Ile | Arg | Ile | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Phe | Asn | Thr | Tyr | Gly | Pro | Arg | Met | Asn | Ile | Asp | Asp | Gly | Arg | Val |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Val | Ser | Asn | Phe | Ile | Ala | Gln | Ala | Leu | Arg | Gly | Glu | Ala | Leu | Thr | Val |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Gln | Lys | Pro | Gly | Thr | Gln | Thr | Arg | Ser | Phe | Cys | Tyr | Val | Ser | Asp | Met |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Val | Asp | Gly | Leu | Met | Arg | Leu | Met | Glu | Gly | Asp | Asp | Thr | Gly | Pro | Ile |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Asn | Ile | Gly | Asn | Pro | Gly | Glu | Phe | Thr | Met | Val | Glu | Leu | Ala | Glu | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Lys | Glu | Leu | Ile | Asn | Pro | Ser | Ile | Glu | Ile | Lys | Met | Val | Glu | Asn |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |

Thr Pro Asp Asp Pro Arg Gln Arg Lys Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

Met Asn Ile Asp Asp Gly Arg Val Val Ser Asn Phe Ile Ala Gln Ala  
1 5 10 15  
Leu Arg Gly Glu Ala Leu Thr Val Gln Lys Pro Gly Thr Gln Thr Arg  
20 25 30  
Ser Phe Cys Tyr Val Ser Asp Met Val Asp Gly Leu Met Arg Leu Met  
35 40 45  
Glu Gly Asp Asp Thr Gly Pro Ile Asn Ile Gly Asn Pro Gly Glu Phe  
50 55 60  
Thr Met Val Glu Leu Ala Glu Thr Val Lys Glu Leu Ile Asn Pro Ser  
65 70 75 80  
Ile Glu Ile Lys Met Val Glu Asn Thr Pro Asp Asp Pro Arg Gln Arg  
85 90 95  
Lys Pro

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

ttcaatcccc tttttttttt cgttttcgtcg tttgttcggt ttctctatcg ctctcgttca 60  
tctacgcaat ctctctcact aggtacagtt ttaaattgggt aagaagaagt cagacgagag 120  
tgctgctacc acaaagggtga agccaagtgg gaaagatgct tcgaaagatt ctaaaaaaga 180  
gaaattgtca gtctcggcta tgcttgccagg catggatcag aaagatgata aaccgaagaa 240  
gggctcatca tctagaacca aggctgctcc gaaatctaca tcttacactg atggcataga 300  
tcttctctct tctgatgaag aagacgcagg tgaatctgat gaggaagaga gacagaagga 360  
agctaggagg aagctgaaga gtgaacaaag gcaccttgag atatctgtga ctgataagga 420  
acaaaagaag cgagaggcga aagaaagatt agctcttcag gctgcagagt cggcaaagag 480  
ggaggctatg aaggacgatc atgatgcatt cacggttggt attggaagca agacctcagt 540  
gcttgaagga gacgacatgg ctgatgcaaa tggttaaggat attaccatag aatctttttc 600  
tgtatctgct cgaggtaaag agcttttgaa gaatgcttct gtcaggattt cacatggtaa 660  
aaggtatggg ttgatcgggc caaacggaat gggaaagtct acactgttaa agcttttagc 720  
ttggaggaag attccagtgc caaagaatat tgatgttctt cttgttgagc aagaggtggg 780  
tggtgatgaa aagagtgtc tgaatgcagt tgtctctgcc aatgaagagt tggttaagct 840  
acgtgaagag gctgaagtc tgcagaagtc gtcttctgga gctgatggag aaaatgttga 900  
tggtgaggat gatgatgata ctggagaaaa gcttgctgaa ctgtatgaca ggctgcagat 960  
tttaggggtca gatgctgctg aagcacaggc atccaaaatt cttgcggggg taggtttcac 1020  
aaaaAgatat gcaagtgcgt gcgactcagt ccttcagtgg tggctggagg atgcgaatat 1080  
cattagctag agctctcttc gtgcaacctt cccttttgct gttagatgaa ccactaacc 1140  
atcttgacct gagagctggt ctatgggttag aggagtattt gtgtcgctgg aagaagacac 1200  
tagttgttgt ttcacatgac cgggacttcc tcaacacagt ctgcacggag ataatacatc 1260

```
tccatgacca gaatctccac ttctaccgtg gtaatttcga tggttttgaa agcggatatg 1320
agcagcgtcg caaggagatg aacaaaaaat ttgatgtcta cgacaaacag atgaaagcag 1380
cgaagaggac tggaaccggg ggtcaacagg agaaggtaaa ggacagggcc aagtttactg 1440
ctgcaaaaga agcatccaag agtaagtcaa agggcaagac agtggatgaa gaaggcccag 1500
caccagaagc tccaaggaag tggagagatt acagtgtggt gttccacttc ccagaaccaa 1560
ctgagctcac tctctctctt ctgcagttaa ttgagggttag cttcagctat cccaacaggc 1620
cagatttcag actctcgaat gttgatgtag gtatcgatat ggggacacgg gttgcgatag 1680
ttgggcctaa cggagcagga aagtccactc tattaatctt tcttgcgga gatttagttc 1740
caacagaggg tgaaatgaga agaagccaga agctgaggat tggcaggtat tctcagcatt 1800
ttgttgacct ttaacaatg ggggaaacac cggttcagta tctccttcgt cttcatcctg 1860
accaagaggg atttagcaag caagaggcag tgcgagcgaa gctaggcaag tttgggctac 1920
caagtcacaa tcacttatct ccaattgcga aattgtctag aggacaaaag gctagggttg 1980
tggtcacctc gatctcaatg tcaaaaccac acattttgct cctggacgag cctacaaatc 2040
acttagacat gcagagtata gatgccttgg cggatgcact agatgagttc acaggtggag 2100
ttgtgttggg gagtacagac tcgagactca tatcacgtgt atgtgcggaa gaggagaaga 2160
gtcaaatttg ggtttagtaa gacggaacag tgaatttctt cccaggcaca tttgaagagt 2220
acaaagaaga tctccaaaga gaaatcaaag cagaagttga tgagtgaagt tttgttgta 2280
gcttctaagg taaactcaaa ctcttttatg ttttataaca aactcaaaaa gttttggaca 2340
attttatttt
```

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1568214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

```
Met Gly Lys Lys Lys Ser Asp Glu Ser Ala Ala Thr Thr Lys Val Lys
1 5 10 15
Pro Ser Gly Lys Asp Ala Ser Lys Asp Ser Lys Lys Glu Lys Leu Ser
20 25 30
Val Ser Ala Met Leu Ala Gly Met Asp Gln Lys Asp Asp Lys Pro Lys
35 40 45
Lys Gly Ser Ser Ser Arg Thr Lys Ala Ala Pro Lys Ser Thr Ser Tyr
50 55 60
Thr Asp Gly Ile Asp Leu Pro Pro Ser Asp Glu Glu Asp Asp Gly Glu
65 70 75 80
Ser Asp Glu Glu Glu Arg Gln Lys Glu Ala Arg Arg Lys Leu Lys Ser
85 90 95
Glu Gln Arg His Leu Glu Ile Ser Val Thr Asp Lys Glu Gln Lys Lys
100 105 110
Arg Glu Ala Lys Glu Arg Leu Ala Leu Gln Ala Ala Glu Ser Ala Lys
115 120 125
Arg Glu Ala Met Lys Asp Asp His Asp Ala Phe Thr Val Val Ile Gly
130 135 140
Ser Lys Thr Ser Val Leu Glu Gly Asp Asp Met Ala Asp Ala Asn Val
145 150 155 160
Lys Asp Ile Thr Ile Glu Ser Phe Ser Val Ser Ala Arg Gly Lys Glu
165 170 175
Leu Leu Lys Asn Ala Ser Val Arg Ile Ser His Gly Lys Arg Tyr Gly
180 185 190
Leu Ile Gly Pro Asn Gly Met Gly Lys Ser Thr Leu Leu Lys Leu Leu
195 200 205
Ala Trp Arg Lys Ile Pro Val Pro Lys Asn Ile Asp Val Leu Leu Val
210 215 220
Glu Gln Glu Val Val Gly Asp Glu Lys Ser Ala Leu Asn Ala Val Val
225 230 235 240
```



(2) INFORMATION FOR SEQ ID NO:877:

(A) LENGTH: 412 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1568215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Val | Arg | Ala | Thr | Gln | Ser | Phe | Ser | Gly | Gly | Trp | Arg | Met | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ser | Leu | Ala | Arg | Ala | Leu | Phe | Val | Gln | Pro | Thr | Leu | Leu | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Glu | Pro | Thr | Asn | His | Leu | Asp | Leu | Arg | Ala | Val | Leu | Trp | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Tyr | Leu | Cys | Arg | Trp | Lys | Lys | Thr | Leu | Val | Val | Val | Ser | His | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Asp | Phe | Leu | Asn | Thr | Val | Cys | Thr | Glu | Ile | Ile | His | Leu | His | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Asn | Leu | His | Phe | Tyr | Arg | Gly | Asn | Phe | Asp | Gly | Phe | Glu | Ser | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Glu | Gln | Arg | Arg | Lys | Glu | Met | Asn | Lys | Lys | Phe | Asp | Val | Tyr | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Gln | Met | Lys | Ala | Ala | Lys | Arg | Thr | Gly | Asn | Arg | Gly | Gln | Gln | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Val | Lys | Asp | Arg | Ala | Lys | Phe | Thr | Ala | Ala | Lys | Glu | Ala | Ser | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Lys | Ser | Lys | Gly | Lys | Thr | Val | Asp | Glu | Glu | Gly | Pro | Ala | Pro | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Pro | Arg | Lys | Trp | Arg | Asp | Tyr | Ser | Val | Val | Phe | His | Phe | Pro | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Thr | Glu | Leu | Thr | Pro | Pro | Leu | Leu | Gln | Leu | Ile | Glu | Val | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Tyr | Pro | Asn | Arg | Pro | Asp | Phe | Arg | Leu | Ser | Asn | Val | Asp | Val | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Asp | Met | Gly | Thr | Arg | Val | Ala | Ile | Val | Gly | Pro | Asn | Gly | Ala | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Ser | Thr | Leu | Leu | Asn | Leu | Leu | Ala | Gly | Asp | Leu | Val | Pro | Thr | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Glu | Met | Arg | Arg | Ser | Gln | Lys | Leu | Arg | Ile | Gly | Arg | Tyr | Ser | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Phe | Val | Asp | Leu | Leu | Thr | Met | Gly | Glu | Thr | Pro | Val | Gln | Tyr | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Arg | Leu | His | Pro | Asp | Gln | Glu | Gly | Phe | Ser | Lys | Gln | Glu | Ala | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ala | Lys | Leu | Gly | Lys | Phe | Gly | Leu | Pro | Ser | His | Asn | His | Leu | Ser |

(2) INFORMATION FOR SEO ID NO:878:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1568216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1 | Arg | Ile | Ser | Leu<br>5 | Ala | Arg | Ala | Leu | Phe<br>10 | Val | Gln | Pro | Thr | Leu<br>15 | Leu |
| Leu      | Leu | Asp | Glu | Pro      | Thr | Asn | His | Leu | Asp       | Leu | Arg | Ala | Val | Leu       | Trp |
|          |     |     | 20  |          |     |     |     | 25  |           |     |     |     | 30  |           |     |
| Leu      | Glu | Glu | Tyr | Leu      | Cys | Arg | Trp | Lys | Lys       | Thr | Leu | Val | Val | Val       | Ser |
|          |     |     | 35  |          |     |     | 40  |     |           |     |     | 45  |     |           |     |
| His      | Asp | Arg | Asp | Phe      | Leu | Asn | Thr | Val | Cys       | Thr | Glu | Ile | Ile | His       | Leu |
|          |     |     | 50  |          |     | 55  |     |     |           |     | 60  |     |     |           |     |
| His      | Asp | Gln | Asn | Leu      | His | Phe | Tyr | Arg | Gly       | Asn | Phe | Asp | Gly | Phe       | Glu |
| 65       |     |     |     |          | 70  |     |     |     |           | 75  |     |     |     |           | 80  |
| Ser      | Gly | Tyr | Glu | Gln      | Arg | Arg | Lys | Glu | Met       | Asn | Lys | Lys | Phe | Asp       | Val |
|          |     |     |     | 85       |     |     |     |     | 90        |     |     |     |     | 95        |     |
| Tyr      | Asp | Lys | Gln | Met      | Lys | Ala | Ala | Lys | Arg       | Thr | Gly | Asn | Arg | Gly       | Gln |
|          |     |     | 100 |          |     |     |     | 105 |           |     |     |     | 110 |           |     |
| Gln      | Glu | Lys | Val | Lys      | Asp | Arg | Ala | Lys | Phe       | Thr | Ala | Ala | Lys | Glu       | Ala |
|          |     |     | 115 |          |     |     | 120 |     |           |     |     | 125 |     |           |     |
| Ser      | Lys | Ser | Lys | Ser      | Lys | Gly | Lys | Thr | Val       | Asp | Glu | Glu | Gly | Pro       | Ala |
|          |     |     | 130 |          |     | 135 |     |     |           |     | 140 |     |     |           |     |
| Pro      | Glu | Ala | Pro | Arg      | Lys | Trp | Arg | Asp | Tyr       | Ser | Val | Val | Phe | His       | Phe |
| 145      |     |     |     | 150      |     |     |     |     | 155       |     |     |     |     |           | 160 |
| Pro      | Glu | Pro | Thr | Glu      | Leu | Thr | Pro | Pro | Leu       | Leu | Gln | Leu | Ile | Glu       | Val |
|          |     |     |     | 165      |     |     |     |     | 170       |     |     |     |     | 175       |     |
| Ser      | Phe | Ser | Tyr | Pro      | Asn | Arg | Pro | Asp | Phe       | Arg | Leu | Ser | Asn | Val       | Asp |
|          |     |     | 180 |          |     |     |     | 185 |           |     |     |     | 190 |           |     |
| Val      | Gly | Ile | Asp | Met      | Gly | Thr | Arg | Val | Ala       | Ile | Val | Gly | Pro | Asn       | Gly |
|          |     |     | 195 |          |     |     | 200 |     |           |     |     | 205 |     |           |     |
| Ala      | Gly | Lys | Ser | Thr      | Leu | Leu | Asn | Leu | Leu       | Ala | Gly | Asp | Leu | Val       | Pro |
|          |     |     | 210 |          |     | 215 |     |     |           |     | 220 |     |     |           |     |
| Thr      | Glu | Gly | Glu | Met      | Arg | Arg | Ser | Gln | Lys       | Leu | Arg | Ile | Gly | Arg       | Tyr |
| 225      |     |     |     | 230      |     |     |     |     | 235       |     |     |     |     |           | 240 |
| Ser      | Gln | His | Phe | Val      | Asp | Leu | Leu | Thr | Met       | Gly | Glu | Thr | Pro | Val       | Gln |
|          |     |     |     | 245      |     |     |     |     | 250       |     |     |     |     | 255       |     |
| Tyr      | Leu | Leu | Arg | Leu      | His | Pro | Asp | Gln | Glu       | Gly | Phe | Ser | Lys | Gln       | Glu |
|          |     |     | 260 |          |     |     |     | 265 |           |     |     |     | 270 |           |     |

Ala Val Arg Ala Lys Leu Gly Lys Phe Gly Leu Pro Ser His Asn His  
275 280 285  
Leu Ser Pro Ile Ala Lys Leu Ser Arg Gly Gln Lys Ala Arg Val Val  
290 295 300  
Phe Thr Ser Ile Ser Met Ser Lys Pro His Ile Leu Leu Leu Asp Glu  
305 310 315 320  
Pro Thr Asn His Leu Asp Met Gln Ser Ile Asp Ala Leu Ala Asp Ala  
325 330 335  
Leu Asp Glu Phe Thr Gly Gly Val Val Leu Val Ser His Asp Ser Arg  
340 345 350  
Leu Ile Ser Arg Val Cys Ala Glu Glu Lys Ser Gln Ile Trp Val  
355 360 365  
Val Glu Asp Gly Thr Val Asn Phe Phe Pro Gly Thr Phe Glu Glu Tyr  
370 375 380  
Lys Glu Asp Leu Gln Arg Glu Ile Lys Ala Glu Val Asp Glu  
385 390 395

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaagaaaga | aaaaaatgcc | ttcttttgc  | tttgatctc  | atcaccattt | ggcgaatcct | 60  |
| acagactcgc | cgccgtactc | cgtcgaaatt | agcatcgacg | gtgactcctc | cgacttggat | 120 |
| tctttgtctc | aggtcgattt | agagtcgggc | ggtgtaccgg | cgccggagaa | acagctacat | 180 |
| tccggtggta | agaagaggag | aactaggagg | agaaagagga | ggaagaagaa | gaagaagaag | 240 |
| aaaggtggaa | gagattgcag | gatctgtcat | cttcctttag | agactaacia | agaagctgaa | 300 |
| gatgaagatg | aagaagaaga | agatgattct | gatgatgatg | aagatgaaga | agatgaagaa | 360 |
| gaagaagaag | aagaagaaga | atattatggt | ttgcctttgc | aattaggttg | ctcttgtaaa | 420 |
| ggtgatattg | gtgttgctca | tagtaagtgt | gctgagactt | ggtttaagat | caaaggaaac | 480 |
| atgacatgtg | agatatgcgg | cgcaatggct | ctaaAcgtgg | ctggtgaaca | atctaaNtcc | 540 |
| ggagagcact | gcttctacac | attcacaagc | agctgcggga | caatctctaa | ctcagacaga | 600 |
| gccacgagga | atctggcatg | gtgcacctgt | tatgaacttc | ttacttgctg | ctatggtcct | 660 |
| cgccttcgtt | gtttcttggc | tttttcaact | caaagtcctc | aagtgaacg  | ttttccatct | 720 |
| ctctctctct | ctctctttcg | cccacccgca | cgagctcact | cttctcctgt | tcttgagccg | 780 |
| cttgcaatcg | ctgaatcaat | ccctcctggt | gcttgattat | tcacacgttt | tgtagctgta | 840 |
| aaaacttggt | agtgtttaga | ttgttgtaac | ttgtgagatt | tacattttgt | ataatattgt | 900 |
| tctctgctcc | ggcttcgtg  |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Lys Arg Lys Lys Lys Met Pro Ser Phe Ala Phe Gly Ser His His His  
1 5 10 15  
Leu Ala Asn Pro Thr Asp Ser Pro Pro Tyr Ser Val Glu Ile Ser Ile  
20 25 30  
Asp Gly Asp Ser Ser Asp Leu Asp Ser Leu Ser Gln Val Asp Leu Glu

2025 RELEASE UNDER E.O. 14176

```
(2) INFORMATION FOR SEQ ID NO:881:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..266
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568219
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ser | Phe | Ala | Phe | Gly | Ser | His | His | His | Leu | Ala | Asn | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ser | Pro | Pro | Tyr | Ser | Val | Glu | Ile | Ser | Ile | Asp | Gly | Asp | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Asp | Ser | Leu | Ser | Gln | Val | Asp | Leu | Glu | Ser | Gly | Gly | Val | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Pro | Glu | Lys | Gln | Leu | His | Ser | Gly | Gly | Lys | Lys | Arg | Arg | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Lys | Arg | Arg | Lys | Lys | Lys | Lys | Lys | Lys | Lys | Gly | Gly | Arg | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Arg | Ile | Cys | His | Leu | Pro | Leu | Glu | Thr | Asn | Lys | Glu | Ala | Glu | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Glu | Glu | Glu | Glu | Asp | Asp | Ser | Asp | Asp | Asp | Glu | Asp | Glu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Glu | Glu | Glu | Glu | Glu | Glu | Glu | Glu | Glu | Tyr | Tyr | Gly | Leu | Pro | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Leu | Gly | Cys | Ser | Cys | Lys | Gly | Asp | Leu | Gly | Val | Ala | His | Ser | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Ala | Glu | Thr | Trp | Phe | Lys | Ile | Lys | Gly | Asn | Met | Thr | Cys | Glu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:882:

(A) LENGTH: 1475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1475

(D) OTHER INFORMATION: / Ceres Seq. ID 1568230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| aaaatagaga | cctttcttta  | acacagagaa | agagcctgag | agacaagtga  | gaaacgcaac | 60   |
| aacaacaccg | aaagagagag  | tccaaattcg | aaagagaaaa | agaatcaaat  | tccttcttct | 120  |
| tccttttttg | attttcaatt  | attactttta | tcttctttcc | cgctctctat  | tcttcttctt | 180  |
| ctttaggatc | aatcaccggt  | tagctttctt | cccatacgtc | tctccgttta  | cgaccagtat | 240  |
| acagaggctg | gagctgggga  | agaaaaggat | tgtctatgga | gggagacgtc  | ggaatagggt | 300  |
| tggtatgcca | gaatactatg  | gatgggaagg | cgagtaatgg | aaatggttta  | gagaagactg | 360  |
| taccttcttg | ttgccttaag  | gctatggcat | gtttacctga | ggatgatgct  | aagtgtcact | 420  |
| ccactgttgt | ttctgggtgg  | ttttcggaac | ctcaccctcg | ctctgggaaa  | aaaggcggca | 480  |
| aagcagtcta | tttcaacaac  | cctatgtggc | caggagaagc | acactcactg  | aaagttgaga | 540  |
| aagttctgtt | caaagacaag  | tccgattttc | aggaagtctt | agtgttcgag  | tcagccacgt | 600  |
| acggaaaggt | gcttgttcta  | gatggtatcg | tacagctgac | cgaaaaagat  | gaatgtgcat | 660  |
| atcaggagat | gatagcccat  | ctgcctttat | gctctatatc | ttcccctaaa  | aatgttcttg | 720  |
| ttgttggtgg | aggtgatggt  | ggtgttcttc | gagagatttc | tcgccatagt  | tctgttgagg | 780  |
| ttattgatat | ctgtgagata  | gacaagatgg | ttatagatgt | gtctaagaag  | ttcttccccg | 840  |
| agtttagcgt | tgggtttgac  | gatoctcgtg | ttcaacttca | ctgttgtagt  | gctgctgagt | 900  |
| tcctccgtaa | atccctgaa   | gggaagtatg | atgccatcat | tatttgattct | tcagatcccg | 960  |
| taggtctcgc | tcttgcgctt  | gttgagaagc | ctttcttcga | gacactggct  | agagcgttga | 1020 |
| agcctggggg | agttctttgt  | aacatggcag | aaagtatgtg | gctccatact  | catcttattg | 1080 |
| aagatatgat | ctccatttgc  | cgtcaaacat | tcaaaagtgt | tcactatgcg  | tgagcagcgc | 1140 |
| tccccacata | tccaagcggc  | gtgattgggt | tcgtcttggt | ctctactgaa  | ggaccagctg | 1200 |
| ttgacttcaa | gaacccaatc  | aaccctattg | agaaactaga | cggtgcgatg  | acccataaaa | 1260 |
| gagaattgaa | gttctataac  | tctgatatgc | acagagccgc | atttgctttg  | cccacattCc | 1320 |
| tcgggagaga | agttagcttca | cttctggctt | cttgacttct | gtttggctct  | accatatccc | 1380 |
| tgcatcaaaa | ctttgtagaa  | ctcttgaa   | ggaataataa | atcattgaag  | gctttgtatc | 1440 |
| tctaagttta | ctcctttata  | aaaagactta | tattt      |             |            |      |

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1568231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

Met Glu Gly Asp Val Gly Ile Gly Leu Val Cys Gln Asn Thr Met Asp  
1 5 10 15  
Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro Ser Cys  
20 25 30  
Cys Leu Lys Ala Met Ala Cys Leu Pro Glu Asp Asp Ala Lys Cys His  
35 40 45  
Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly  
50 55 60  
Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly  
65 70 75 80  
Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser  
85 90 95  
Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val  
100 105 110  
Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala  
115 120 125  
Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro  
130 135 140  
Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu  
145 150 155 160  
Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp  
165 170 175  
Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val  
180 185 190  
Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala Ala Glu  
195 200 205  
Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp  
210 215 220  
Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe  
225 230 235 240  
Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn  
245 250 255  
Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile  
260 265 270  
Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser  
275 280 285  
Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr  
290 295 300  
Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys  
305 310 315 320  
Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser  
325 330 335  
Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu  
340 345 350  
Val Ala Ser Leu Leu Ala Ser  
355

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1568232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro

```

1 5 10 15
Ser Cys Cys Leu Lys Ala Met Ala Cys Leu Pro Glu Asp Asp Ala Lys
20 25 30
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg
35 40 45
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp
50 55 60
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp
65 70 75
Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85 90 95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100 105 110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115 120 125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130 135 140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145 150 155
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165 170 175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala
180 185 190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195 200 205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210 215 220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225 230 235
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245 250 255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260 265 270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275 280 285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290 295 300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305 310 315
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325 330 335
Arg Glu Val Ala Ser Leu Leu Ala Ser
340 345

```

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1568233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

```

Met Ala Cys Leu Pro Glu Asp Asp Ala Lys Cys His Ser Thr Val Val
1 5 10 15
Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly Lys Lys Gly Gly
20 25 30
Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly Glu Ala His Ser
35 40 45

```

Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser Asp Phe Gln Glu  
50 55 60  
Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val Leu Val Leu Asp  
65 70 75 80  
Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala Tyr Gln Glu Met  
85 90 95  
Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro Lys Asn Val Leu  
100 105 110  
Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Ile Ser Arg His  
115 120 125  
Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp Lys Met Val Ile  
130 135 140  
Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val Gly Phe Asp Asp  
145 150 155 160  
Pro Arg Val Gln Leu His Ile Gly Asp Ala Ala Glu Phe Leu Arg Lys  
165 170 175  
Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp Ser Ser Asp Pro  
180 185 190  
Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe Phe Glu Thr Leu  
195 200 205  
Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn Met Ala Glu Ser  
210 215 220  
Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile Ser Ile Cys Arg  
225 230 235 240  
Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser Val Pro Thr Tyr  
245 250 255  
Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr Glu Gly Pro Ala  
260 265 270  
Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys Leu Asp Gly Ala  
275 280 285  
Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser Asp Met His Arg  
290 295 300  
Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu Val Ala Ser Leu  
305 310 315 320  
Leu Ala Ser

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cacaaattca gaagaaCaag aacagagaaaa acagaggaag aggtgagatg gaggaacttg | 60  |
| tagggcttct gagaatccga gtgaagagag ggatcaatct tgctcagcga gacactctaa  | 120 |
| gcagcgaccc tttgtgtgtc ataaccatgg gatcacagaa gctgaagact cgtgttgtgg  | 180 |
| aaaataactg caaccctgag tggaacgagg aattaaccct tgcgttaaga catcccgatg  | 240 |
| aacctgtgaa tctgatagtg tatgataaag atacattcac atcgcacgac aagatgggag  | 300 |
| atgcaaagat agatattaaa ccatttctgg aggttcacaa aatggggttg caagaacttc  | 360 |
| cagatggaac agagatcaag agagttgtga taactttgat ggatagtgtt ctgaaatcac  | 420 |
| tctttttggt ttggagccc                                               |     |

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..145  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

Gln Ile Gln Lys Asn Lys Asn Arg Glu Asn Arg Gly Arg Gly Glu Met  
1                  5                  10                  15  
Glu Glu Leu Val Gly Leu Leu Arg Ile Arg Val Lys Arg Gly Ile Asn  
                  20                  25                  30  
Leu Ala Gln Arg Asp Thr Leu Ser Ser Asp Pro Phe Val Val Ile Thr  
                  35                  40                  45  
Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys Asn  
50                  55                  60  
Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp Glu  
65                  70                  75                  80  
Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His Asp  
                  85                  90                  95  
Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val His  
                  100                  105                  110  
Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg Val  
115                  120                  125  
Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val Trp  
130                  135                  140  
Ser  
145

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 130 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..130

    (D) OTHER INFORMATION: / Ceres Seq. ID 1568236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

Met Glu Glu Leu Val Gly Leu Leu Arg Ile Arg Val Lys Arg Gly Ile  
1                  5                  10                  15  
Asn Leu Ala Gln Arg Asp Thr Leu Ser Ser Asp Pro Phe Val Val Ile  
                  20                  25                  30  
Thr Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys  
35                  40                  45  
Asn Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp  
50                  55                  60  
Glu Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His  
65                  70                  75                  80  
Asp Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val  
                  85                  90                  95  
His Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg  
                  100                  105                  110  
Val Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val  
115                  120                  125  
Trp Ser  
130

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 97 amino acids  
    (B) TYPE: amino acid

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(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568237  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:  
Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys Asn  
1 5 10 15  
Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp Glu  
20 25 30  
Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His Asp  
35 40 45  
Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val His  
50 55 60  
Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg Val  
65 70 75 80  
Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val Trp  
85 90 95  
Ser

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..602  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

aacaagagcg tccttttgatt ggttttggat tttgtttgtg tctctcctcaaa atgacaaaaac 60  
tatggacttc tctctctgct ctccattccc tcgctggacc cgtgggtgatg ctgctctatc 120  
cgttatatgc gtcggtgata gcaatagaga gcccatcaaa agtagatgac gagcaatggc 180  
ttgcttattg gattctctat tctttccctta ctctatcaga actcatcctt caatctctcc 240  
tagagtggat accgatatgg tacacggcga aGctagtgtt tgtggcatgg ttggttttac 300  
cacaatttag aggagctgct tttatatata acaaagtcgt gaggggaacag ttcaagaagt 360  
acggcatcct caaacctaag gttagagcatc aggctgagtg agtcaaaaag aggagggggac 420  
acaagagggc ttcaactgtt gggtctccag tttctaattct ctttttgctt tthctatttt 480  
gtcttatatc tcttttgata tacggaaaaa tggggtagtt cttattatga gcctctgctt 540  
gaatgtatgt gaaaagacct tttattcgac gttaaaatat tatattagag attataaatt 600  
tt

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..132  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Gln Glu Arg Pro Leu Ile Gly Phe Gly Phe Cys Cys Val Pro Leu Lys  
1 5 10 15  
Met Thr Lys Leu Trp Thr Ser Leu Ser Ala Leu His Ser Leu Ala Gly  
20 25 30

Pro Val Val Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile  
35 40 45  
Glu Ser Pro Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile  
50 55 60  
Leu Tyr Ser Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu  
65 70 75 80  
Glu Trp Ile Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp  
85 90 95  
Leu Val Leu Pro Gln Phe Arg Gly Ala Ala Phe Ile Tyr Asn Lys Val  
100 105 110  
Val Arg Glu Gln Phe Lys Lys Tyr Gly Ile Leu Lys Pro Lys Val Glu  
115 120 125  
His Gln Ala Glu  
130

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met Thr Lys Leu Trp Thr Ser Leu Ser Ala Leu His Ser Leu Ala Gly  
1 5 10 15  
Pro Val Val Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile  
20 25 30  
Glu Ser Pro Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile  
35 40 45  
Leu Tyr Ser Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu  
50 55 60  
Glu Trp Ile Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp  
65 70 75 80  
Leu Val Leu Pro Gln Phe Arg Gly Ala Ala Phe Ile Tyr Asn Lys Val  
85 90 95  
Val Arg Glu Gln Phe Lys Lys Tyr Gly Ile Leu Lys Pro Lys Val Glu  
100 105 110  
His Gln Ala Glu  
115

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile Glu Ser Pro  
1 5 10 15  
Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile Leu Tyr Ser  
20 25 30  
Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu Glu Trp Ile  
35 40 45  
Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp Leu Val Leu

(2) INFORMATION FOR SEQ ID NO:894:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

(2) INFORMATION FOR SEQ ID NO:895:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1568268

|          |     |     |     |     |          |     |     |     |     |     |     |     |     |     |     |           |
|----------|-----|-----|-----|-----|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|
| Arg<br>1 | Leu | Leu | Ile |     | Phe<br>5 | Tyr | His | Leu | Gln | Ala | Tyr | Ser | Ile | Phe | Phe | Arg<br>15 |
| Phe      | Glu | Met | Val |     | Ser      | Phe | Lys | Val | Ser | Leu | Val | Ser | Thr | Ser | Pro | Ile       |
|          |     |     | 20  |     |          |     |     |     | 25  |     |     |     |     | 30  |     |           |
| Asp      | Gly | Gln | Lys | Pro | Gly      | Thr | Ser | Gly | Leu | Arg | Lys | Lys | Val | Lys | Val |           |
|          |     | 35  |     |     |          |     | 40  |     |     |     |     | 45  |     |     |     |           |
| Phe      | Lys | Gln | Pro | Asn | Tyr      | Leu | Glu | Asn | Phe | Val | Gln | Ala | Thr | Phe | Asn |           |
|          | 50  |     |     |     | 55       |     |     |     |     | 60  |     |     |     |     |     |           |
| Ala      | Leu | Thr | Thr | Glu | Lys      | Val | Lys | Gly | Ala | Thr | Leu | Val | Val | Ser | Gly |           |
| 65       |     |     |     |     | 70       |     |     |     |     | 75  |     |     |     |     | 80  |           |
| Asp      | Gly | Arg | Tyr | Tyr | Ser      | Glu | Gln | Ala | Ile | Gln | Ile | Ile | Val | Lys | Met |           |
|          |     |     |     | 85  |          |     |     |     | 90  |     |     |     |     | 95  |     |           |
| Ala      | Ala | Ala | Asn | Gly | Val      | Arg | Arg | Val | Trp | Val | Gly | Gln | Asn | Ser | Leu |           |
|          |     |     | 100 |     |          |     |     | 105 |     |     |     |     | 110 |     |     |           |
| Leu      | Ser | Thr | Pro | Ala | Val      | Ser | Ala | Ile | Ile | Arg | Glu | Arg | Val | Gly | Ala |           |
|          |     | 115 |     |     |          |     | 120 |     |     |     |     | 125 |     |     |     |           |
| Asp      | Gly | Ser | Lys | Ala | Thr      | Gly | Ala | Phe | Ile | Leu | Thr | Ala | Ser | His | Asn |           |
|          | 130 |     |     |     |          | 135 |     |     |     |     | 140 |     |     |     |     |           |
| Pro      | Gly | Gly | Pro | Thr | Glu      | Asp | Phe | Gly | Ile | Lys | Tyr | Asn | Met | Glu | Asn |           |
| 145      |     |     |     |     | 150      |     |     |     |     | 155 |     |     |     |     | 160 |           |
| Gly      | Gly | Pro | Ala | Pro | Glu      | Ser | Ile | Thr | Asp | Lys | Ile | Tyr | Glu | Asn | Thr |           |
|          |     |     | 165 |     |          |     |     |     | 170 |     |     |     |     | 175 |     |           |
| Lys      | Thr | Ile | Lys | Glu | Tyr      | Pro | Ile | Ala | Glu | Asp | Leu | Pro | Arg | Val | Asp |           |
|          |     | 180 |     |     |          |     |     | 185 |     |     |     |     | 190 |     |     |           |
| Ile      | Ser | Thr | Ile | Gly | Ile      | Thr | Ser | Phe | Glu | Gly | Pro | Glu | Gly | Lys | Phe |           |
|          | 195 |     |     |     |          |     | 200 |     |     |     |     | 205 |     |     |     |           |
| Asp      | Val | Glu | Val | Phe | Asp      | Ser | Ala | Asp | Asp | Tyr | Val | Lys | Leu | Met | Lys |           |
|          | 210 |     |     |     |          | 215 |     |     |     |     | 220 |     |     |     |     |           |
| Ser      | Ile | Phe | Asp | Phe | Glu      | Ser | Ile | Lys | Lys | Leu | Leu | Ser | Tyr | Pro | Lys |           |
| 225      |     |     |     | 230 |          |     |     |     |     | 235 |     |     |     |     | 240 |           |
| Phe      | Thr | Phe | Cys | Tyr | Asp      | Ala | Leu | His | Gly | Val | Ala | Gly | Ala | Tyr | Ala |           |
|          |     |     | 245 |     |          |     |     |     | 250 |     |     |     |     | 255 |     |           |
| His      | Arg | Ile | Phe | Val | Glu      | Glu | Leu | Gly | Ala | Pro | Glu | Ser | Ser | Leu | Leu |           |
|          |     | 260 |     |     |          |     |     | 265 |     |     |     |     | 270 |     |     |           |
| Asn      | Cys | Val | Pro | Lys | Glu      | Asp | Phe | Gly | Gly | Gly | His | Pro | Asp | Pro | Asn |           |
|          | 275 |     |     |     |          |     | 280 |     |     |     |     | 285 |     |     |     |           |
| Leu      | Thr | Tyr | Ala | Lys | Glu      | Leu | Val | Ala | Arg | Met | Gly | Leu | Ser | Lys | Thr |           |
|          | 290 |     |     |     |          | 295 |     |     |     |     | 300 |     |     |     |     |           |
| Asp      | Asp | Ala | Gly | Gly | Glu      | Pro | Pro | Glu | Phe | Gly | Ala | Ala | Ala | Asp | Gly |           |
| 305      |     |     |     | 310 |          |     |     |     | 315 |     |     |     |     |     | 320 |           |
| Asp      | Ala | Asp | Arg | Asn | Met      | Ile | Leu | Gly | Lys | Arg | Phe | Phe | Val | Thr | Pro |           |
|          |     |     | 325 |     |          |     |     |     | 330 |     |     |     |     | 335 |     |           |
| Ser      | Asp | Ser | Val | Ala | Ile      | Ile | Ala | Ala | Asn | Ala | Val | Gly | Ala | Ile | Pro |           |
|          |     |     | 340 | </  |          |     |     |     |     |     |     |     |     |     |     |           |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

|                                                                 |   |  |    |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------------------------------|---|--|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SEQUENCE DESCRIPTION: SEQ ID NO:1555                            |   |  |    |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met Val Ser Phe Lys Val Ser Leu Val Ser Thr Ser Pro Ile Asp Gly | 1 |  |    |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gln Lys Pro Gly Thr Ser Gly Leu Arg Lys Lys Val Lys Val Phe Lys |   |  |    | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
|                                                                 |   |  | 20 |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Gln Pro Asn Tyr Leu Glu Asn Phe Val Gln Ala Thr Phe Asn Ala Leu |   |  |    |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr Thr Glu Lys Val Lys Gly Ala Thr Leu Val Val Ser Gly Asp Gly |   |  |    |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg Tyr Tyr Ser Glu Gln Ala Ile Gln Ile Ile Val Lys Met Ala Ala |   |  |    |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ala Asn Gly Val Arg Arg Val Trp Val Gly Gln Asn Ser Leu Leu Ser |   |  |    | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr Pro Ala Val Ser Ala Ile Ile Arg Glu Arg Val Gly Ala Asp Gly |   |  |    |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser Lys Ala Thr Gly Ala Phe Ile Leu Thr Ala Ser His Asn Pro Gly |   |  |    |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
| Gly Pro Thr Glu Asp Phe Gly Ile Lys Tyr Asn Met Glu Asn Gly Gly |   |  |    |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Pro Ala Pro Glu Ser Ile Thr Asp Lys Ile Tyr Glu Asn Thr Lys Thr |   |  |    |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Ile Lys Glu Tyr Pro Ile Ala Glu Asp Leu Pro Arg Val Asp Ile Ser |   |  |    | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr Ile Gly Ile Thr Ser Phe Glu Gly Pro Glu Gly Lys Phe Asp Val |   |  |    |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Glu Val Phe Asp Ser Ala Asp Asp Tyr Val Lys Leu Met Lys Ser Ile |   |  |    |     |     | 200 |     |     |     |     | 205 |     |     |     |     |     |
| Phe Asp Phe Glu Ser Ile Lys Lys Leu Leu Ser Tyr Pro Lys Phe Thr |   |  |    |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Phe Cys Tyr Asp Ala Leu His Gly Val Ala Gly Ala Tyr Ala His Arg |   |  |    |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Ile Phe Val Glu Glu Leu Gly Ala Pro Glu Ser Ser Leu Leu Asn Cys |   |  |    |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val Pro Lys Glu Asp Phe Gly Gly Gly His Pro Asp Pro Asn Leu Thr |   |  |    |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr Ala Lys Glu Leu Val Ala Arg Met Gly Leu Ser Lys Thr Asp Asp |   |  |    |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ala Gly Gly Glu Pro Pro Glu Phe Gly Ala Ala Ala Asp Gly Asp Ala |   |  |    |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Asp Arg Asn Met Ile Leu Gly Lys Arg Phe Phe Val Thr Pro Ser Asp |   |  |    |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser Val Ala Ile Ile Ala Ala Asn Ala Val Gly Ala Ile Pro Tyr Phe |   |  |    |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser Ser Gly Leu Lys Gly Val Ala Arg Ser Met Pro Thr Ser Ala Ala |   |  |    |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu Asp Val Val Ala Lys Asn Leu Gly Leu Lys Phe Phe Glu Val Pro |   |  |    |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Gly Met Cys Ser |   |  |    |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Val Cys Gly Glu Glu Ser Phe Gly Thr Gly Ser Asp His Ile Arg     |   |  |    |     | 390 |     |     |     |     |     | 395 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:897:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..322
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Asn | Gly | Val | Arg | Arg | Val | Trp | Val | Gly | Gln | Asn | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ser | Thr | Pro | Ala | Val | Ser | Ala | Ile | Ile | Arg | Glu | Arg | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asp | Gly | Ser | Lys | Ala | Thr | Gly | Ala | Phe | Ile | Leu | Thr | Ala | Ser | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Pro | Gly | Gly | Pro | Thr | Glu | Asp | Phe | Gly | Ile | Lys | Tyr | Asn | Met | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Gly | Gly | Pro | Ala | Pro | Glu | Ser | Ile | Thr | Asp | Lys | Ile | Tyr | Glu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Lys | Thr | Ile | Lys | Glu | Tyr | Pro | Ile | Ala | Glu | Asp | Leu | Pro | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ile | Ser | Thr | Ile | Gly | Ile | Thr | Ser | Phe | Glu | Gly | Pro | Glu | Gly | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Asp | Val | Glu | Val | Phe | Asp | Ser | Ala | Asp | Asp | Tyr | Val | Lys | Leu | Met |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Ser | Ile | Phe | Asp | Phe | Glu | Ser | Ile | Lys | Lys | Leu | Leu | Ser | Tyr | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Phe | Thr | Phe | Cys | Tyr | Asp | Ala | Leu | His | Gly | Val | Ala | Gly | Ala | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | His | Arg | Ile | Phe | Val | Glu | Glu | Leu | Gly | Ala | Pro | Glu | Ser | Ser | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Asn | Cys | Val | Pro | Lys | Glu | Asp | Phe | Gly | Gly | Gly | His | Pro | Asp | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Leu | Thr | Tyr | Ala | Lys | Glu | Leu | Val | Ala | Arg | Met | Gly | Leu | Ser | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Thr | Asp | Asp | Ala | Gly | Gly | Glu | Pro | Pro | Glu | Phe | Gly | Ala | Ala | Ala | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Asp | Ala | Asp | Arg | Asn | Met | Ile | Leu | Gly | Lys | Arg | Phe | Phe | Val | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Ser | Asp | Ser | Val | Ala | Ile | Ile | Ala | Ala | Asn | Ala | Val | Gly | Ala | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Tyr | Phe | Ser | Ser | Gly | Leu | Lys | Gly | Val | Ala | Arg | Ser | Met | Pro | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ala | Ala | Leu | Asp | Val | Val | Ala | Lys | Asn | Leu | Gly | Leu | Lys | Phe | Phe |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Val | Pro | Thr | Gly | Trp | Lys | Phe | Phe | Gly | Asn | Leu | Met | Asp | Ala | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Cys | Ser | Val | Cys | Gly | Glu | Glu | Ser | Phe | Gly | Thr | Gly | Ser | Asp | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:898:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1445 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..1445

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(D) OTHER INFORMATION: / Ceres Seq. ID 1568286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| gcaaaaaccac | cgccgtatat  | ccacggccgt | cttatcaccg  | gcaacaaccg | taggtttttg | 60   |
| ttttccgtcg  | cgatggaggt  | ggataagaag | gacgagagag  | aggtggaatc | ttcggagcaa | 120  |
| gtggtgaatc  | catgggaagt  | gtccgccaaa | gacggcgagg  | agatcgatta | cgacaagctt | 180  |
| attgacaaat  | ttggatgtca  | aaggcttgac | gagtcactga  | ttgatcgtgt | tcagagactg | 240  |
| acttctcgtc  | aaccacacgt  | gttcctccgc | cgtagtgtct  | tcttcgcca  | Ccgggatttc | 300  |
| aatgagattt  | tggacgctta  | tgagagagga | gacaagttct  | atctctacac | tggaagagga | 360  |
| ccttcacag   | aagcattgca  | tttggggcat | ttgattcctt  | tcatgtttac | caaatacttg | 420  |
| caagaagctt  | tcaaggttcc  | ccttggtata | cagctcacgg  | atgatgaaaa | aagtatatgg | 480  |
| aagaacttat  | cgggtggagga | aagtcaaaga | cttgccagag  | aaaatgcgaa | agatattatt | 540  |
| gcttggtgat  | tcgatgtaac  | aaagaccttc | attttctcgg  | acttcgacta | tggtggcggt | 600  |
| gctttctata  | aaaatatggt  | gaagggttgc | aagtgcgtta  | cacttaataa | ggctatggga | 660  |
| atctttgggt  | tttcgggtga  | agatcctatc | gcgaaactca  | gtttccctcc | tgtgcaggca | 720  |
| gttccatctt  | ttcctagctc  | attccacat  | ttgttcctg   | gcaaggacaa | tctccgctgc | 780  |
| ttgattcctt  | gtgctattga  | ccaggatcct | tattttagaa  | tgactcgtga | tgtcgcaccc | 840  |
| cggttaggct  | atagcaagcc  | cgccctgatt | gagtcacat   | tttttcctgc | gttgcaggga | 900  |
| gagaatggaa  | aaatgtctgc  | tagtgatcca | aattctgcta  | tctatgtgac | tgattccgca | 960  |
| aaggacatta  | aaaacaagat  | aaacagatat | gcgttttagtg | gtgggcaaga | ctccattgag | 1020 |
| aagcaccgag  | aacttgagc   | aaatctcgag | gttgacatac  | ccgtcaagta | tctgagtttc | 1080 |
| ttcctcgaag  | acgattctga  | actagaacac | attaaaaagg  | aatatggaga | aggaagaatg | 1140 |
| ctaacaggag  | agtaaaagaa  | gagacttacg | gaagtgttga  | cagaaattgt | ggagaaacac | 1200 |
| cgcagggctc  | gagctgctgt  | tactgatgag | atggttgatg  | cgttcatggc | ggtgagacct | 1260 |
| ctcccaagca  | agttcgaata  | gaaaaagtca | gaaacccttt  | ttggctcctc | agcaacttca | 1320 |
| caTcYactcc  | gtttgatttg  | gattcagaca | tctttgggtg  | tctattgata | gatttgatcc | 1380 |
| ttgaaattga  | accatacttg  | ttagttacaa | ttttcatatt  | tacatttatt | tatgaatcac | 1440 |
| attct       |             |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1568287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Pro | Pro | Tyr | Ile | His | Gly | Arg | Leu | Ile | Thr | Gly | Asn | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Phe | Leu | Phe | Ser | Val | Ala | Met | Glu | Val | Asp | Lys | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Glu |
| Arg | Glu | Ala | Glu | Ser | Ser | Glu | Gln | Val | Val | Asn | Pro | Trp | Glu | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     | Ser |
| Ala | Lys | Asp | Gly | Gly | Lys | Ile | Asp | Tyr | Asp | Lys | Leu | Ile | Asp | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     | Phe |
| Gly | Cys | Gln | Arg | Leu | Asp | Glu | Ser | Leu | Ile | Asp | Arg | Val | Gln | Arg |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Thr | Ser | Arg | Gln | Pro | His | Val | Phe | Leu | Arg | Arg | Ser | Val | Phe | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | Ala |
| His | Arg | Asp | Phe | Asn | Glu | Ile | Leu | Asp | Ala | Tyr | Glu | Arg | Gly | Asp |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     | Lys |
| Phe | Tyr | Leu | Tyr | Thr | Gly | Arg | Gly | Pro | Ser | Ser | Glu | Ala | Leu | His |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     | Leu |
| Gly | His | Leu | Ile | Pro | Phe | Met | Phe | Thr | Lys | Tyr | Leu | Gln | Glu | Ala |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     | Phe |
| Lys | Val | Pro | Leu | Val | Ile | Gln | Leu | Thr | Asp | Asp | Glu | Lys | Ser | Ile |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Lys | Asn | Leu | Ser | Val | Glu | Glu | Ser | Gln | Arg | Leu | Ala | Arg | Glu | Asn |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 | Ala |



Lys Asp Ile Ile Ala Cys Gly Phe Asp Val Thr Lys Thr Phe Ile Phe  
180 185 190  
Ser Asp Phe Asp Tyr Val Gly Gly Ala Phe Tyr Lys Asn Met Val Lys  
195 200 205  
Val Gly Lys Cys Val Thr Leu Asn Lys Ala Met Gly Ile Phe Gly Phe  
210 215 220  
Ser Gly Glu Asp Pro Ile Ala Lys Leu Ser Phe Pro Pro Val Gln Ala  
225 230 235 240  
Val Pro Ser Phe Pro Ser Ser Phe Pro His Leu Phe Pro Gly Lys Asp  
245 250 255  
Asn Leu Arg Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe  
260 265 270  
Arg Met Thr Arg Asp Val Ala Pro Arg Leu Gly Tyr Ser Lys Pro Ala  
275 280 285  
Leu Ile Glu Ser Thr Phe Phe Pro Ala Leu Gln Gly Glu Asn Gly Lys  
290 295 300  
Met Ser Ala Ser Asp Pro Asn Ser Ala Ile Tyr Val Thr Asp Ser Ala  
305 310 315 320  
Lys Asp Ile Lys Asn Lys Ile Asn Arg Tyr Ala Phe Ser Gly Gly Gln  
325 330 335  
Asp Ser Ile Glu Lys His Arg Glu Leu Gly Ala Asn Leu Glu Val Asp  
340 345 350  
Ile Pro Val Lys Tyr Leu Ser Phe Phe Leu Glu Asp Asp Ser Glu Leu  
355 360 365  
Glu His Ile Lys Lys Glu Tyr Gly Glu Gly Arg Met Leu Thr Gly Glu  
370 375 380  
Val Lys Lys Arg Leu Thr Glu Val Leu Thr Glu Ile Val Glu Lys His  
385 390 395 400  
Arg Arg Ala Arg Ala Val Thr Asp Glu Met Val Asp Ala Phe Met  
405 410 415  
Ala Val Arg Pro Leu Pro Ser Lys Phe Glu  
420 425

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..402

(D) OTHER INFORMATION: / Ceres Seq. ID 1568288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met Glu Val Asp Lys Lys Asp Glu Arg Glu Ala Glu Ser Ser Glu Gln  
1 5 10 15  
Val Val Asn Pro Trp Glu Val Ser Ala Lys Asp Gly Gly Lys Ile Asp  
20 25 30  
Tyr Asp Lys Leu Ile Asp Lys Phe Gly Cys Gln Arg Leu Asp Glu Ser  
35 40 45  
Leu Ile Asp Arg Val Gln Arg Leu Thr Ser Arg Gln Pro His Val Phe  
50 55 60  
Leu Arg Arg Ser Val Phe Phe Ala His Arg Asp Phe Asn Glu Ile Leu  
65 70 75 80  
Asp Ala Tyr Glu Arg Gly Asp Lys Phe Tyr Leu Tyr Thr Gly Arg Gly  
85 90 95  
Pro Ser Ser Glu Ala Leu His Leu Gly His Leu Ile Pro Phe Met Phe  
100 105 110  
Thr Lys Tyr Leu Gln Glu Ala Phe Lys Val Pro Leu Val Ile Gln Leu  
115 120 125  
Thr Asp Asp Glu Lys Ser Ile Trp Lys Asn Leu Ser Val Glu Glu Ser

SEQUENCE 1568288

130 135 140  
Gln Arg Leu Ala Arg Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe  
145 150 155 160  
Asp Val Thr Lys Thr Phe Ile Phe Ser Asp Phe Asp Tyr Val Gly Gly  
165 170 175  
Ala Phe Tyr Lys Asn Met Val Lys Val Gly Lys Cys Val Thr Leu Asn  
180 185 190  
Lys Ala Met Gly Ile Phe Gly Phe Ser Gly Glu Asp Pro Ile Ala Lys  
195 200 205  
Leu Ser Phe Pro Pro Val Gln Ala Val Pro Ser Phe Pro Ser Ser Phe  
210 215 220  
Pro His Leu Phe Pro Gly Lys Asp Asn Leu Arg Cys Leu Ile Pro Cys  
225 230 235 240  
Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro  
245 250 255  
Arg Leu Gly Tyr Ser Lys Pro Ala Leu Ile Glu Ser Thr Phe Phe Pro  
260 265 270  
Ala Leu Gln Gly Glu Asn Gly Lys Met Ser Ala Ser Asp Pro Asn Ser  
275 280 285  
Ala Ile Tyr Val Thr Asp Ser Ala Lys Asp Ile Lys Asn Lys Ile Asn  
290 295 300  
Arg Tyr Ala Phe Ser Gly Gly Gln Asp Ser Ile Glu Lys His Arg Glu  
305 310 315 320  
Leu Gly Ala Asn Leu Glu Val Asp Ile Pro Val Lys Tyr Leu Ser Phe  
325 330 335  
Phe Leu Glu Asp Asp Ser Glu Leu Glu His Ile Lys Lys Glu Tyr Gly  
340 345 350  
Glu Gly Arg Met Leu Thr Gly Glu Val Lys Lys Arg Leu Thr Glu Val  
355 360 365  
Leu Thr Glu Ile Val Glu Lys His Arg Arg Ala Arg Ala Ala Val Thr  
370 375 380  
Asp Glu Met Val Asp Ala Phe Met Ala Val Arg Pro Leu Pro Ser Lys  
385 390 395 400  
Phe Glu

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1568289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

Met Phe Thr Lys Tyr Leu Gln Glu Ala Phe Lys Val Pro Leu Val Ile  
1 5 10 15  
Gln Leu Thr Asp Asp Glu Lys Ser Ile Trp Lys Asn Leu Ser Val Glu  
20 25 30  
Glu Ser Gln Arg Leu Ala Arg Glu Asn Ala Lys Asp Ile Ile Ala Cys  
35 40 45  
Gly Phe Asp Val Thr Lys Thr Phe Ile Phe Ser Asp Phe Asp Tyr Val  
50 55 60  
Gly Gly Ala Phe Tyr Lys Asn Met Val Lys Val Gly Lys Cys Val Thr  
65 70 75 80  
Leu Asn Lys Ala Met Gly Ile Phe Gly Phe Ser Gly Glu Asp Pro Ile  
85 90 95  
Ala Lys Leu Ser Phe Pro Pro Val Gln Ala Val Pro Ser Phe Pro Ser  
100 105 110

Ser Phe Pro His Leu Phe Pro Gly Lys Asp Asn Leu Arg Cys Leu Ile  
115 120 125  
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val  
130 135 140  
Ala Pro Arg Leu Gly Tyr Ser Lys Pro Ala Leu Ile Glu Ser Thr Phe  
145 150 155 160  
Phe Pro Ala Leu Gln Gly Glu Asn Gly Lys Met Ser Ala Ser Asp Pro  
165 170 175  
Asn Ser Ala Ile Tyr Val Thr Asp Ser Ala Lys Asp Ile Lys Asn Lys  
180 185 190  
Ile Asn Arg Tyr Ala Phe Ser Gly Gly Gln Asp Ser Ile Glu Lys His  
195 200 205  
Arg Glu Leu Gly Ala Asn Leu Glu Val Asp Ile Pro Val Lys Tyr Leu  
210 215 220  
Ser Phe Phe Leu Glu Asp Asp Ser Glu Leu Glu His Ile Lys Lys Glu  
225 230 235 240  
Tyr Gly Glu Gly Arg Met Leu Thr Gly Glu Val Lys Lys Arg Leu Thr  
245 250 255  
Glu Val Leu Thr Glu Ile Val Glu Lys His Arg Arg Ala Arg Ala Ala  
260 265 270  
Val Thr Asp Glu Met Val Asp Ala Phe Met Ala Val Arg Pro Leu Pro  
275 280 285  
Ser Lys Phe Glu  
290

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| cttttttttcg agaaaaacgA agtttttctga gctaaactag atcagctatg gcgaccggtg | 60  |
| gtgctgcggc ggatttggaa gatgttcaga cgggtgatct catgtcggag ctccctccgcc  | 120 |
| gcctcaagtg ttctcagaag cccgacaaac gctcatctt cattggacct ccagggtcag    | 180 |
| ggaaaggtag tcaatctcca gtagtgaagg atgagtattg cttgtgtcac ttatccactg   | 240 |
| gagacatggt aagagctgct gttgcttcta agaccctct tgggtgtcaag gctaaagaag   | 300 |
| ctatggaaaa aggagagctc gtctctgatg atttggttgt tgggtataatt gatgaagcca  | 360 |
| tgaacaagcc aaaatgtcaa aaaggattta tccttgatGg gttccccagg actgttactc   | 420 |
| aggcagagaa gctcgatgag atgcttaaga ggcgaggaac tgaaattgac aaagttctca   | 480 |
| actttgctat tgatgacgca atcttgagg aaagaataac cgggcgatgg atccacccat    | 540 |
| cgagtggcag gagttaccac accaaatttg ctccctccaa aaccctgga gttgatgata    | 600 |
| ttactggaga gcctctgac caacgtaaag atgataacgc tgatgttcta aagtcgaggc    | 660 |
| ttgcagcttt ccacagtcaa actcaaccgg tgattgatta ctacgcaaag aaggccgttc   | 720 |
| tcacaaacat ccaggccgag aaggctcccc aagaagttac atcagaggtt aaaaaagcat   | 780 |
| tgatcatgac aaagactcct caagcaaadc atctcctctg gttagaatcc attcttttcc   | 840 |
| ttactacaag agagagacac atctatataa tccactcatc tgcggaatga cagttttttc   | 900 |
| tttt                                                                |     |

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1568301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

Met Ala Thr Gly Gly Ala Ala Ala Asp Leu Glu Asp Val Gln Thr Val  
1 5 10 15  
Asp Leu Met Ser Glu Leu Leu Arg Arg Leu Lys Cys Ser Gln Lys Pro  
20 25 30  
Asp Lys Arg Leu Ile Phe Ile Gly Pro Pro Gly Ser Gly Lys Gly Thr  
35 40 45  
Gln Ser Pro Val Val Lys Asp Glu Tyr Cys Leu Cys His Leu Ser Thr  
50 55 60  
Gly Asp Met Leu Arg Ala Val Ala Ser Lys Thr Pro Leu Gly Val  
65 70 75 80  
Lys Ala Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu  
85 90 95  
Val Val Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys  
100 105 110  
Gly Phe Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys  
115 120 125  
Leu Asp Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu  
130 135 140  
Asn Phe Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg  
145 150 155 160  
Trp Ile His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro  
165 170 175  
Pro Lys Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln  
180 185 190  
Arg Lys Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe  
195 200 205  
His Ser Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val  
210 215 220  
Leu Thr Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu  
225 230 235 240  
Val Lys Lys Ala Leu Ser  
245

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1568302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

Met Ser Glu Leu Leu Arg Arg Leu Lys Cys Ser Gln Lys Pro Asp Lys  
1 5 10 15  
Arg Leu Ile Phe Ile Gly Pro Pro Gly Ser Gly Lys Gly Thr Gln Ser  
20 25 30  
Pro Val Val Lys Asp Glu Tyr Cys Leu Cys His Leu Ser Thr Gly Asp  
35 40 45  
Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val Lys Ala  
50 55 60  
Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu Val Val  
65 70 75 80  
Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys Gly Phe  
85 90 95  
Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys Leu Asp  
100 105 110

Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu Asn Phe  
115 120 125  
Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg Trp Ile  
130 135 140  
His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro Pro Lys  
145 150 155 160  
Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln Arg Lys  
165 170 175  
Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe His Ser  
180 185 190  
Gln Thr Gln Pro Val Ile Asp Tyr Ala Lys Lys Ala Val Leu Thr  
195 200 205  
Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu Val Lys  
210 215 220  
Lys Ala Leu Ser  
225

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val Lys Ala  
1 5 10 15  
Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu Val Val  
20 25 30  
Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys Gly Phe  
35 40 45  
Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys Leu Asp  
50 55 60  
Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu Asn Phe  
65 70 75 80  
Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg Trp Ile  
85 90 95  
His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro Pro Lys  
100 105 110  
Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln Arg Lys  
115 120 125  
Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe His Ser  
130 135 140  
Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val Leu Thr  
145 150 155 160  
Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu Val Lys  
165 170 175  
Lys Ala Leu Ser  
180

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

002404-7666960

(B) LOCATION: 1..1303

(D) OTHER INFORMATION: / Ceres Seq. ID 1568304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| aaagctcaga  | tatctgaata  | actcgcttgc | gtgcctctct | ctctctaaaa  | gcccattctct | 60   |
| ttctcctcct  | cctcctccat  | tgaagaagaa | acctaccttc | gtaatatattc | ctcaattacg  | 120  |
| atcatggtga  | atgttaaagg  | gtcaacccaa | aaatcgaatc | ttgatcgatt  | ccttcattgc  | 180  |
| ataacaccct  | tagtgccacc  | ccaatctctc | cccaagacgg | agattagaac  | cctaaatoga  | 240  |
| ttgtggcatc  | catgggagag  | acaaaagggt | gagtttttca | ggttgagtga  | tttgtgggat  | 300  |
| tgttatgatg  | aatggagcgc  | ttatggagct | agcgttccta | ttcatgttac  | caacggagaa  | 360  |
| tctcttggtc  | aatactatgt  | tccttatctc | tctgccatcc | agattttcac  | ctctcattcc  | 420  |
| tccttgatcc  | gcttaaggga  | agagtctgaa | gatggggaat | gtgagggtag  | agatccgttt  | 480  |
| agcgattcag  | gtagcgaatg  | gagtgctctc | gaggaaggac | ttgagaacaa  | cacgctcttg  | 540  |
| catccaagtg  | atcgtttggg  | ttatctttat | ctccaatact | ttgagagatc  | agctccttat  | 600  |
| accagagttc  | ctctgatgga  | taagatcaat | gaattggctc | aaagataccc  | gggattgatg  | 660  |
| tcgttgagaa  | gcgttgatct  | ttctccagct | agttggatgt | cagtagcatg  | gtaccogatt  | 720  |
| taccatatac  | caatgggaag  | aaccattaaa | gacttatcca | cgtgtttcct  | cacttatcac  | 780  |
| actctttcct  | cttcttttca  | agatatggaa | ccggaagaaa | atggtgggga  | caaggagaga  | 840  |
| gtgcggaggg  | aaggggaaga  | tataactctg | ctcccatttg | ggatggctac  | ttacaagatg  | 900  |
| caaggcgatg  | tttggttttc  | gcaggaccac | gatgatcaag | agagattggC  | ttcgctttac  | 960  |
| agtgttgccg  | attcttggct  | taaacagctc | agggtccaac | atcatgactt  | caactacttc  | 1020 |
| tgcaatatgt  | caatgactca  | tcgtggctaa | acctcggttg | gatgacacca  | tgatgtttgc  | 1080 |
| ttgtttcctc  | atatatagtc  | taattcttgc | tttgttctgg | aaccgcttgc  | gttttgtaaa  | 1140 |
| acgcaatgga  | gcgattcgct  | ttgcagtgtt | ttggttagaa | tagcgttttg  | agtcttctaa  | 1200 |
| cctttgagag  | agtatatgtc  | gtatatagag | ttttgttgct | tgttgaaaca  | gagtacaatt  | 1260 |
| gttggttgctt | gttaaaaaaca | gagtgattgt | ttcttataag | ttg         |             |      |

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1568305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asn | Val | Lys | Gly | Ser | Thr | Lys | Ser | Asn | Leu | Asp | Arg | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | His | Cys | Ile | Thr | Pro | Leu | Val | Pro | Pro | Gln | Ser | Leu | Pro | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Glu | Ile | Arg | Thr | Leu | Asn | Arg | Leu | Trp | His | Pro | Trp | Glu | Arg | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     | Lys |
| Val | Glu | Phe | Phe | Arg | Leu | Ser | Asp | Leu | Trp | Asp | Cys | Tyr | Asp | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     | Trp |
| Ser | Ala | Tyr | Gly | Ala | Ser | Val | Pro | Ile | His | Val | Thr | Asn | Gly | Glu |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Leu | Val | Gln | Tyr | Tyr | Val | Pro | Tyr | Leu | Ser | Ala | Ile | Gln | Ile | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |
| Ser | His | Ser | Ser | Leu | Ile | Arg | Leu | Arg | Glu | Glu | Ser | Glu | Asp | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     | Glu |
| Cys | Glu | Gly | Arg | Asp | Pro | Phe | Ser | Asp | Ser | Gly | Ser | Asp | Glu | Ser |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     | Val |
| Ser | Glu | Gly | Gly | Leu | Glu | Asn | Asn | Thr | Leu | Leu | His | Pro | Ser | Asp |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     | Arg |
| Leu | Gly | Tyr | Leu | Tyr | Leu | Gln | Tyr | Phe | Glu | Arg | Ser | Ala | Pro | Tyr |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Arg | Val | Pro | Leu | Met | Asp | Lys | Ile | Asn | Glu | Leu | Ala | Gln | Arg | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Gly | Leu | Met | Ser | Leu | Arg | Ser | Val | Asp | Leu | Ser | Pro | Ala | Ser | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Met |

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 5001 |             |             |             |             |             |      |
|--------------------------------------------|-------------|-------------|-------------|-------------|-------------|------|
| atttaaatggc                                | aaagccggaa  | aatgacgtca  | tcttaaccga  | gaaacaaaaca | tggagcacat  | 60   |
| gggaagagct                                 | tctcctcgcc  | tgcgccgtac  | accgtcacgg  | taccgaatca  | tggaaactctg | 120  |
| tttcgcgtga                                 | aatccagaaa  | ctgagtccca  | acctctgttc  | cctcacccgc  | tccgcttgcc  | 180  |
| gccacaagta                                 | cttcgacctc  | aaaagccggt  | tcactcaaga  | gctggccgta  | ccggaatccg  | 240  |
| tcgctgcat                                  | ctcaaccgct  | ccttggttag  | aggagttaag  | gaagctccgc  | gtcgatgagc  | 300  |
| tccgtcgcca                                 | agttgaacag  | tacgatttat  | ccatctcaac  | gttgcactcg  | aaggtgaagc  | 360  |
| aattggaaga                                 | agagagagag  | atgagtttca  | ttaaaccgga  | cacggaaacc  | gagaatttag  | 420  |
| atctagagag                                 | gaagaagag   | ctgtacCGATG | tccggtgaac  | cagtcctaaa  | cccgccggtt  | 480  |
| cagctaatag                                 | acgaaaccat  | ttctccagat  | cccaaagaaa  | tcggatcgga  | aaacacggag  | 540  |
| agggaggagg                                 | aaatggccgg  | aagcggcgcc  | ggagaatcga  | agcttgccgg  | agaggattct  | 600  |
| tgtagaggaa                                 | gctgtgaaag  | tgtggagaag  | gaactgacga  | cgaactcgga  | gagagttgaa  | 660  |
| ccggtgagtg                                 | tgaccgagtt  | gatagagtcg  | gaggacggag  | cgagtcgtgg  | agaggagatt  | 720  |
| actagtgatg                                 | tgagagctc   | ggcgagcttg  | ccaagaaagg  | gaacgtcgga  | gccggataag  | 780  |
| gaagatcaat                                 | ctccgacgag  | cgccaaagat  | ttcacccgtt  | aatcacagcc  | gttgattagt  | 840  |
| tttgtcgaga                                 | ttctttctgtc | tcctcctgt   | ggttcccact  | tttcgcccgc  | actcgaacgt  | 900  |
| caggaaacaa                                 | tttgatagct  | tacaataatt  | agagagcacg  | tagattttga  | gataaattcg  | 960  |
| aagcgaagt                                  | aaggaggctt  | gtacaaaagt  | tggaggatca  | acttctttcg  | tgatttgctg  | 1020 |
| ctacttgtaa                                 | ataatgcaag  | agtgttttat  | cacagaggat  | cttcagagtt  | taaatttgct  | 1080 |
| gagcagcttc                                 | accaactcgt  | caagaaacag  | atgactacta  | ctctcaagg   | acttagtaat  | 1140 |
| agagatgaga                                 | tctcaatctc  | accaccaaaa  | gaagaagttg  | ttgcaatccc  | ttcatcaaag  | 1200 |
| cctgtttctt                                 | ctaaaccaag  | aatgtctgtt  | cctaataattg | tagcttgctg  | gaaacgtagt  | 1260 |
| gccttggtcg                                 | ctaaaccttt  | gctattattg  | cctcctggac  | cagataaaaa  | ggccaagaaa  | 1320 |
| acagatcatg                                 | ttgtggacta  | tgatgagaag  | ccggtttacg  | acaaggatgg  | tgaagcctct  | 1380 |
| gggaatagcg                                 | atgtgactc   | ctgtgatttg  | aagataataa  | ctagagggaag | aaacctcctcg | 1440 |
| acgggaaaag                                 | tagctaacag  | gaacgtcaag  | aaccgtgact  | ccagtttgaa  | tgttgatgat  | 1500 |
| agcaaagata                                 | aggttaagaa  | aactgatgaa  | gagaagaaag  | gtggctcgaa  | aaagaaaggg  | 1560 |
| gctgcgagtt                                 | ttctcaggag  | aatgaaagt   | ggctcttcgg  | atgacacatt  | gaagcgtagc  | 1620 |
| tctgctgctg                                 | attcttctac  | tacgggaaaa  | ggaggaggag  | cggaacagag  | gaagaataac  | 1680 |
| agcaacaaag                                 | ctgataataa  | gaaaacaccg  | ataccaagga  | taagacaaac  | aaataagaaa  | 1740 |
| gcaagtcctg                                 | tgaagagaag  | caataatggt  | cgaacctcag  | aaagagaagc  | tgctccattct | 1800 |
| tatcctattc                                 | tagcaaaagc  | aagcagagaa  | gctggtgaaa  | aagaggaggc  | gtcttcttat  | 1860 |
| tcaccacgat                                 | tgaagaaacg  | tgcaggagg   | tgatgtagtt  | gttggtactac | ttatataact  | 1920 |
| taacttgaga                                 | tqaaaatcag  | aaactaataa  | attccaaaga  | gtc         |             |      |

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1568310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Glu | Pro | Val | Pro | Asn | Pro | Pro | Val | Gln | Leu | Met | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Ile | Ser | Pro | Asp | Pro | Lys | Glu | Ile | Gly | Ser | Glu | Asn | Thr | Glu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Glu | Met | Ala | Gly | Ser | Gly | Gly | Gly | Glu | Ser | Lys | Leu | Ala | Gly |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Glu | Asp | Ser | Cys | Arg | Gly | Ser | Cys | Glu | Ser | Val | Glu | Lys | Glu | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Asn | Ser | Glu | Arg | Val | Glu | Pro | Val | Ser | Val | Thr | Glu | Leu | Ile | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Glu | Asp | Gly | Ala | Ser | Arg | Gly | Glu | Glu | Ile | Thr | Ser | Asp | Val | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Ala | Ser | Leu | Pro | Arg | Lys | Gly | Thr | Ser | Glu | Pro | Asp | Lys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Gln | Ser | Pro | Thr | Ser | Ala | Lys | Asp | Phe | Thr | Val | Glu | Ser | Gln | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ile | Ser | Phe | Val | Glu | Ile | Leu | Leu | Ser | His | Pro | Cys | Gly | Ser | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Arg | Arg | Leu | Glu | Arg | Gln | Glu | Thr | Ile | Glu | Tyr | Gly | Thr | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Arg | Glu | His | Val | Asp | Phe | Glu | Ile | Ile | Arg | Lys | Arg | Val | Glu | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Leu | Tyr | Lys | Ser | Trp | Arg | Ile | Asn | Phe | Phe | Arg | Asp | Leu | Leu | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Val | Asn | Asn | Ala | Arg | Val | Phe | Tyr | His | Arg | Gly | Ser | Ser | Glu | Phe |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Phe | Ala | Glu | Gln | Leu | His | Gln | Leu | Val | Lys | Lys | Gln | Met | Thr | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Leu | Lys | Gly | Leu | Ser | Asn | Arg | Asp | Glu | Ile | Ser | Ile | Ser | Pro | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Glu | Glu | Val | Val | Ala | Ile | Pro | Ser | Ser | Lys | Pro | Val | Ser | Ser | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Arg | Met | Ser | Val | Pro | Asn | Ile | Val | Ala | Cys | Arg | Lys | Arg | Ser | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Ala | Ala | Lys | Pro | Leu | Leu | Leu | Pro | Pro | Gly | Pro | Asp | Lys | Lys |     |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ala | Lys | Lys | Thr | Asp | His | Val | Val | Asp | Tyr | Asp | Glu | Lys | Pro | Val | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Lys | Asp | Gly | Glu | Ala | Ser | Gly | Lys | Asp | Asp | Asp | Asp | Ser | Leu | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Val | Lys | Ile | Ile | Thr | Arg | Gly | Arg | Thr | Ser | Ser | Thr | Gly | Lys | Val | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Arg | Asn | Val | Lys | Asn | Arg | Asp | Ser | Ser | Leu | Asn | Val | Asp | Asp | Ser |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Asp | Lys | Val | Lys | Lys | Thr | Asp | Glu | Glu | Lys | Lys | Gly | Gly | Ser | Lys |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Lys | Lys | Gly | Ala | Ala | Ser | Phe | Leu | Arg | Arg | Met | Lys | Val | Gly | Ser | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Asp | Thr | Leu | Lys | Arg | Ser | Ser | Ala | Ala | Asp | Ser | Ser | Thr | Thr | Gly |



[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1568311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Glu | Thr | Ile | Ser | Pro | Asp | Pro | Lys | Glu | Ile | Gly | Ser | Glu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Glu | Arg | Glu | Glu | Glu | Met | Ala | Gly | Ser | Gly | Gly | Gly | Glu | Ser | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Gly | Glu | Asp | Ser | Cys | Arg | Gly | Ser | Cys | Glu | Ser | Val | Glu | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Leu | Thr | Thr | Asn | Ser | Glu | Arg | Val | Glu | Pro | Val | Ser | Val | Thr | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Ile | Glu | Ser | Glu | Asp | Gly | Ala | Ser | Arg | Gly | Glu | Glu | Ile | Thr | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Gln | Ser | Ser | Ala | Ser | Leu | Pro | Arg | Lys | Gly | Thr | Ser | Glu | Pro |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Lys | Glu | Asp | Gln | Ser | Pro | Thr | Ser | Ala | Lys | Asp | Phe | Thr | Val | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gln | Pro | Leu | Ile | Ser | Phe | Val | Glu | Ile | Leu | Leu | Ser | His | Pro | Cys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | His | Phe | Ser | Arg | Arg | Leu | Glu | Arg | Gln | Glu | Thr | Ile | Glu | Tyr |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gly | Thr | Ile | Ile | Arg | Glu | His | Val | Asp | Phe | Glu | Ile | Ile | Arg | Lys | Arg |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Glu | Gly | Gly | Leu | Tyr | Lys | Ser | Trp | Arg | Ile | Asn | Phe | Phe | Arg | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Leu | Leu | Leu | Val | Asn | Asn | Ala | Arg | Val | Phe | Tyr | His | Arg | Gly | Ser |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Glu | Phe | Lys | Phe | Ala | Glu | Gln | Leu | His | Gln | Leu | Val | Lys | Lys | Gln |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Met | Thr | Thr | Thr | Leu | Lys | Gly | Leu | Ser | Asn | Arg | Asp | Glu | Ile | Ser | Ile |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ser | Pro | Pro | Lys | Glu | Glu | Val | Val | Ala | Ile | Pro | Ser | Ser | Lys | Pro | Val |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ser | Ser | Lys | Pro | Arg | Met | Ser | Val | Pro | Asn | Ile | Val | Ala | Cys | Arg | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Arg | Ser | Ala | Leu | Ala | Ala | Lys | Pro | Leu | Leu | Leu | Leu | Pro | Pro | Gly | Pro |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Asp | Lys | Lys | Ala | Lys | Lys | Thr | Asp | His | Val | Val | Asp | Tyr | Asp | Glu | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Pro Val Ser Asp Lys Asp Gly Glu Ala Ser Gly Lys Asp Asp Asp Asp  
290 295 300  
Ser Leu Ile Val Lys Ile Thr Arg Gly Arg Thr Ser Ser Thr Gly  
305 310 315 320  
Lys Val Ala Asn Arg Asn Val Lys Asn Arg Asp Ser Ser Leu Asn Val  
325 330 335  
Asp Asp Ser Lys Asp Lys Val Lys Lys Thr Asp Glu Glu Lys Lys Gly  
340 345 350  
Gly Ser Lys Lys Lys Gly Ala Ala Ser Phe Leu Arg Arg Met Lys Val  
355 360 365  
Gly Ser Ser Asp Asp Thr Leu Lys Arg Ser Ser Ala Ala Asp Ser Ser  
370 375 380  
Thr Thr Gly Lys Gly Gly Glu Ala Glu Gln Arg Lys Asn Asn Ser Asn  
385 390 395 400  
Lys Ala Asp Asn Lys Lys Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn  
405 410 415  
Lys Lys Ala Ser Pro Val Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu  
420 425 430  
Arg Glu Ala Ala Pro Ser Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu  
435 440 445  
Ala Gly Glu Lys Glu Glu Ala Ser Ser Tyr Ser Pro Arg Leu Lys Lys  
450 455 460  
Arg Ala Arg Arg  
465

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1568312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

Met Ala Gly Ser Gly Gly Gly Glu Ser Lys Leu Ala Gly Glu Asp Ser  
1 5 10 15  
Cys Arg Gly Ser Cys Glu Ser Val Glu Lys Glu Leu Thr Thr Asn Ser  
20 25 30  
Glu Arg Val Glu Pro Val Ser Val Thr Glu Leu Ile Glu Ser Glu Asp  
35 40 45  
Gly Ala Ser Arg Gly Glu Glu Ile Thr Ser Asp Val Gln Ser Ser Ala  
50 55 60  
Ser Leu Pro Arg Lys Gly Thr Ser Glu Pro Asp Lys Glu Asp Gln Ser  
65 70 75 80  
Pro Thr Ser Ala Lys Asp Phe Thr Val Glu Ser Gln Pro Leu Ile Ser  
85 90 95  
Phe Val Glu Ile Leu Leu Ser His Pro Cys Gly Ser His Phe Ser Arg  
100 105 110  
Arg Leu Glu Arg Gln Glu Thr Ile Glu Tyr Gly Thr Ile Ile Arg Glu  
115 120 125  
His Val Asp Phe Glu Ile Ile Arg Lys Arg Val Glu Gly Gly Leu Tyr  
130 135 140  
Lys Ser Trp Arg Ile Asn Phe Phe Arg Asp Leu Leu Leu Val Asn  
145 150 155 160  
Asn Ala Arg Val Phe Tyr His Arg Gly Ser Ser Glu Phe Lys Phe Ala  
165 170 175  
Glu Gln Leu His Gln Leu Val Lys Lys Gln Met Thr Thr Thr Leu Lys  
180 185 190  
Gly Leu Ser Asn Arg Asp Glu Ile Ser Ile Ser Pro Pro Lys Glu Glu

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| Variable                       | Mean        | SD      | Min         | Max     |
|--------------------------------|-------------|---------|-------------|---------|
| Age                            | 34.5        | 10.2    | 21          | 55      |
| Gender                         | Male        | Female  | Male        | Female  |
| Marital status                 | Married     | Single  | Married     | Single  |
| Education                      | High school | College | High school | College |
| Occupation                     | Manager     | Worker  | Manager     | Worker  |
| Income                         | Low         | High    | Low         | High    |
| Health status                  | Good        | Poor    | Good        | Poor    |
| Stress level                   | Low         | High    | Low         | High    |
| Life satisfaction              | High        | Low     | High        | Low     |
| Resilience                     | High        | Low     | High        | Low     |
| Optimism                       | High        | Low     | High        | Low     |
| Self-efficacy                  | High        | Low     | High        | Low     |
| Perceived stress               | Low         | High    | Low         | High    |
| Depression                     | Low         | High    | Low         | High    |
| Anxiety                        | Low         | High    | Low         | High    |
| Quality of life                | High        | Low     | High        | Low     |
| Health-related quality of life | High        | Low     | High        | Low     |
| Physical health                | High        | Low     | High        | Low     |
| Mental health                  | High        | Low     | High        | Low     |
| Social health                  | High        | Low     | High        | Low     |
| Environmental health           | High        | Low     | High        | Low     |
| Overall health                 | High        | Low     | High        | Low     |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..635

- (D) OTHER INFORMATION: / Ceres Seq. ID 1568313

| (A1) SEQUENCE DESCRIPTION: SEQ ID: 1 |            |            |            |            |             |            |     |
|--------------------------------------|------------|------------|------------|------------|-------------|------------|-----|
| ttacagtc                             | cc         | atgatccgtg | cttggTttga | tcctcaccat | catcaccaat  | ccatctccac | 60  |
| cgacgatctc                           | aaccaccacc | atcaccttcc | tccaccggtt | caccaatcag | caatccccgg  |            | 120 |
| aatcggattc                           | gcctcaggtg | aattatcttc | gggttttcgc | ataccagcac | ggtttcaggg  |            | 180 |
| ccaagaagag                           | gagcagcacg | acggtctcac | tcacaagccg | tcctctgctt | cctctatttc  |            | 240 |
| tcgccattga                           | caatcgaaac | taatcctcta | agtttcaggg | cttgctagc  | ttccatgcac  |            | 300 |
| attgaagctt                           | gacttagatt | gtccggaaca | gggaaggtgt | tctcggtttg | tgtagtcaat  |            | 360 |
| ggcctgaatc                           | tagaaaacgc | aaggaaatga | agaaagaaca | acagtttcag | gttctttctc  |            | 420 |
| ttcttcttcc                           | aatatcttaa | ccttgccgat | tgtaattttt | catattttca | ccagtttagac |            | 480 |
| caacgttctt                           | ctgtagctca | attatggtta | gattccaagg | tttcgtcttg | ttgtgttatg  |            | 540 |
| tttgtAacct                           | tgtatcatca | tcatCctatt | gttactgctc | cctgttctta | ttgtgtaact  |            | 600 |
| ccgtggatgt                           | tctaataaag | tctgaaactt | tctcc      |            |             |            |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Tyr Ser Pro Met Ile Arg Ala Trp Phe Asp Pro His His His His Gln  
1 5 10 15  
Ser Ile Ser Thr Asp Asp Leu Asn His His His His Leu Pro Pro Pro  
20 25 30  
Val His Gln Ser Ala Ile Pro Gly Ile Gly Phe Ala Ser Gly Glu Leu  
35 40 45  
Ser Ser Gly Phe Arg Ile Pro Ala Arg Phe Gln Gly Gln Glu Glu Glu  
50 55 60  
Gln His Asp Gly Leu Thr His Lys Pro Ser Ser Ala Ser Ser Ile Ser  
65 70 75 80  
Arg His

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met Ile Arg Ala Trp Phe Asp Pro His His His Gln Ser Ile Ser  
1 5 10 15  
Thr Asp Asp Leu Asn His His His His Leu Pro Pro Pro Val His Gln  
20 25 30  
Ser Ala Ile Pro Gly Ile Gly Phe Ala Ser Gly Glu Leu Ser Ser Gly  
35 40 45  
Phe Arg Ile Pro Ala Arg Phe Gln Gly Gln Glu Glu Gln His Asp  
50 55 60  
Gly Leu Thr His Lys Pro Ser Ser Ala Ser Ser Ile Ser Arg His  
65 70 75

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

Met Val Arg Phe Gln Gly Phe Val Leu Leu Cys Tyr Val Cys Asn Phe  
1 5 10 15  
Val Ser Ser Ser Tyr Cys Tyr Cys Ser Leu Phe Leu Leu Cys Asn  
20 25 30  
Ser Val Asp Val Leu Ile Lys Ser Glu Thr Phe Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..407
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| tttgggggttg | gtggagatga  | tgaaggga   | agagagagt  | tgggaggaga | tggtaagga  | 60  |
| gaatcaattg  | caagagaaga  | agcttgagga | agttggtgtg | tgggtggttg | ctgatgttat | 120 |
| acttgagggg  | attgcgactg  | tggcttggtt | tttcttttac | actttcttgc | cggagacgca | 180 |
| agggaggatg  | cttgaggata  | tggatgagct | tttcagtggg | ttcaggtgga | gagattccaa | 240 |
| gagtaagcct  | aagggttaacc | ccgagaagac | ggtaccgaat | cccagggttg | agattggatc | 300 |
| aaacaagcag  | tgggaaggag  | gagacacaca | aagttcgtag | gaaatttgat | cagatatgta | 360 |
| atttgatgg   | tatgGtgggt  | ttaatgataa | aacgaacaaa | ttagcgt    |            |     |

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..112
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568322
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Leu | Val | Glu | Met | Met | Lys | Gly | Lys | Glu | Arg | Val | Trp | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Val | Lys | Glu | Asn | Gln | Leu | Gln | Glu | Lys | Lys | Leu | Glu | Glu | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Trp | Trp | Phe | Ala | Asp | Val | Ile | Leu | Gly | Gly | Ile | Ala | Thr | Val | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Val | Phe | Phe | Tyr | Thr | Phe | Leu | Pro | Glu | Thr | Gln | Gly | Arg | Met | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Asp | Met | Asp | Glu | Leu | Phe | Ser | Gly | Phe | Arg | Trp | Arg | Asp | Ser | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Lys | Pro | Lys | Gly | Asn | Pro | Glu | Lys | Thr | Val | Pro | Asn | Pro | Glu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ile | Gly | Ser | Asn | Lys | Gln | Trp | Lys | Glu | Gly | Asp | Thr | Gln | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:918:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..107
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568323
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Lys | Gly | Lys | Glu | Arg | Val | Trp | Glu | Glu | Met | Val | Lys | Glu | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Leu | Gln | Glu | Lys | Lys | Leu | Glu | Glu | Val | Gly | Val | Trp | Trp | Phe | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Ile | Leu | Gly | Gly | Ile | Ala | Thr | Val | Ala | Trp | Val | Phe | Phe | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

Thr Phe Leu Pro Glu Thr Gln Gly Arg Met Leu Glu Asp Met Asp Glu  
50 55 60  
Leu Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys Ser Lys Pro Lys Gly  
65 70 75 80  
Asn Pro Glu Lys Thr Val Pro Asn Pro Glu Val Glu Ile Gly Ser Asn  
85 90 95  
Lys Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1568324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

Met Lys Gly Lys Glu Arg Val Trp Glu Glu Met Val Lys Glu Asn Gln  
1 5 10 15  
Leu Gln Glu Lys Leu Glu Glu Val Gly Val Trp Trp Phe Ala Asp  
20 25 30  
Val Ile Leu Gly Gly Ile Ala Thr Val Ala Trp Val Phe Phe Tyr Thr  
35 40 45  
Phe Leu Pro Glu Thr Gln Gly Arg Met Leu Glu Asp Met Asp Glu Leu  
50 55 60  
Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys Ser Lys Pro Lys Gly Asn  
65 70 75 80  
Pro Glu Lys Thr Val Pro Asn Pro Glu Val Glu Ile Gly Ser Asn Lys  
85 90 95  
Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..821

(D) OTHER INFORMATION: / Ceres Seq. ID 1568333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

aaaaaaagga gaaagcttga aacgccgctt cttcttcttc tctgtcgttc tctctgtaaa 60  
tcgcttcttc aatcatctct gtggatttgt ctctattcat aacttggtga agaagatgtt 120  
gacggaagag gagctcaaaa gattgtacag aatccagaag acgttgatgc agatgttaag 180  
ggatcggtga tattttatcg cggattctga acttacgatg actaaacaac agttttattag 240  
gaaacatggt gataacatga aaagagagga tcttggtact ctttaaggcta agcgaaatga 300  
taatagtgat cagctctata tattcttccc tgatgagggc aaagttggtg tgaagacgat 360  
gaaaatgtac acgaacagga tgaaatcaga gaatgtgttc agagctatatt tggttgtgcA 420  
acagaacttg accccgtttg ctcgaaacttg cattagtgag atctcttcta aGgtttcatc 480  
tggaagtgtt ccaGggaggc ggaaatgcta gtgaacatta aagaacatgt tcttgttcct 540  
gagcatcaag ttcttaccac tgaagagaag aaaactttac tggagagata cacagtgaag 600  
gagacacagc ttccaaggat ccaagtgcact gatccaatcg caagatactt tggactaaaa 660  
cgtgggcaag tcgtgaagat cattcgtccg agtgaaacgg ctggtcgtta tgttacctat 720  
cgttatgttg tataagccaa agcaaaaggc ttttgtggat tgtaatgcga attgaacgct 780  
gagagttgtg aaacataaga gtaatgcttt tgtactaaac c

(2) INFORMATION FOR SEQ ID NO:921:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 169 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..169  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568334  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

Lys Lys Gly Glu Ser Leu Lys Arg Arg Phe Phe Phe Ser Val Val  
1                   5                   10                   15  
Leu Ser Val Asn Arg Phe Phe Asn His Leu Cys Gly Phe Val Ser Ile  
                  20                   25                   30  
His Asn Leu Val Lys Lys Met Leu Thr Glu Glu Glu Leu Lys Arg Leu  
                  35                   40                   45  
Tyr Arg Ile Gln Lys Thr Leu Met Gln Met Leu Arg Asp Arg Gly Tyr  
50                   55                   60  
Phe Ile Ala Asp Ser Glu Leu Thr Met Thr Lys Gln Gln Phe Ile Arg  
65                   70                   75                   80  
Lys His Gly Asp Asn Met Lys Arg Glu Asp Leu Val Thr Leu Lys Ala  
                  85                   90                   95  
Lys Arg Asn Asp Asn Ser Asp Gln Leu Tyr Ile Phe Phe Pro Asp Glu  
                  100                   105                   110  
Ala Lys Val Gly Val Lys Thr Met Lys Met Tyr Thr Asn Arg Met Lys  
                  115                   120                   125  
Ser Glu Asn Val Phe Arg Ala Ile Leu Val Val Gln Gln Asn Leu Thr  
130                   135                   140  
Pro Phe Ala Arg Thr Cys Ile Ser Glu Ile Ser Ser Lys Val Ser Ser  
145                   150                   155                   160  
Gly Ser Phe Pro Gly Arg Arg Lys Cys  
                  165

- (2) INFORMATION FOR SEQ ID NO:922:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 131 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..131  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1568335  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met Leu Thr Glu Glu Leu Lys Arg Leu Tyr Arg Ile Gln Lys Thr  
1                   5                   10                   15  
Leu Met Gln Met Leu Arg Asp Arg Gly Tyr Phe Ile Ala Asp Ser Glu  
                  20                   25                   30  
Leu Thr Met Thr Lys Gln Gln Phe Ile Arg Lys His Gly Asp Asn Met  
                  35                   40                   45  
Lys Arg Glu Asp Leu Val Thr Leu Lys Ala Lys Arg Asn Asp Asn Ser  
50                   55                   60  
Asp Gln Leu Tyr Ile Phe Phe Pro Asp Glu Ala Lys Val Gly Val Lys  
65                   70                   75                   80  
Thr Met Lys Met Tyr Thr Asn Arg Met Lys Ser Glu Asn Val Phe Arg  
                  85                   90                   95  
Ala Ile Leu Val Val Gln Gln Asn Leu Thr Pro Phe Ala Arg Thr Cys  
                  100                   105                   110  
Ile Ser Glu Ile Ser Ser Lys Val Ser Ser Gly Ser Phe Pro Gly Arg  
115                   120                   125

Arg Lys Cys  
130

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1568336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Met | Leu | Arg | Asp | Arg | Gly | Tyr | Phe | Ile | Ala | Asp | Ser | Glu | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Met | Thr | Lys | Gln | Gln | Phe | Ile | Arg | Lys | His | Gly | Asp | Asn | Met | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Glu | Asp | Leu | Val | Thr | Leu | Lys | Ala | Lys | Arg | Asn | Asp | Asn | Ser | Asp |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gln | Leu | Tyr | Ile | Phe | Phe | Pro | Asp | Glu | Ala | Lys | Val | Gly | Val | Lys | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Met | Lys | Met | Tyr | Thr | Asn | Arg | Met | Lys | Ser | Glu | Asn | Val | Phe | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Leu | Val | Val | Gln | Gln | Asn | Leu | Thr | Pro | Phe | Ala | Arg | Thr | Cys | Ile |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Glu | Ile | Ser | Ser | Lys | Val | Ser | Ser | Gly | Ser | Phe | Pro | Gly | Arg | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Lys | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1264

(D) OTHER INFORMATION: / Ceres Seq. ID 1568357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| aatggattac | ttttcttcca  | cacatatata | acttaactct | ctctttttct  | cttttgcttt | 60   |
| aacccctca  | aagaaaagat  | aagagccttt | taaagttttt | ttttttacct  | tctcttcag  | 120  |
| gacttgctg  | tacttgatag  | gcttaagtgg | ctgcaacagc | aacaaatggt  | ttcacctgag | 180  |
| tttcttcaga | tacttggtc   | agatgggaga | gaagagctca | aaagagttga  | gagttacttg | 240  |
| ggaaaAcaac | aatgatgagc  | tgcagagttt | cagacatttt | cccgaattcg  | gaccggatta | 300  |
| tgatactact | gatggctgca  | tttctaggac | aagtagcttc | catatggagc  | cagtgaagaa | 360  |
| taatggacac | agcagagcca  | ttaccttgca | gaacaagaga | aaaccagagg  | gtaagacaga | 420  |
| aaagagagag | aagaagaaga  | tcaaagcaga | ggatgaaaca | gagccaagca  | tgaaagggaa | 480  |
| atcaaacatg | agtaacRcag  | agacatcttc | agaaattoag | aaaccagatt  | acattcatgt | 540  |
| tagggctaga | cgagggtgaag | ccaccgacag | acatagctta | gcagagaggg  | caagaagaga | 600  |
| aaagataaag | aagaagatga  | aatgtctaca | agatattgtt | cctggatgca  | acaaagtta  | 660  |
| tggaaaagct | ggtatgcttg  | atgagatcat | caactatgtc | caatctctgc  | aacaacaagt | 720  |
| cgagttcttg | tcgatgaaac  | tctctgtcat | aaatccagaa | cttgagtgtc  | atatcgatga | 780  |
| tttatccgca | aaacagtttc  | aggcttactt | cacaggtcct | ccagaagggtg | actcgaagca | 840  |
| gtcaatcatg | gcggattttc  | ggtcttttcc | attacatcag | caaggatctt  | tagattactc | 900  |
| agtcataaac | tcagaccaca  | ccacatctct | cggcgctaaa | gatcatacat  | catcaagctg | 960  |
| ggaaactcac | tcacagtgtc  | tttacaacag | cttgagaacc | gattctattt  | ccaatttctt | 1020 |
| cagcctcaag | taaaaaaatt  | agggatagcc | tcattaaaaa | aatcgcggtt  | ttttgttgtt | 1080 |
| gtcttatcca | tttatctatc  | ttatctgaaa | tttgaaccag | aaagacagag  | gaaaccaaat | 1140 |



(2) INFORMATION FOR SEQ ID NO:925:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1568358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1568359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met Glu Pro Val Lys Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln  
1 5 10 15  
Asn Lys Arg Lys Pro Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys Lys  
20 25 30  
Ile Lys Ala Glu Asp Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn  
35 40 45  
Met Ser Asn Xaa Glu Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile  
50 55 60  
His Val Arg Ala Arg Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala  
65 70 75 80  
Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln  
85 90 95  
Asp Ile Val Pro Gly Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu  
100 105 110  
Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe  
115 120 125  
Leu Ser Met Lys Leu Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile  
130 135 140  
Asp Asp Leu Ser Ala Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro  
145 150 155 160  
Glu Gly Asp Ser Lys Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro  
165 170 175  
Leu His Gln Gln Gly Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His  
180 185 190  
Thr Thr Ser Leu Gly Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr  
195 200 205  
His Ser Gln Cys Leu Tyr Asn Ser Leu Arg Thr Asp Ser Ile Ser Asn  
210 215 220  
Phe Phe Ser Leu Lys  
225

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1568360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Lys Gly Lys Ser Asn Met Ser Asn Xaa Glu Thr Ser Ser Glu Ile  
1 5 10 15  
Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala Thr  
20 25 30  
Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys  
35 40 45  
Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val Thr  
50 55 60  
Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu  
65 70 75 80  
Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn Pro  
85 90 95  
Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln Ala  
100 105 110  
Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met Ala  
115 120 125  
Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr Ser

130 135 140  
Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly Ala Lys Asp His Thr  
145 150 155 160  
Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu Tyr Asn Ser Leu Arg  
165 170 175  
Thr Asp Ser Ile Ser Asn Phe Phe Ser Leu Lys  
180 185

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1273
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

accacacac aaagattcca ttacaaataa acaattttca tatatatcta taacaaaaaa 60  
aaacaatggc gacctcaagc atgaagagca ttccaatggc gatcccaagt ttctccatgt 120  
gtcacaaagt cgagctcctt aaagaaggca aaactcgca cgtcccgaag gccgaagaag 180  
atgaagggct aagctgagag ttccaagaga tggttgattc tcttcctaag gagagaggat 240  
ggagaactcg ttacctttac ctattccaag ggttttggtg ccaagccaaa gagattcaag 300  
ccatcatgtc ttccaaaaa cattttccat ccctcgaaaa cgacgtcgtt ctcgccacca 360  
tacctaaatc cgggtacaacc tggctaaaag ctttaacttt caccatcctt aaccgtcacc 420  
ggtttgatcc gggtgcctcg agtaccaacc accctctttt cacttccaac cctcatgacc 480  
ttgtaccttt cttcgagtac aagctttacg ccaacggaga tgttcccgat ctctcgggtc 540  
tagccagtc aagaacgttc gcaaccact taccgttcgg ttccttaaag gaaacgatcg 600  
agaaacccgg tgtgaaggtc gtgtacttgt gccggaacc gtttgacaca ttcatctctt 660  
cgtggcatta caccaacaac atcaaaccg agtcagttag cccagtcttg ctagaccaag 720  
cttttgatct gtattgccgg ggagtgatcg ggtttgccc gttttgggaa cacatggttg 780  
gatactggag agagagcttg aagagaccag agaaagtctt ctttttaagg tacgaggatc 840  
tcaaagacga catcgagacc aacttgaaga ggcttgcaac tttcttagag cttcctttca 900  
ccgaagaaga ggaacgaaag ggagttgtga aGgctatcgc cgagctgtgt agcttcgaga 960  
atctgaagaa gttggaggtg aacaagtcaa acaagtcgat caagaacttt gagaatcgat 1020  
tcttgtttcg gaaaggagaa gtgagtgatt gggtttaacta tttgtcacct tcacaagtgg 1080  
aaagattgtc agccttagtg gatgacaagt taggtggatc tgggtctact ttcaggttga 1140  
gctaaatata aggccacgtg cccccatttc tactcttggt ctgagggcct actatatacg 1200  
ttaagctaaag ttaaggcagt tgtattgttg ttacagatag acatcgaagc aacgtaacgt 1260  
ccataattaa gtc

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

Met Ala Thr Ser Ser Met Lys Ser Ile Pro Met Ala Ile Pro Ser Phe  
1 5 10 15  
Ser Met Cys His Lys Leu Glu Leu Leu Lys Glu Gly Lys Thr Arg Asp  
20 25 30  
Val Pro Lys Ala Glu Glu Asp Glu Gly Leu Ser Cys Glu Phe Gln Glu  
35 40 45  
Met Leu Asp Ser Leu Pro Lys Glu Arg Gly Trp Arg Thr Arg Tyr Leu  
50 55 60

Tyr Leu Phe Gln Gly Phe Trp Cys Gln Ala Lys Glu Ile Gln Ala Ile  
65 70 75 80  
Met Ser Phe Gln Lys His Phe Gln Ser Leu Glu Asn Asp Val Val Leu  
85 90 95  
Ala Thr Ile Pro Lys Ser Gly Thr Thr Trp Leu Lys Ala Leu Thr Phe  
100 105 110  
Thr Ile Leu Asn Arg His Arg Phe Asp Pro Val Ala Ser Ser Thr Asn  
115 120 125  
His Pro Leu Phe Thr Ser Asn Pro His Asp Leu Val Pro Phe Phe Glu  
130 135 140  
Tyr Lys Leu Tyr Ala Asn Gly Asp Val Pro Asp Leu Ser Gly Leu Ala  
145 150 155 160  
Ser Pro Arg Thr Phe Ala Thr His Leu Pro Phe Gly Ser Leu Lys Glu  
165 170 175  
Thr Ile Glu Lys Pro Gly Val Lys Val Val Tyr Leu Cys Arg Asn Pro  
180 185 190  
Phe Asp Thr Phe Ile Ser Ser Trp His Tyr Thr Asn Asn Ile Lys Ser  
195 200 205  
Glu Ser Val Ser Pro Val Leu Leu Asp Gln Ala Phe Asp Leu Tyr Cys  
210 215 220  
Arg Gly Val Ile Gly Phe Gly Pro Phe Trp Glu His Met Leu Gly Tyr  
225 230 235 240  
Trp Arg Glu Ser Leu Lys Arg Pro Glu Lys Val Phe Phe Leu Arg Tyr  
245 250 255  
Glu Asp Leu Lys Asp Asp Ile Glu Thr Asn Leu Lys Arg Leu Ala Thr  
260 265 270  
Phe Leu Glu Leu Pro Phe Thr Glu Glu Glu Glu Arg Lys Gly Val Val  
275 280 285  
Lys Ala Ile Ala Glu Leu Cys Ser Phe Glu Asn Leu Lys Lys Leu Glu  
290 295 300  
Val Asn Lys Ser Asn Lys Ser Ile Lys Asn Phe Glu Asn Arg Phe Leu  
305 310 315 320  
Phe Arg Lys Gly Glu Val Ser Asp Trp Val Asn Tyr Leu Ser Pro Ser  
325 330 335  
Gln Val Glu Arg Leu Ser Ala Leu Val Asp Asp Lys Leu Gly Gly Ser  
340 345 350  
Gly Leu Thr Phe Arg Leu Ser  
355

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

Met Lys Ser Ile Pro Met Ala Ile Pro Ser Phe Ser Met Cys His Lys  
1 5 10 15  
Leu Glu Leu Leu Lys Glu Gly Lys Thr Arg Asp Val Pro Lys Ala Glu  
20 25 30  
Glu Asp Glu Gly Leu Ser Cys Glu Phe Gln Glu Met Leu Asp Ser Leu  
35 40 45  
Pro Lys Glu Arg Gly Trp Arg Thr Arg Tyr Leu Tyr Leu Phe Gln Gly  
50 55 60  
Phe Trp Cys Gln Ala Lys Glu Ile Gln Ala Ile Met Ser Phe Gln Lys  
65 70 75 80  
His Phe Gln Ser Leu Glu Asn Asp Val Val Leu Ala Thr Ile Pro Lys

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85 90 95  
Ser Gly Thr Thr Trp Leu Lys Ala Leu Thr Phe Thr Ile Leu Asn Arg  
100 105 110  
His Arg Phe Asp Pro Val Ala Ser Ser Thr Asn His Pro Leu Phe Thr  
115 120 125  
Ser Asn Pro His Asp Leu Val Pro Phe Phe Glu Tyr Lys Leu Tyr Ala  
130 135 140  
Asn Gly Asp Val Pro Asp Leu Ser Gly Leu Ala Ser Pro Arg Thr Phe  
145 150 155 160  
Ala Thr His Leu Pro Phe Gly Ser Leu Lys Glu Thr Ile Glu Lys Pro  
165 170 175  
Gly Val Lys Val Val Tyr Leu Cys Arg Asn Pro Phe Asp Thr Phe Ile  
180 185 190  
Ser Ser Trp His Tyr Thr Asn Asn Ile Lys Ser Glu Ser Val Ser Pro  
195 200 205  
Val Leu Leu Asp Gln Ala Phe Asp Leu Tyr Cys Arg Gly Val Ile Gly  
210 215 220  
Phe Gly Pro Phe Trp Glu His Met Leu Gly Tyr Trp Arg Glu Ser Leu  
225 230 235 240  
Lys Arg Pro Glu Lys Val Phe Phe Leu Arg Tyr Glu Asp Leu Lys Asp  
245 250 255  
Asp Ile Glu Thr Asn Leu Lys Arg Leu Ala Thr Phe Leu Glu Leu Pro  
260 265 270  
Phe Thr Glu Glu Glu Glu Arg Lys Gly Val Val Lys Ala Ile Ala Glu  
275 280 285  
Leu Cys Ser Phe Glu Asn Leu Lys Lys Leu Glu Val Asn Lys Ser Asn  
290 295 300  
Lys Ser Ile Lys Asn Phe Glu Asn Arg Phe Leu Phe Arg Lys Gly Glu  
305 310 315 320  
Val Ser Asp Trp Val Asn Tyr Leu Ser Pro Ser Gln Val Glu Arg Leu  
325 330 335  
Ser Ala Leu Val Asp Asp Lys Leu Gly Gly Ser Gly Leu Thr Phe Arg  
340 345 350  
Leu Ser

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1568368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

Met Ala Ile Pro Ser Phe Ser Met Cys His Lys Leu Glu Leu Leu Lys  
1 5 10 15  
Glu Gly Lys Thr Arg Asp Val Pro Lys Ala Glu Glu Asp Glu Gly Leu  
20 25 30  
Ser Cys Glu Phe Gln Glu Met Leu Asp Ser Leu Pro Lys Glu Arg Gly  
35 40 45  
Trp Arg Thr Arg Tyr Leu Tyr Leu Phe Gln Gly Phe Trp Cys Gln Ala  
50 55 60  
Lys Glu Ile Gln Ala Ile Met Ser Phe Gln Lys His Phe Gln Ser Leu  
65 70 75 80  
Glu Asn Asp Val Val Leu Ala Thr Ile Pro Lys Ser Gly Thr Thr Trp  
85 90 95  
Leu Lys Ala Leu Thr Phe Thr Ile Leu Asn Arg His Arg Phe Asp Pro  
100 105 110

Val Ala Ser Ser Thr Asn His Pro Leu Phe Thr Ser Asn Pro His Asp  
115 120 125  
Leu Val Pro Phe Phe Glu Tyr Lys Leu Tyr Ala Asn Gly Asp Val Pro  
130 135 140  
Asp Leu Ser Gly Leu Ala Ser Pro Arg Thr Phe Ala Thr His Leu Pro  
145 150 155 160  
Phe Gly Ser Leu Lys Glu Thr Ile Glu Lys Pro Gly Val Lys Val Val  
165 170 175  
Tyr Leu Cys Arg Asn Pro Phe Asp Thr Phe Ile Ser Ser Trp His Tyr  
180 185 190  
Thr Asn Asn Ile Lys Ser Glu Ser Val Ser Pro Val Leu Leu Asp Gln  
195 200 205  
Ala Phe Asp Leu Tyr Cys Arg Gly Val Ile Gly Phe Gly Pro Phe Trp  
210 215 220  
Glu His Met Leu Gly Tyr Trp Arg Glu Ser Leu Lys Arg Pro Glu Lys  
225 230 235 240  
Val Phe Phe Leu Arg Tyr Glu Asp Leu Lys Asp Asp Ile Glu Thr Asn  
245 250 255  
Leu Lys Arg Leu Ala Thr Phe Leu Glu Leu Pro Phe Thr Glu Glu Glu  
260 265 270  
Glu Arg Lys Gly Val Val Lys Ala Ile Ala Glu Leu Cys Ser Phe Glu  
275 280 285  
Asn Leu Lys Lys Leu Glu Val Asn Lys Ser Asn Lys Ser Ile Lys Asn  
290 295 300  
Phe Glu Asn Arg Phe Leu Phe Arg Lys Gly Glu Val Ser Asp Trp Val  
305 310 315 320  
Asn Tyr Leu Ser Pro Ser Gln Val Glu Arg Leu Ser Ala Leu Val Asp  
325 330 335  
Asp Lys Leu Gly Ser Gly Leu Thr Phe Arg Leu Ser  
340 345

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..797
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaattcggat agcttgcaaa taacgctgac aaaaaaagaa acagtgaaga agaaaaaaaa  | 60  |
| aaaaggtcat ttccattttc tccatttgat ttttgccgac cggagaaaat atcttcttgc  | 120 |
| cgtcttcttc ttcatattcac caggaacttt tatttgaaat cggtttgatt tagccatggc | 180 |
| aaacgcggca tcgggaatgg ctgtgcatga tgattgcaag ctgaaattta tggaactgaa  | 240 |
| ggcgaagaaga acattccgta ccatagtcta caagattgag gataagcaag tgattgtaga | 300 |
| gaaactcggg gaacctgaac aatcatatga tgactttgca gctagtcttc cagctgatga  | 360 |
| ttgccgatat tgcatttacg atttcgactt tGgtcactgc ggagaactgc cagaagagca  | 420 |
| agatcttctt cattgcatgg tctccggaca ctgccaaagt gagagacaag atgatttacg  | 480 |
| cgagctctaa agatagggtc aagagagaac tagatggaat tcaagtggaa cttcaagcta  | 540 |
| ctgatccaac agaaatgggt cttgatgttt tcaaaagccg caccaactaa gtaaaacaaa  | 600 |
| accctgtaag ggcatttgaa taagtttggg ttctggagtg aatatgtttc ctctgactgt  | 660 |
| tatgaaaact ttttaacacc ttcaacttca ttctacttgg tattattgta tgtctttgat  | 720 |
| gtgttatgtg tgccttgatga tggttttcaa ttagttttac atgtacaata cttgaaatca | 780 |
| gattgttgct aagcttc                                                 |     |

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..104  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

Met Ala Asn Ala Ala Ser Gly Met Ala Val His Asp Asp Cys Lys Leu  
1                    5                    10                    15  
Lys Phe Met Glu Leu Lys Ala Lys Arg Thr Phe Arg Thr Ile Val Tyr  
                    20                    25                    30  
Lys Ile Glu Asp Lys Gln Val Ile Val Glu Lys Leu Gly Glu Pro Glu  
                    35                    40                    45  
Gln Ser Tyr Asp Asp Phe Ala Ala Ser Leu Pro Ala Asp Asp Cys Arg  
                    50                    55                    60  
Tyr Cys Ile Tyr Asp Phe Asp Phe Gly His Cys Gly Glu Leu Pro Glu  
65                    70                    75                    80  
Glu Gln Asp Leu Leu His Cys Met Val Ser Gly His Cys Gln Ser Glu  
                    85                    90                    95  
Arg Gln Asp Asp Leu Arg Glu Leu  
                    100

(2) INFORMATION FOR SEQ ID NO:934:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 97 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..97  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

Met Ala Val His Asp Asp Cys Lys Leu Lys Phe Met Glu Leu Lys Ala  
1                    5                    10                    15  
Lys Arg Thr Phe Arg Thr Ile Val Tyr Lys Ile Glu Asp Lys Gln Val  
                    20                    25                    30  
Ile Val Glu Lys Leu Gly Glu Pro Glu Gln Ser Tyr Asp Asp Phe Ala  
                    35                    40                    45  
Ala Ser Leu Pro Ala Asp Asp Cys Arg Tyr Cys Ile Tyr Asp Phe Asp  
                    50                    55                    60  
Phe Gly His Cys Gly Glu Leu Pro Glu Glu Gln Asp Leu Leu His Cys  
65                    70                    75                    80  
Met Val Ser Gly His Cys Gln Ser Glu Arg Gln Asp Asp Leu Arg Glu  
                    85                    90                    95  
Leu

(2) INFORMATION FOR SEQ ID NO:935:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 87 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..87  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

Met Met Thr Leu Gln Leu Val Phe Gln Leu Met Ile Ala Asp Ile Ala  
1                    5                    10                    15

Phe Thr Ile Ser Thr Leu Val Thr Ala Glu Asn Cys Gln Lys Ser Lys  
20 25 30  
Ile Phe Phe Ile Ala Trp Ser Pro Asp Thr Ala Lys Val Arg Asp Lys  
35 40 45  
Met Ile Tyr Ala Ser Ser Lys Asp Arg Phe Lys Arg Glu Leu Asp Gly  
50 55 60  
Ile Gln Val Glu Leu Gln Ala Thr Asp Pro Thr Glu Met Gly Leu Asp  
65 70 75 80  
Val Phe Lys Ser Arg Thr Asn  
85

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1327
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| actggttcgt  | ctctttcttc | gatttctctt  | tctatctggt  | ttccattttc | gtctcgttgg | 60   |
| tggtctggtg  | ggtttggttt | gtctctgttc  | ttctatttgt  | ggcgttattc | atcggttcaa | 120  |
| ttgtcatctt  | catcgtttcc | gtcgtgttat  | ttggtgtttc  | tcgtttgggt | ctttcgaaca | 180  |
| tctttcattc  | ttctcttttt | ggtgttgctc  | cccacgaaca  | ggtagattga | tgaaaagcaa | 240  |
| ccatggatga  | cctacatgga | agcaatgctc  | gaatgcacat  | tagagaagct | caagatccaa | 300  |
| tgcattgtgca | atttgaacat | catgctttgc  | atcacatcca  | caatggaagc | ggtatggttg | 360  |
| atgaccaggc  | tgatgatggc | aatgctggtg  | ggatgagtga  | gggtgtggaa | acagacattc | 420  |
| cttctcacc   | tggaatgta  | actgacaatc  | gtggtgaagt  | ggtcgaccgt | ggtagtgaac | 480  |
| aaggagatca  | gttaacattg | tcttttcagg  | gccaaagtcta | cgtttttgac | agtgtcttgc | 540  |
| ctgagaaggt  | tcaagctgtg | cttctattat  | tgggtgggtc  | tgaattacct | cagcagcccc | 600  |
| tcttgacctc  | ggatcacctc | atcagaacaa  | cagagtatcg  | agtttacctg | gtactcctca | 660  |
| aagggttagt  | attccgcagc | gattagcttc  | tttggtcaga  | tttcgagaga | aacggaaagg | 720  |
| aaggaatttt  | gataagaaga | ttcgggtatac | agtccgcaag  | gaggtagctt | tgaggatgca | 780  |
| acgcaataaa  | ggtcagttca | catctgccaa  | gtcaaacaat  | gatgaagctg | catctgcttg | 840  |
| atctagctgg  | gggtcgaatc | aaacctgggc  | catagaaaagt | agtgaggctc | agcatcaaga | 900  |
| gatctcatgt  | cggcactgtg | gaattggcga  | gaagtcaact  | ccaatgatgc | gacgtggacc | 960  |
| tgccggggcca | agaacacttt | gcaatgcattg | tggacttatg  | tgggcaaaca | aggggtgctt | 1020 |
| tagggactta  | tccaaagcct | ctcctcaaac  | agccagaat   | cttcctttta | ataagaatga | 1080 |
| agatgcaaat  | cttgagactg | atcatcaaat  | aatgataaca  | gtggccaatg | acataagcaa | 1140 |
| ctcacagtga  | gggcatgttg | gctcttccca  | ttacaagcaa  | gagaaagatc | tcaacagagt | 1200 |
| ttgcatcgcc  | tcaggttctg | tagctttatc  | attccctttg  | aaagaatctg | actcgattta | 1260 |
| ggttatcagg  | atttgatcta | tgacaAtgta  | atctgagtga  | taatgatctg | caatgttttg | 1320 |
| cttcttc     |            |             |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asp | Leu | His | Gly | Ser | Asn | Ala | Arg | Met | His | Ile | Arg | Glu | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Asp | Pro | Met | His | Val | Gln | Phe | Glu | His | His | Ala | Leu | His | His | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asn | Gly | Ser | Gly | Met | Val | Asp | Asp | Gln | Ala | Asp | Asp | Gly | Asn | Ala |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Met | Ser | Glu | Gly | Val | Glu | Thr | Asp | Ile | Pro | Ser | His | Pro | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Asn | Val | Thr | Asp | Asn | Arg | Gly | Glu | Val | Val | Asp | Arg | Gly | Ser | Glu | Gln |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Asp | Gln | Leu | Thr | Leu | Ser | Phe | Gln | Gly | Gln | Val | Tyr | Val | Phe | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Val | Leu | Pro | Glu | Lys | Val | Gln | Ala | Val | Leu | Leu | Leu | Leu | Gly | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Arg | Glu | Leu | Pro | Gln | Gln | Pro | Leu | Leu | Ala |     |     |     |     |     |     |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ile | Arg | Glu | Ala | Gln | Asp | Pro | Met | His | Val | Gln | Phe | Glu | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ala | Leu | His | His | Ile | His | Asn | Gly | Ser | Gly | Met | Val | Asp | Asp | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asp | Asp | Gly | Asn | Ala | Gly | Gly | Met | Ser | Glu | Gly | Val | Glu | Thr | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Ser | His | Pro | Gly | Asn | Val | Thr | Asp | Asn | Arg | Gly | Glu | Val | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Arg | Gly | Ser | Glu | Gln | Gly | Asp | Gln | Leu | Thr | Leu | Ser | Phe | Gln | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Gln | Val | Tyr | Val | Phe | Asp | Ser | Val | Leu | Pro | Glu | Lys | Val | Gln | Ala | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Leu | Leu | Leu | Gly | Gly | Arg | Glu | Leu | Pro | Gln | Gln | Pro | Leu | Leu | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Arg | Asn | Lys | Gly | Gln | Phe | Thr | Ser | Ala | Lys | Ser | Asn | Asn | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Ala | Ala | Ser | Ala | Gly | Ser | Ser | Trp | Gly | Ser | Asn | Gln | Thr | Trp | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Glu | Ser | Ser | Glu | Ala | Gln | His | Gln | Glu | Ile | Ser | Cys | Arg | His | Cys |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Ile | Gly | Glu | Lys | Ser | Thr | Pro | Met | Met | Arg | Arg | Gly | Pro | Ala | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Arg | Thr | Leu | Cys | Asn | Ala | Cys | Gly | Leu | Met | Trp | Ala | Asn | Lys | Gly |

(2) INFORMATION FOR SEQ ID NO:940:

(A) LENGTH: 1289 base pairs

(C) STRANDEDNESS: single

MOLECULE TYPE: DNA (α

(A) NAM

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:940:

attaaa ttctctataa aacataagag agtctaaaca c

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gactttttaga | tatgtgtagt  | aaaataacat  | tagtgttaac  | tttattttcc  | agttatttca  | 120  |
| tatcaacaga  | tgtgtgaat   | ggatcatttc  | ctgcgctttt  | ggcttttgga  | gattcaattc  | 180  |
| tcgatactgg  | caacaacaat  | tttctcctga  | cttttatgaa  | aggaaatatc  | tggccatatg  | 240  |
| gaaggagttt  | cagcatgaga  | agggcgacag  | gaagatttgg  | aatggaaga   | gttttctctg  | 300  |
| acatagttgc  | tgaaggttta  | gggactcaaga | agatttttacc | agcttatcgt  | aagttgttca  | 360  |
| attctccaag  | tgacctttaga | actggtgttt  | gcttcgcatac | aggtggtgca  | ggagttgacc  | 420  |
| ctgtttacatc | caaatgtctg  | agagtgtttaa | cgccaaagga  | tcaagtaaac  | gatttcaaag  | 480  |
| ggtacataag  | aaagctaaag  | gccacagcag  | gtccttcaag  | agcaagtagt  | atagtttcaa  | 540  |
| atgcagtgat  | tcttgtttct  | caaggaaata  | atgatattgg  | aatctcatat  | tttggaaactc | 600  |
| caactgctgc  | tttccgagga  | ttaactccca  | atagatatac  | cactaaacta  | gctggttgga  | 660  |
| acaaacagtt  | tatgaaagaa  | ttatacgcac  | aaggagcgag  | aaaattcgcg  | gtaatgggag  | 720  |
| tgataccggt  | gggatgtttg  | cctatgacaa  | gaattcttct  | tgggtgggttc | gtcatcacgt  | 780  |
| gtaacttctt  | cgcgaataga  | gtcgcagaac  | agtacaacgg  | aaaattgagg  | agcggaaacta | 840  |
| aaagttgggg  | acgtgaagca  | gggttttaggg | gtacaaaatt  | tgtctatgtc  | gacatgtaca  | 900  |
| acactcttat  | ggatgtttat  | aaaaattata  | gaagatacgg  | attttctaat  | gagaaaaatg  | 960  |
| ggtgtttgtt  | tatgattacg  | gctataatac  | catgccccaa  | cccagataaa  | tacgtcttct  | 1020 |
| acgacttcgt  | tcatccatcc  | gagaaagctt  | acagaacaat  | ttctaaaaag  | cttgtccagg  | 1080 |
| atatcaagaa  | tggccttgcc  | tgattttatta | tatatacaat  | gctttatttt  | aatttttaata | 1140 |
| acagccatgc  | ttaataaatg  | aaatgagaag  | acaaaaatca  | tacatggcga  | tctctctgtt  | 1200 |
| tttcttatgt  | taaagaatgt  | ataatccagt  | ttatgtattg  | ttcactttat  | ataatcccag  | 1260 |
| aacaacaaag  | gagttttggtt | acaaCatgt   |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:941:

(A) LENGTH: 343 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAM

(B) LOCATION: 1..343

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:941:

Cys Ser Lys Ile Thr Leu Val Leu Thr Leu P

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Leu | Ala | Val | Leu | Val | Leu | Ala | Ser | Ser | Leu | Ala | Val | Met |
|     |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Ser | Thr | Asp | Ala | Val | Asn | Gly | Ser | Phe | Pro | Ala | Leu | Leu | Ala | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ser | Ile | Leu | Asp | Thr | Gly | Asn | Asn | Asn | Phe | Leu | Leu | Thr | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Lys | Gly | Asn | Ile | Trp | Pro | Tyr | Gly | Arg | Ser | Phe | Ser | Met | Arg | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp Ile Val Ala  
65 70 75 80  
Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg Lys Leu Phe  
85 90 95  
Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala Ser Gly Gly  
100 105 110  
Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val Leu Thr Pro  
115 120 125  
Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys Leu Lys Ala  
130 135 140  
Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn Ala Val Ile  
145 150 155 160  
Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr Phe Gly Thr  
165 170 175  
Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr Thr Thr Lys  
180 185 190  
Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr Asp Gln Gly  
195 200 205  
Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly Cys Leu Pro  
210 215 220  
Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys Asn Phe Phe  
225 230 235 240  
Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg Ser Gly Thr  
245 250 255  
Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys Phe Val Tyr  
260 265 270  
Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn Tyr Arg Arg  
275 280 285  
Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met Ile Thr Ala  
290 295 300  
Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr Asp Phe Val  
305 310 315 320  
His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys Leu Val Gln  
325 330 335  
Asp Ile Lys Asn Gly Leu Ala  
340

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1568411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

Met Lys Gly Asn Ile Trp Pro Tyr Gly Arg Ser Phe Ser Met Arg Arg  
1 5 10 15  
Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp Ile Val Ala  
20 25 30  
Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg Lys Leu Phe  
35 40 45  
Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala Ser Gly Gly  
50 55 60  
Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val Leu Thr Pro  
65 70 75 80  
Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys Leu Lys Ala  
85 90 95  
Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn Ala Val Ile

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr Phe Gly Thr |     |     |
| 115                                                             | 120 | 125 |
| Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr Thr Thr Lys |     |     |
| 130                                                             | 135 | 140 |
| Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr Asp Gln Gly |     |     |
| 145                                                             | 150 | 155 |
| Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly Cys Leu Pro |     |     |
| 165                                                             | 170 | 175 |
| Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys Asn Phe Phe |     |     |
| 180                                                             | 185 | 190 |
| Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg Ser Gly Thr |     |     |
| 195                                                             | 200 | 205 |
| Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys Phe Val Tyr |     |     |
| 210                                                             | 215 | 220 |
| Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn Tyr Arg Arg |     |     |
| 225                                                             | 230 | 235 |
| Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met Ile Thr Ala |     |     |
| 245                                                             | 250 | 255 |
| Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr Asp Phe Val |     |     |
| 260                                                             | 265 | 270 |
| His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys Leu Val Gln |     |     |
| 275                                                             | 280 | 285 |
| Asp Ile Lys Asn Gly Leu Ala                                     |     |     |
| 290                                                             | 295 |     |

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1568412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Arg Arg Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp |     |     |
| 1                                                               | 5   | 10  |
| Ile Val Ala Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg |     |     |
| 20                                                              | 25  | 30  |
| Lys Leu Phe Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala |     |     |
| 35                                                              | 40  | 45  |
| Ser Gly Gly Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val |     |     |
| 50                                                              | 55  | 60  |
| Leu Thr Pro Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys |     |     |
| 65                                                              | 70  | 75  |
| Leu Lys Ala Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn |     |     |
| 85                                                              | 90  | 95  |
| Ala Val Ile Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr |     |     |
| 100                                                             | 105 | 110 |
| Phe Gly Thr Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr |     |     |
| 115                                                             | 120 | 125 |
| Thr Thr Lys Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr |     |     |
| 130                                                             | 135 | 140 |
| Asp Gln Gly Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly |     |     |
| 145                                                             | 150 | 155 |
| Cys Leu Pro Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys |     |     |
| 165                                                             | 170 | 175 |
| Asn Phe Phe Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg |     |     |
| 180                                                             | 185 | 190 |

Ser Gly Thr Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys  
195 200 205  
Phe Val Tyr Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn  
210 215 220  
Tyr Arg Arg Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met  
225 230 235 240  
Ile Thr Ala Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr  
245 250 255  
Asp Phe Val His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys  
260 265 270  
Leu Val Gln Asp Ile Lys Asn Gly Leu Ala  
275 280

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..593
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcaaaatct ttacaatatt tatcatgtat gattctatca agtgagatgg aacggtatgc   | 60  |
| aattttttccg ttttaataatg tgttttcgct tacaggttga acaagtcact ccagtagcag | 120 |
| tagagaacgt tgaggtacca acaaagacag tggaggagac agtggtggag acagaggtga   | 180 |
| cccaacagcc ggaagaatcc gtccccgccg tgacagaaca aaaatccgaa gcaccaattg   | 240 |
| tagaaacaaa cgaagaagtg gttgtggaag aggcagagaa gaaagatgaa gaaaccgaga   | 300 |
| agaaaacaga ggagaaagac gagaagacag aagtgatcac ggaaactccg gtagttgagg   | 360 |
| aggaggagaa gaaagctgag gaagtgaccg aaactccggc gggttgaggag gaggagaaga  | 420 |
| agacagaggt gggtgaggag aaacagactg aggttgccgc tgctgaggaa gtcgccgttg   | 480 |
| agaaggccga ggagtaaaga ggaaggaaga agctatatat gacctttttt ggtctcatat   | 540 |
| cgttttctgt ttatttttatt ttatcaaWca tttcataagt attttctatg ttt         |     |

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gln Phe Phe Arg Leu Ile Met Cys Phe Arg Leu Gln Val Glu Gln |  |
| 1 5 10 15                                                       |  |
| Val Thr Pro Val Ala Val Glu Asn Val Glu Val Pro Thr Lys Thr Val |  |
| 20 25 30                                                        |  |
| Glu Glu Thr Val Val Glu Thr Glu Val Thr Gln Gln Pro Glu Glu Ser |  |
| 35 40 45                                                        |  |
| Val Pro Ala Val Thr Glu Gln Lys Ser Glu Ala Pro Ile Val Glu Thr |  |
| 50 55 60                                                        |  |
| Asn Glu Glu Val Val Val Glu Glu Ala Glu Lys Lys Asp Glu Glu Thr |  |
| 65 70 75 80                                                     |  |
| Glu Lys Lys Thr Glu Glu Lys Asp Glu Lys Thr Glu Val Ile Thr Glu |  |
| 85 90 95                                                        |  |
| Thr Pro Val Val Glu Glu Glu Glu Lys Lys Ala Glu Glu Val Thr Glu |  |
| 100 105 110                                                     |  |
| Thr Pro Ala Val Val Glu Glu Glu Lys Lys Thr Glu Val Val Glu Glu |  |

115 120 125  
Lys Gln Thr Glu Val Ala Ala Glu Glu Val Ala Val Glu Lys Ala  
130 135 140  
Glu Glu  
145

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..139  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

Met Cys Phe Arg Leu Gln Val Glu Gln Val Thr Pro Val Ala Val Glu  
1 5 10 15  
Asn Val Glu Val Pro Thr Lys Thr Val Glu Glu Thr Val Val Glu Thr  
20 25 30  
Glu Val Thr Gln Gln Pro Glu Glu Ser Val Pro Ala Val Thr Glu Gln  
35 40 45  
Lys Ser Glu Ala Pro Ile Val Glu Thr Asn Glu Glu Val Val Val Glu  
50 55 60  
Glu Ala Glu Lys Lys Asp Glu Glu Thr Glu Lys Lys Thr Glu Glu Lys  
65 70 75 80  
Asp Glu Lys Thr Glu Val Ile Thr Glu Thr Pro Val Val Glu Glu Glu  
85 90 95  
Glu Lys Lys Ala Glu Glu Val Thr Glu Thr Pro Ala Val Val Glu Glu  
100 105 110  
Glu Lys Lys Thr Glu Val Val Glu Glu Lys Gln Thr Glu Val Ala Ala  
115 120 125  
Ala Glu Glu Val Ala Val Glu Lys Ala Glu Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1157  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

cgagatatat cgactccgcg accctccaact actctgctga tctacacaca cacacacaaa 60  
cacaatcgcc ggcaacaatg gcgaagctca cacttctctt ctctcctttcc tttctcatct 120  
tctcctcatc catcgctttc caatcagacg agctcctcgt tgacgacgac gaatttggtc 180  
tagaaggagc aaagccccgc tccaccgatc ttcacacatc ttcttcttct tcgccacagc 240  
agcagcaaca gactccaact attcggagaa gatactcaga tccctacgat ttggattcaa 300  
aagtccaatt tactctcgaa catgccttcg gtgactctga tttctccccc gccggtactt 360  
tctccgctcg tctcaaaacc tggagtcatt gcggaagac attaacgaag ctgcgattct 420  
ctagaaatga tttttctgct gaagagaaaag atgcattcaa gaatctgctg aaaggagatg 480  
gcttttatcg gattcggctt ccatctaatt tggttagtcc accagggaga gaggttgtga 540  
ttgcatcagt gagagctaga tgtctaccac gggatggctt ggatgagcat ttcattatac 600  
acatggaagg tgctaacatc ttggcagtta gttatggttc tcttggggcg tgtcaatatac 660  
ctcgacaatt gaaacttcca gcaaatgggt cgtttaactc tcacacaatt ctgaaaagca 720  
gtgagcaggc gccaaagaact ccaatattca ctgaggagat tctaggchdK tgagaatgta 780  
gagggagaag ttgaaccacc accagagaga tcattttggg cgaaatattg gatgtatttg 840

```
ataccgctgg gactcgtagt gatgaatgcc gtgacacaag catcaaacat ggctgaagaa 900
cCtgcggggtg gacaggcagg aggtgcacaa gtgcaaccag ctgccaggag aagatgattc 960
cacttttact tctcccaaag caatgaaagc tgcagctggt tagagatgat gattcaacag 1020
atcttcatgt aaaccatctt gccatcattt gggtttatgt aacctttaat tttaatcctc 1080
gatcgggtgtg ttttagtact caccaatcgg gaaatcaaaa atcttgtctt catgacatat 1140
caagaacaaa gacattt
```

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1568437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

Arg Tyr Ile Asp Ser Ala Thr Leu His Tyr Ser Ala Asp Leu His Thr  
1 5 10 15  
His Thr Gln Thr Gln Ser Pro Ala Thr Met Ala Lys Leu Thr Leu Leu  
20 25 30  
Phe Phe Leu Ser Phe Leu Ile Phe Ser Ser Ser Ile Ala Phe Gln Ser  
35 40 45  
Asp Glu Leu Leu Val Asp Asp Asp Glu Phe Gly Leu Glu Gly Ala Lys  
50 55 60  
Pro Arg Ser Thr Asp Leu His Thr Ser Ser Ser Ser Ser Pro Gln Gln  
65 70 75 80  
Gln Gln Gln Thr Pro Thr Ile Arg Arg Arg Tyr Ser Asp Pro Thr Asp  
85 90 95  
Leu Asp Ser Lys Val Gln Phe Thr Leu Glu His Ala Phe Gly Asp Ser  
100 105 110  
Asp Phe Ser Pro Ala Gly Thr Phe Ser Ala Arg Leu Lys Thr Trp Ser  
115 120 125  
His Gly Gly Lys Thr Leu Thr Lys Leu Arg Phe Ser Arg Asn Asp Phe  
130 135 140  
Ser Ala Glu Glu Lys Asp Ala Phe Lys Asn Leu Lys Gly Asp Gly  
145 150 155 160  
Phe Tyr Arg Ile Arg Leu Pro Ser Asn Val Val Ser Pro Pro Gly Arg  
165 170 175  
Glu Phe Val Ile Ala Ser Val Arg Ala Arg Cys Leu Pro Arg Asp Gly  
180 185 190  
Leu Asp Glu His Phe Ile Ile His Met Glu Gly Ala Asn Ile Leu Ala  
195 200 205  
Val Ser Tyr Gly Ser Pro Gly Ala Cys Gln Tyr Pro Arg Gln Leu Lys  
210 215 220  
Leu Pro Ala Lys Trp Ser Phe Asn Ser His Thr Ile Leu Lys Ser Ser  
225 230 235 240  
Glu Gln Ala Pro Arg Thr Pro Ile Phe Thr Glu Glu Ile Leu Gly Xaa  
245 250 255

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

Met Ala Lys Leu Thr Leu Leu Phe Phe Leu Ser Phe Leu Ile Phe Ser  
1 5 10 15  
Ser Ser Ile Ala Phe Gln Ser Asp Glu Leu Leu Val Asp Asp Asp Glu  
20 25 30  
Phe Gly Leu Glu Gly Ala Lys Pro Arg Ser Thr Asp Leu His Thr Ser  
35 40 45  
Ser Ser Ser Ser Pro Gln Gln Gln Gln Thr Pro Thr Ile Arg Arg  
50 55 60  
Arg Tyr Ser Asp Pro Thr Asp Leu Asp Ser Lys Val Gln Phe Thr Leu  
65 70 75 80  
Glu His Ala Phe Gly Asp Ser Asp Phe Ser Pro Ala Gly Thr Phe Ser  
85 90 95  
Ala Arg Leu Lys Thr Trp Ser His Gly Gly Lys Thr Leu Thr Lys Leu  
100 105 110  
Arg Phe Ser Arg Asn Asp Phe Ser Ala Glu Glu Lys Asp Ala Phe Lys  
115 120 125  
Asn Leu Leu Lys Gly Asp Gly Phe Tyr Arg Ile Arg Leu Pro Ser Asn  
130 135 140  
Val Val Ser Pro Pro Gly Arg Glu Phe Val Ile Ala Ser Val Arg Ala  
145 150 155 160  
Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu His Phe Ile Ile His Met  
165 170 175  
Glu Gly Ala Asn Ile Leu Ala Val Ser Tyr Gly Ser Pro Gly Ala Cys  
180 185 190  
Gln Tyr Pro Arg Gln Leu Lys Leu Pro Ala Lys Trp Ser Phe Asn Ser  
195 200 205  
His Thr Ile Leu Lys Ser Ser Glu Gln Ala Pro Arg Thr Pro Ile Phe  
210 215 220  
Thr Glu Glu Ile Leu Gly Xaa  
225 230

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1568490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

atatacCttc ttcttcttca ctttatgcaa gataatggac aaagttatga gaatgtcgtc 60  
cgaaaaaagg gtggttatat ttaccaagag ctctctgttg ttgtcctatg cggttcaagt 120  
tctcttccaa gatcttggtg ttaaccctaa gatccacgag attgataagg accctgaatg 180  
ccgagagata gagaaggctc ttatgaggct aggggtgttca aagccggtcc cagccgtctt 240  
cattggtggc aagctcgttg gttcgaccaa cgaagtaatg tccatgcacc taagcagctc 300  
gctcgttccc ctagtgaagc catatttatg ttaaacaaca acgaaggagt atttatgata 360  
ttaattagct atgtatatgt tattcaataa ggaacaaaat tgagccaaat ctttgtaatg 420  
tgttttttgg tattattatt ggttgataaa cattgggaaa gtgtacgtat aattataaga 480  
ctgttatatt gattcgaagg t

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1568491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Thr | Phe | Phe | Phe | Phe | Thr | Leu | Cys | Lys | Ile | Met | Asp | Lys | Val | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Met | Ser | Ser | Glu | Lys | Gly | Val | Val | Ile | Phe | Thr | Lys | Ser | Ser | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Leu | Ser | Tyr | Ala | Val | Gln | Val | Leu | Phe | Gln | Asp | Leu | Gly | Val | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Lys | Ile | His | Glu | Ile | Asp | Lys | Asp | Pro | Glu | Cys | Arg | Glu | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Leu | Met | Arg | Leu | Gly | Cys | Ser | Lys | Pro | Val | Pro | Ala | Val | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Gly | Gly | Lys | Leu | Val | Gly | Ser | Thr | Asn | Glu | Val | Met | Ser | Met | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ser | Ser | Ser | Leu | Val | Pro | Leu | Val | Lys | Pro | Tyr | Leu | Cys |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1568492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Lys | Val | Met | Arg | Met | Ser | Ser | Glu | Lys | Gly | Val | Val | Ile | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Lys | Ser | Ser | Cys | Cys | Leu | Ser | Tyr | Ala | Val | Gln | Val | Leu | Phe | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Gly | Val | Asn | Pro | Lys | Ile | His | Glu | Ile | Asp | Lys | Asp | Pro | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Arg | Glu | Ile | Glu | Lys | Ala | Leu | Met | Arg | Leu | Gly | Cys | Ser | Lys | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Pro | Ala | Val | Phe | Ile | Gly | Gly | Lys | Leu | Val | Gly | Ser | Thr | Asn | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Met | Ser | Met | His | Leu | Ser | Ser | Ser | Leu | Val | Pro | Leu | Val | Lys | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Leu | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1568493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Met | Ser | Ser | Glu | Lys | Gly | Val | Val | Ile | Phe | Thr | Lys | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Cys | Leu | Ser | Tyr | Ala | Val | Gln | Val | Leu | Phe | Gln | Asp | Leu | Gly | Val |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |

Asn Pro Lys Ile His Glu Ile Asp Lys Asp Pro Glu Cys Arg Glu Ile  
35 40 45  
Glu Lys Ala Leu Met Arg Leu Gly Cys Ser Lys Pro Val Pro Ala Val  
50 55 60  
Phe Ile Gly Gly Lys Leu Val Gly Ser Thr Asn Glu Val Met Ser Met  
65 70 75 80  
His Leu Ser Ser Ser Leu Val Pro Leu Val Lys Pro Tyr Leu Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1075
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| atgaaaccgg  | atactcgaga | gtcgccggag  | tgctcttccc | ttcttctatc  | agctctgctt | 60   |
| ctccttttaga | aattagggtt | tttgaggaag  | acgagtattc | acttcttttc  | accgtgaagc | 120  |
| gatggcttct  | ttgttcaagg | agcaagcaaa  | gctctcagct | tatcgagata  | gaagattttc | 180  |
| aggaacacaa  | gaggagtttg | atgaagcgtt  | aagggcattc | acaacggttt  | acattggcaa | 240  |
| tgtgtctttt  | tacactactg | aagaacagct  | ttacgagctt | ttctctagag  | ctggagaaat | 300  |
| caaaaagatc  | atcatgggtt | tggataagaa  | cactaaaaca | ccttggtggc  | tttgtttcgt | 360  |
| cctgttctac  | tctagagagg | atactgaaga  | tgcagtcaag | tatataagtg  | ggGactattc | 420  |
| tcgatgaccg  | gcctattcgt | gtggattttg  | attggggatt | ccaagaagga  | agacaatggg | 480  |
| gacgtggtag  | aagcgggtgt | cagggttcgtg | atgaataccg | tacagattac  | gatcctgcta | 540  |
| gaggttatgg  | gaaattagtt | cagaaggaac  | tcgaagcaca | aaggcagctc  | gtggattacg | 600  |
| gtactggctc  | attgggagct | tatcctcaag  | Ctgcgccaac | gaattatgga  | aatggaaggc | 660  |
| gtggtggagg  | aaactatggt | caaggaggag  | aaaatcgcca | tggaagagga  | ggagactacc | 720  |
| atcggaacg   | acaaagagac | gatgatcgct  | atggacgtga | taactcaaga  | agaaacacag | 780  |
| atcatgagtc  | taggagagac | actgatagtg  | acatgagacc | ggagaagaac  | ccacgattcc | 840  |
| gtgagagcgg  | tgactccgat | gacgatggtg  | aagatgatcg | gaagagaaga  | tcttaaaaca | 900  |
| aaacttttaga | agttgtcaat | gttgctgaat  | ggtcaatgta | atcttttagat | tgatgagtct | 960  |
| gaactcagtt  | tgggttttct | agattttcat  | tacaaccttt | cttaagtggg  | ttcgttcaat | 1020 |
| atcagtgtcc  | tcattaactt | ttgctccttg  | atcaacagat | atgtcattac  | tagtt      |      |

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

Glu Thr Gly Tyr Ser Arg Val Ala Gly Val Ser Phe Pro Ser Ser Ile  
1 5 10 15  
Ser Ser Ala Ser Pro Leu Glu Ile Arg Val Phe Glu Glu Asp Glu Tyr  
20 25 30  
Ser Leu Leu Phe Thr Val Lys Arg Trp Leu Leu Cys Ser Arg Ser Lys  
35 40 45  
Gln Ser Ser Gln Leu Ile Glu Ile Glu Asp Phe Gln Glu His Lys Arg  
50 55 60  
Ser Leu Met Lys Arg  
65

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 101 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..101  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568496  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:  
Met Ala Ser Leu Phe Lys Glu Gln Ala Lys Leu Ser Ala Tyr Arg Asp  
1                    5                    10                    15  
Arg Arg Phe Ser Gly Thr Gln Glu Glu Phe Asp Glu Ala Leu Arg Ala  
                    20                    25                    30  
Ser Thr Thr Val Tyr Ile Gly Asn Val Ser Phe Tyr Thr Thr Glu Glu  
                    35                    40                    45  
Gln Leu Tyr Glu Leu Phe Ser Arg Ala Gly Glu Ile Lys Lys Ile Ile  
50                    55                    60  
Met Gly Leu Asp Lys Asn Thr Lys Thr Pro Cys Gly Phe Cys Phe Val  
65                    70                    75                    80  
Leu Phe Tyr Ser Arg Glu Asp Thr Glu Asp Ala Val Lys Tyr Ile Ser  
                    85                    90                    95  
Gly Asp Tyr Ser Arg  
                    100

(2) INFORMATION FOR SEQ ID NO:957:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 56 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..56  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1568497  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:  
Met Glu Met Glu Gly Val Val Glu Glu Thr Met Val Lys Glu Asp Lys  
1                    5                    10                    15  
Ile Ala Met Glu Glu Glu Glu Thr Thr Ile Gly Asn Asp Lys Glu Thr  
                    20                    25                    30  
Met Ile Ala Met Asp Val Ile Thr Gln Glu Glu Thr Gln Ile Met Ser  
                    35                    40                    45  
Leu Gly Glu Thr Leu Ile Val Thr  
50                    55

(2) INFORMATION FOR SEQ ID NO:958:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 1230 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..1230  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1568508  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:  
acgtcaaaaa ttcaaaaacc ccaaaaccct ataattctct atataaatat tcagccctag          60  
atcttataat tcatcaatca aacaattctt tcaatcaaatt ctcttcttca atcaaattctt         120  
caaattccctt caaagatgcc ttcaatgcCa gaagagccgc tcctaaccacc aaccccagac         180  
agattTctgt atgttcccaa ttactaccc acagatctgg gaaatgtaca aaaaagccga         240

agcatcattc tggaccgccc aagaagtaga tctatcacaa gacaaccgcg actgggaaaa 300  
cagtctcaac gacggtgaac gtcacttcat caaacacgtc ctcgctttct tcgctgcac 360  
tgacggaatc gtactagaga atctcgcttc tcgcttcatg tccgatgttc aagtctcgga 420  
ggcgcgtgct ttctacgggt tccagatcgc gattgaaaac atccactcgg agatgtatag 480  
tctccttctc gatacttata tcaaagataa caaagagaga gatcatctct ttcgtgccat 540  
tgaaacaatc ccttgcgctc ccaagaaagc tcaatgggct atgaaatgga tcgacgggtc 600  
tcagactttc gccgaacgaa tcactcgctt cgcttgcgtc gaaggatatc tcttctccgg 660  
aagcttttgt tcaatcttct ggctgaagaa acggggactc atgcctggat taacattctc 720  
aaacgaattg atctctcgtg acgaagggtt aactgcgcac ttcgcttgct tactctacac 780  
gctactcaaa acaaagctta gcgaagaacg cgtgaaatca aNtcGtctgc gacgcggtcg 840  
aaatcgagag agagtttgtg tgcgacgcgc ttccgtgcgc gttgggtggg atgaaccgtg 900  
atttgatgag tcagtatatg gagtttgttg cggataggct tttgggtgcg cttgggtacg 960  
ggaagggtga cgggtgtact aatccgtttg attggatgga acttatttctg cttcaaggga 1020  
aaacgaattt cttcgagaaa cgtgttggtg attaccaaaa ggcttccgtt atgtctagcg 1080  
ttaatggtaa cggcgcgttt gataaccatg tcttctctct cgacgaagat ttttaaagag 1140  
cgtttgtttt gatgctataa ttacgattct actcttgat tattaccgtg tattatcctt 1200  
ggtttttgaa ttaatgaata attagttgcc

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1568509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

Met Phe Pro Ile His Tyr Pro Gln Ile Trp Glu Met Tyr Lys Lys Ala  
1 5 10 15  
Glu Ala Ser Phe Trp Thr Ala Glu Glu Val Asp Leu Ser Gln Asp Asn  
20 25 30  
Arg Asp Trp Glu Asn Ser Leu Asn Asp Gly Glu Arg His Phe Ile Lys  
35 40 45  
His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Leu Glu Asn  
50 55 60  
Leu Ala Ser Arg Phe Met Ser Asp Val Gln Val Ser Glu Ala Arg Ala  
65 70 75 80  
Phe Tyr Gly Phe Gln Ile Ala Ile Glu Asn Ile His Ser Glu Met Tyr  
85 90 95  
Ser Leu Leu Leu Asp Thr Tyr Ile Lys Asp Asn Lys Glu Arg Asp His  
100 105 110  
Leu Phe Arg Ala Ile Glu Thr Ile Pro Cys Val Ala Lys Lys Ala Gln  
115 120 125  
Trp Ala Met Lys Trp Ile Asp Gly Ser Gln Thr Phe Ala Glu Arg Ile  
130 135 140  
Ile Ala Phe Ala Cys Val Glu Gly Ile Phe Phe Ser Gly Ser Phe Cys  
145 150 155 160  
Ser Ile Phe Trp Leu Lys Lys Arg Gly Leu Met Pro Gly Leu Thr Phe  
165 170 175  
Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe Ala  
180 185 190  
Cys Leu Leu Tyr Thr Leu Leu Lys Thr Lys Leu Ser Glu Glu Arg Val  
195 200 205  
Lys Ser Xaa Arg Leu Arg Arg Gly Arg Asn Arg Glu Arg Val Cys Val  
210 215 220  
Arg Arg Ala Ser Val Arg Val Gly Trp Asp Glu Pro  
225 230 235

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..225
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568510
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

Met Tyr Lys Lys Ala Glu Ala Ser Phe Trp Thr Ala Glu Glu Val Asp  
1 5 10 15  
Leu Ser Gln Asp Asn Arg Asp Trp Glu Asn Ser Leu Asn Asp Gly Glu  
20 25 30  
Arg His Phe Ile Lys His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly  
35 40 45  
Ile Val Leu Glu Asn Leu Ala Ser Arg Phe Met Ser Asp Val Gln Val  
50 55 60  
Ser Glu Ala Arg Ala Phe Tyr Gly Phe Gln Ile Ala Ile Glu Asn Ile  
65 70 75 80  
His Ser Glu Met Tyr Ser Leu Leu Leu Asp Thr Tyr Ile Lys Asp Asn  
85 90 95  
Lys Glu Arg Asp His Leu Phe Arg Ala Ile Glu Thr Ile Pro Cys Val  
100 105 110  
Ala Lys Lys Ala Gln Trp Ala Met Lys Trp Ile Asp Gly Ser Gln Thr  
115 120 125  
Phe Ala Glu Arg Ile Ile Ala Phe Ala Cys Val Glu Gly Ile Phe Phe  
130 135 140  
Ser Gly Ser Phe Cys Ser Ile Phe Trp Leu Lys Lys Arg Gly Leu Met  
145 150 155 160  
Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu  
165 170 175  
His Cys Asp Phe Ala Cys Leu Leu Tyr Thr Leu Leu Lys Thr Lys Leu  
180 185 190  
Ser Glu Glu Arg Val Lys Ser Xaa Arg Leu Arg Arg Gly Arg Asn Arg  
195 200 205  
Glu Arg Val Cys Val Arg Arg Ala Ser Val Arg Val Gly Trp Asp Glu  
210 215 220  
Pro  
225

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 167 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..167
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568511
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met Ser Asp Val Gln Val Ser Glu Ala Arg Ala Phe Tyr Gly Phe Gln  
1 5 10 15  
Ile Ala Ile Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Asp  
20 25 30  
Thr Tyr Ile Lys Asp Asn Lys Glu Arg Asp His Leu Phe Arg Ala Ile  
35 40 45  
Glu Thr Ile Pro Cys Val Ala Lys Lys Ala Gln Trp Ala Met Lys Trp  
50 55 60  
Ile Asp Gly Ser Gln Thr Phe Ala Glu Arg Ile Ile Ala Phe Ala Cys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Glu | Gly | Ile | Phe | Phe | Ser | Gly | Ser | Phe | Cys | Ser | Ile | Phe | Trp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Lys | Arg | Gly | Leu | Met | Pro | Gly | Leu | Thr | Phe | Ser | Asn | Glu | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Asp | Glu | Gly | Leu | His | Cys | Asp | Phe | Ala | Cys | Leu | Leu | Tyr | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Lys | Thr | Lys | Leu | Ser | Glu | Glu | Arg | Val | Lys | Ser | Xaa | Arg | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Gly | Arg | Asn | Arg | Glu | Arg | Val | Cys | Val | Arg | Arg | Ala | Ser | Val |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Arg | Val | Gly | Trp | Asp | Glu | Pro |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1388
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| cgaagattct  | ctggtagatc | tatctcgatt  | cgattcgatt | cctctttttt | cccagaaaag | 60   |
| tcgctattgg  | aatcgaacga | aagtgttgaa  | gattttacca | gtcagaggta | tatatatata | 120  |
| gagagagagt  | tatggatttg | gatcaatgga  | tttccaaggt | taaagatggt | cagcatctct | 180  |
| ccgaagacga  | gcttcagctt | ctctgcgaat  | acgtgaaaga | gattctgatt | gaggagtcaa | 240  |
| acgtacagcc  | tgtaaacagt | ccagtcaccg  | tatgtggtga | tatccatggc | cagtttcatg | 300  |
| atcttatgaa  | gctttttcag | accggagggtC | atgttccoga | caccaattac | atttttatgg | 360  |
| gggacctcgt  | ggatagaggt | tacaacagcc  | ttgaagtctt | cactattctt | ttacttctta | 420  |
| aagctagata  | tccagccaat | attacacttt  | tgcgcggaaa | tcatgaaagt | aggcagctaa | 480  |
| cgcagggtgta | tggtttctat | gacgaatgcc  | agaggaagta | tggtaacgct | aatgcgtggc | 540  |
| gatattgcac  | agatgttttt | gactatctta  | cctgtgcagc | tattatagat | ggcacagttc | 600  |
| tatgtgttca  | cggtggcctt | tccccgatg   | tccggacaat | tgatcagata | agactgatcg | 660  |
| agcgaatcg   | cgaaattcct | catgaagggc  | ccttttgoga | tcttatgtgg | agtgatcctg | 720  |
| aagatattga  | aacatgggcg | gttagtccac  | gtggagctgg | ttggcttttc | ggatccaggg | 780  |
| ttaccactga  | gtttaaccat | atcaacaagc  | tggatctagt | atgcoctcog | caccaacttg | 840  |
| tacaagaagg  | tcttaagtac | atgttccaag  | ataaaggcct | tgtaactgta | tggtctgcac | 900  |
| ctaataactg  | ttaccgctgt | gggaatgtcg  | cttctatatt | gagtttcaat | gacaacatgg | 960  |
| aaagggaagt  | gaagttcttc | acagagacag  | aagagaacaa | tcaaatgaga | gggccaagga | 1020 |
| ctggagttcc  | gtatttccta | tgaagaatca  | cacttattat | atttgctgtg | atgatgaagc | 1080 |
| cattgctgcc  | attggcaata | tggtcagttc  | aatgtggaaa | aggttaatat | atgattatat | 1140 |
| atattatcta  | ctgatgggtt | tcgcttacta  | tcattatttt | tgctcctttg | gttacatttc | 1200 |
| ccttgtgaaa  | gttacaagtc | aaacactttg  | gtaatagtct | tagtcatttt | gattctctgc | 1260 |
| tctcttttct  | ttcccccaat | ctttcttctg  | taatgttatt | tttttcattg | ttcacttgta | 1320 |
| ctgtttcttc  | tgtttttggt | gttggtgttg  | tgaagatgac | attaattcta | aaataatcaa | 1380 |
| acatcggt    |            |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

```

Met Asp Leu Asp Gln Trp Ile Ser Lys Val Lys Asp Gly Gln His Leu
1 5 10 15
Ser Glu Asp Glu Leu Gln Leu Leu Cys Glu Tyr Val Lys Glu Ile Leu
20 25 30
Ile Glu Glu Ser Asn Val Gln Pro Val Asn Ser Pro Val Thr Val Cys
35 40 45
Gly Asp Ile His Gly Gln Phe His Asp Leu Met Lys Leu Phe Gln Thr
50 55 60
Gly Gly His Val Pro Asp Thr Asn Tyr Ile Phe Met Gly Asp Phe Val
65 70 75 80
Asp Arg Gly Tyr Asn Ser Leu Glu Val Phe Thr Ile Leu Leu Leu Leu
85 90 95
Lys Ala Arg Tyr Pro Ala Asn Ile Thr Leu Leu Arg Gly Asn His Glu
100 105 110
Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Gln Arg
115 120 125
Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr Cys Thr Asp Val Phe Asp
130 135 140
Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly Thr Val Leu Cys Val His
145 150 155 160
Gly Gly Leu Ser Pro Asp Val Arg Thr Ile Asp Gln Ile Arg Leu Ile
165 170 175
Glu Arg Asn Arg Glu Ile Pro His Glu Gly Pro Phe Cys Asp Leu Met
180 185 190
Trp Ser Asp Pro Glu Asp Ile Glu Thr Trp Ala Val Ser Pro Arg Gly
195 200 205
Ala Gly Trp Leu Phe Gly Ser Arg Val Thr Thr Glu Phe Asn His Ile
210 215 220
Asn Lys Leu Asp Leu Val Cys Arg Ser His Gln Leu Val Gln Glu Gly
225 230 235 240
Leu Lys Tyr Met Phe Gln Asp Lys Gly Leu Val Thr Val Trp Ser Ala
245 250 255
Pro Asn Asn Cys Tyr Arg Cys Gly Asn Val Ala Ser Ile Leu Ser Phe
260 265 270
Asn Asp Asn Met Glu Arg Glu Val Lys Phe Phe Thr Glu Thr Glu Glu
275 280 285
Asn Asn Gln Met Arg Gly Pro Arg Thr Gly Val Pro Tyr Phe Leu
290 295 300

```

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1568514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

```

Met Lys Leu Phe Gln Thr Gly Gly His Val Pro Asp Thr Asn Tyr Ile
1 5 10 15
Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Asn Ser Leu Glu Val Phe
20 25 30
Thr Ile Leu Leu Leu Lys Ala Arg Tyr Pro Ala Asn Ile Thr Leu
35 40 45
Leu Arg Gly Asn His Glu Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe
50 55 60
Tyr Asp Glu Cys Gln Arg Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr
65 70 75 80
Cys Thr Asp Val Phe Asp Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Phe | Val | Asp | Arg | Gly | Tyr | Asn | Ser | Leu | Glu | Val | Phe | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Leu | Leu | Leu | Lys | Ala | Arg | Tyr | Pro | Ala | Asn | Ile | Thr | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Gly | Asn | His | Glu | Ser | Arg | Gln | Leu | Thr | Gln | Val | Tyr | Gly | Phe | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Cys | Gln | Arg | Lys | Tyr | Gly | Asn | Ala | Asn | Ala | Trp | Arg | Tyr | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Asp | Val | Phe | Asp | Tyr | Leu | Thr | Leu | Ser | Ala | Ile | Ile | Asp | Gly | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Leu | Cys | Val | His | Gly | Gly | Leu | Ser | Pro | Asp | Val | Arg | Thr | Ile | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ile | Arg | Leu | Ile | Glu | Arg | Asn | Arg | Glu | Ile | Pro | His | Glu | Gly | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Cys | Asp | Leu | Met | Trp | Ser | Asp | Pro | Glu | Asp | Ile | Glu | Thr | Trp | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ser | Pro | Arg | Gly | Ala | Gly | Trp | Leu | Phe | Gly | Ser | Arg | Val | Thr | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Phe | Asn | His | Ile | Asn | Lys | Leu | Asp | Leu | Val | Cys | Arg | Ser | His | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Val | Gln | Glu | Gly | Leu | Lys | Tyr | Met | Phe | Gln | Asp | Lys | Gly | Leu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Val | Trp | Ser | Ala | Pro | Asn | Asn | Cys | Tyr | Arg | Cys | Gly | Asn | Val | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ile | Leu | Ser | Phe | Asn | Asp | Asn | Met | Glu | Arg | Glu | Val | Lys | Phe | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Glu | Thr | Glu | Glu | Asn | Asn | Gln | Met | Arg | Gly | Pro | Arg | Thr | Gly | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |



Pro Tyr Phe Leu  
225

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| gaccaagaaa | tgtatacttt | ataagagaaa  | tgtactttgat | attcaaaaaa | acaaaaaata | 60  |
| aactaggttg | gttaagatta | ttcaaacttc  | aaaggcaaaa  | ccaaatgagc | ttcgtgtggt | 120 |
| ccgctgcggt | ttgggtcata | gctgtagcgg  | ANttgtttgtg | attagcaa   | ggttataccg | 180 |
| atggtcgaac | ccgaagtgc  | atggtaagtt  | accacgggga  | tcaatgggtt | taccgatcat | 240 |
| cggagagaca | tgcgacttct | ttgagcccca  | tggattatac  | gagatcccac | cctttgtcaa | 300 |
| gaagaggatg | ttaaagtacg | ggccattggt  | tccgacaaaac | attttcggat | ccaacaccgt | 360 |
| ggttttgaca | gaagctgata | tcattctttga | ggttttccgg  | caagagaaca | agtcttttgt | 420 |
| gactagctat | ccagaggcca | ttctcaagcc  | atttggaaaa  | gaaacgtggt | cctcaa     | 480 |
| ggaacatcc  | acaagcacgt | caaacaaatc  | agtcttcaac  | ttcttggctc | tgaggcttta | 540 |
| aaaaaacga  | tgataggaga | aatagacaga  | gtaacctatg  | agcatcttag | atcgaaagct | 600 |
| aacgagggta | gcttcgatgc | taaggaggca  | gttaaaagtg  | tacttacata | gtttctta   | 660 |

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Asn | Val | Tyr | Phe | Ile | Arg | Glu | Met | Tyr | Leu | Ile | Phe | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Lys | Asn | Lys | Leu | Gly | Trp | Leu | Arg | Leu | Phe | Lys | Leu | Gln | Arg | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Gln | Met | Ser | Phe | Val | Trp | Ser | Ala | Ala | Val | Trp | Val | Ile | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Xaa | Leu | Leu |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Pro | Ile | Ile | Gly | Glu | Thr | Cys | Asp | Phe | Phe | Glu | Pro | His |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Leu | Tyr | Glu | Ile | Pro | Pro | Phe | Val | Lys | Lys | Arg | Met | Leu | Lys | Tyr |

20 25 30  
Gly Pro Leu Phe Arg Thr Asn Ile Phe Gly Ser Asn Thr Val Val Leu  
35 40 45  
Thr Glu Ala Asp Ile Ile Phe Glu Val Phe Arg Gln Glu Asn Lys Ser  
50 55 60  
Phe Val Thr Ser Tyr Pro Glu Ala Ile Leu Lys Pro Phe Gly Lys Glu  
65 70 75 80  
Thr Cys Ser Ser Asn Met Glu Thr Ser Thr Ser Thr Ser Asn Lys Ser  
85 90 95  
Val Phe Asn Phe Leu Ala Leu Arg Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

Met Leu Lys Tyr Gly Pro Leu Phe Arg Thr Asn Ile Phe Gly Ser Asn  
1 5 10 15  
Thr Val Val Leu Thr Glu Ala Asp Ile Ile Phe Glu Val Phe Arg Gln  
20 25 30  
Glu Asn Lys Ser Phe Val Thr Ser Tyr Pro Glu Ala Ile Leu Lys Pro  
35 40 45  
Phe Gly Lys Glu Thr Cys Ser Ser Asn Met Glu Thr Ser Thr Ser Thr  
50 55 60  
Ser Asn Lys Ser Val Phe Asn Phe Leu Ala Leu Arg Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

aataagtcca tatttggttag ctccaactcc aaagtgaag agagaaagag atagagaatc 60  
gccatggcaa cgaagTcagt actttctatc ttogccatct ttaccatcgt cgttctggtt 120  
atctttgaaa tacctgagat agaagcacat gatagcgagt gtctgaaaga atatgggggt 180  
gatgttgggt ttggcttctg tgcgcctaag atatttccga cgatttggtta tagaaattgc 240  
caaaaggaca aggggggctaa tgggtgaaaa tgcccttggg gagagggtgg taatgtgaaa 300  
tgcttatgag acttctgcag caaggaatct tttaatcagt ttataagtct tacttgaatc 360  
ttgcatgtgt cgtggttttaa tttgtgtact aattaagcaa ggctaatagat ccaagaaata 420  
atgtaacaat gaataagtaa aataaagaaa cgctaggctt tgcttgtg

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

Met Ala Thr Lys Ser Val Leu Ser Ile Phe Ala Ile Phe Thr Ile Val  
1 5 10 15  
Val Leu Val Ile Phe Glu Ile Pro Glu Ile Glu Ala His Asp Ser Glu  
20 25 30  
Cys Leu Lys Glu Tyr Gly Gly Asp Val Gly Phe Gly Phe Cys Ala Pro  
35 40 45  
Lys Ile Phe Pro Thr Ile Cys Tyr Arg Asn Cys Gln Lys Asp Lys Gly  
50 55 60  
Ala Asn Gly Gly Lys Cys Leu Trp Gly Glu Gly Asn Val Lys Cys  
65 70 75 80  
Leu Cys Asp Phe Cys Ser Lys Glu Ser Phe Asn Gln Phe Ile Ser Leu  
85 90 95  
Thr

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..676  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

agatacaaag ctttctttat aaacgctgcg tcacatcact gaatcaaaaa ccctagcgat 60  
acttcatctc tcgagccgga gccgcgttgc gaaagcattt caatcgtagt ctaagagaat 120  
gtcgacagtg ggagagctcg cttgMagvta cgctgttatg atcctcgagg atgagggtat 180  
tgctatcacg gctgacaaaa tcgccacttt ggtgaaagct gctggtgtta ccattgagtc 240  
atactggcca atgctattcg ccaagatggc tgagaaacgt aatgtcactg atctcatcat 300  
gaacgttggt gctggtggtg gaggtggtgc gcctgttgca gctgctgctc ctgctgctgg 360  
cggtggtgct gccgctgctg ctctgctgctc cgaggagaag aagaaggacg aaccagcaga 420  
agagagtgat ggagatttgg gttttggcct gttcgattaa gtgcatttta cttgttkttt 480  
cttcttcgat ttgagactat ttttttttcg tatcgagcta ttacttgttt tggctctggc 540  
gaagaactat aattagttgt tttctgaacc atatgttgta tgacacaagt tttcaagcaa 600  
acccatcggc tccttctttc cttagaaatg attttgtcac ctcttttttt ttttaattcat 660  
tcgagatatt agtctg

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

Met Ser Thr Val Gly Glu Leu Ala Xaa Tyr Ala Val Met Ile Leu  
1 5 10 15  
Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala Thr Leu Val  
20 25 30  
Lys Ala Ala Gly Val Thr Ile Glu Ser Tyr Trp Pro Met Leu Phe Ala  
35 40 45  
Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly

50 55 60  
Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala  
65 70 75 80  
Gly Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu Lys Lys Lys  
85 90 95  
Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly Leu Phe  
100 105 110  
Asp

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1568585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

Met Ile Leu Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala  
1 5 10 15  
Thr Leu Val Lys Ala Ala Gly Val Thr Ile Glu Ser Tyr Trp Pro Met  
20 25 30  
Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met  
35 40 45  
Asn Val Gly Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Ala  
50 55 60  
Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Ala Pro Ala Ala Glu Glu  
65 70 75 80  
Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe  
85 90 95  
Gly Leu Phe Asp  
100

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1568586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

Met Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile  
1 5 10 15  
Met Asn Val Gly Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala  
20 25 30  
Ala Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Ala Pro Ala Ala Glu  
35 40 45  
Glu Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly  
50 55 60  
Phe Gly Leu Phe Asp  
65

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..930  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568595  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| gcgaccacta | gaaggagaaa  | caaattcttca | ttccagcaat | ggcgattcgt | tgtgtagcga | 60  |
| gtagaaaaac | cctagccggc  | ttgaaggaga  | catcatcgag | gctattgagg | atcagaggga | 120 |
| ttcagacttt | tacgtttcct  | gatcttcctt  | acgattatgg | cgcattggaa | ccggccatta | 180 |
| gtggagagat | catgcagatt  | catcaccaga  | agcatcacca | ggcttatgtt | actaattaca | 240 |
| ataatgctct | tgagcagctt  | gatcaagctg  | tgaacaagg  | agatgcttcc | actgttgta  | 300 |
| agttgcagag | cgccatcaaa  | ttcaacggcg  | gaggtcatgt | caaccattcg | attttctgga | 360 |
| agaaccttgc | tcctttccagt | gaaggtggtg  | gagagccacc | aaaaggatct | cttggtagt  | 420 |
| ccattgacgc | tcactttggc  | tcccttgaag  | gtctggtgaa | aaagatgagt | gctgagggtg | 480 |
| ctgcagtgc  | aggctcagga  | tgggtgtggc  | tgggactaga | caaagaactg | aagaagctag | 540 |
| ttgttgacac | aactgccaat  | caggatccat  | tagtgacaaa | aggaggaagc | ttggtacctc | 600 |
| tgtgtggtat | agatgttttg  | gagcagcct   | actacttgca | gtacaaaaat | gtgaggcctg | 660 |
| agtatctgaa | gaatgtatgg  | aaagtgtatca | actggaaata | tgcaagcgag | gtttatgaga | 720 |
| aggaaagcaa | ctgaatcggt  | tacacgatga  | cataaggaga | tgaaccagtt | ccagctcagc | 780 |
| ttttgtttta | aggttgctctg | aaacaaactt  | acagtgtctc | tttggttttt | aagatttgct | 840 |
| caactcagct | gtgtggtacg  | ttgtttttaca | atgaaagttt | Kcaagaataa | aaatttgcta | 900 |
| ttattgtcag | aaagcgctat  | tgttttattct |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:977:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 231 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..231  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568596  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Arg | Cys | Val | Ala | Ser | Arg | Lys | Thr | Leu | Ala | Gly | Leu | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Thr | Ser | Ser | Arg | Leu | Leu | Arg | Ile | Arg | Gly | Ile | Gln | Thr | Phe | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Pro | Asp | Leu | Pro | Tyr | Asp | Tyr | Gly | Ala | Leu | Glu | Pro | Ala | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Glu | Ile | Met | Gln | Ile | His | His | Gln | Lys | His | His | Gln | Ala | Tyr | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Asn | Tyr | Asn | Asn | Ala | Leu | Glu | Gln | Leu | Asp | Gln | Ala | Val | Asn | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Asp | Ala | Ser | Thr | Val | Val | Lys | Leu | Gln | Ser | Ala | Ile | Lys | Phe | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Gly | Gly | His | Val | Asn | His | Ser | Ile | Phe | Trp | Lys | Asn | Leu | Ala | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Ser | Ser | Glu | Gly | Gly | Gly | Glu | Pro | Pro | Lys | Gly | Ser | Leu | Gly | Ser | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ile | Asp | Ala | His | Phe | Gly | Ser | Leu | Glu | Gly | Leu | Val | Lys | Lys | Met | Ser |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ala | Glu | Gly | Ala | Ala | Val | Gln | Gly | Ser | Gly | Trp | Val | Trp | Leu | Gly | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asp | Lys | Glu | Leu | Lys | Lys | Leu | Val | Val | Asp | Thr | Thr | Ala | Asn | Gln | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Pro | Leu | Val | Thr | Lys | Gly | Gly | Ser | Leu | Val | Pro | Leu | Val | Gly | Ile | Asp |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Val | Trp | Glu | His | Ala | Tyr | Tyr | Leu | Gln | Tyr | Lys | Asn | Val | Arg | Pro | Glu |

195 200 205  
Tyr Leu Lys Asn Val Trp Lys Val Ile Asn Trp Lys Tyr Ala Ser Glu  
210 215 220  
Val Tyr Glu Lys Glu Ser Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

Met Gln Ile His His Gln Lys His His Gln Ala Tyr Val Thr Asn Tyr  
1 5 10 15  
Asn Asn Ala Leu Glu Gln Leu Asp Gln Ala Val Asn Lys Gly Asp Ala  
20 25 30  
Ser Thr Val Val Lys Leu Gln Ser Ala Ile Lys Phe Asn Gly Gly Gly  
35 40 45  
His Val Asn His Ser Ile Phe Trp Lys Asn Leu Ala Pro Ser Ser Glu  
50 55 60  
Gly Gly Gly Glu Pro Pro Lys Gly Ser Leu Gly Ser Ala Ile Asp Ala  
65 70 75 80  
His Phe Gly Ser Leu Glu Gly Leu Val Lys Lys Met Ser Ala Glu Gly  
85 90 95  
Ala Ala Val Gln Gly Ser Gly Trp Val Trp Leu Gly Leu Asp Lys Glu  
100 105 110  
Leu Lys Lys Leu Val Val Asp Thr Thr Ala Asn Gln Asp Pro Leu Val  
115 120 125  
Thr Lys Gly Gly Ser Leu Val Pro Leu Val Gly Ile Asp Val Trp Glu  
130 135 140  
His Ala Tyr Tyr Leu Gln Tyr Lys Asn Val Arg Pro Glu Tyr Leu Lys  
145 150 155 160  
Asn Val Trp Lys Val Ile Asn Trp Lys Tyr Ala Ser Glu Val Tyr Glu  
165 170 175  
Lys Glu Ser Asn  
180

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

cgaaaagcat tgatttggtc ctccttcctc ttctattcta ttcattaaga acctaattctt 60  
catcttctcc atcttcttct tcacggactc cacttcgctc atccaggaag gtttattagt 120  
agtaaccaat ccaagtgttc cttttgttg aagcaacaag ctttgtgata ttatcctgag 180  
agacaatggt tggtttaagg aaatcacggg caaatcttcc caagcataac tcagtcgacc 240  
tcaagtcttc caagccaaat cctttcgatt cagatgatga atctgacaac aaacataccc 300  
ttaaccYYtt ctaagaggac tacctctgaa ccctctttgg ctgatatgac aaaccctttt 360  
ggtggtgaga gaggatagat agttcatcca aacagtcatt gttttcgaac 420  
tccaaatacc agtacaagaa caatttcogt gattctggtg gtattgaaaa ccagtcggtt 480

(2) INFORMATION FOR SEQ ID NO:980:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 270 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..270  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568600  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Leu | Thr | Thr | Asn | Ile | Pro | Leu | Thr | Xaa | Ser | Lys | Arg | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Pro | Ser | Leu | Ala | Asp | Met | Thr | Asn | Pro | Phe | Gly | Gly | Glu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gln | Lys | Gly | Asp | Ser | Ser | Ser | Ser | Lys | Gln | Ser | Leu | Phe | Ser | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Tyr | Gln | Tyr | Lys | Asn | Asn | Phe | Arg | Asp | Ser | Gly | Gly | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Gln | Ser | Val | Gln | Glu | Leu | Glu | Gly | Tyr | Ala | Val | Tyr | Lys | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Glu | Thr | Thr | Lys | Ser | Val | Gln | Gly | Cys | Leu | Lys | Val | Ala | Glu | Asp | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Ser | Asp | Ala | Thr | Arg | Thr | Leu | Val | Met | Leu | His | Asp | Gln | Gly | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Ile | Thr | Arg | Thr | His | His | Lys | Ala | Val | Glu | Ile | Asp | His | Asp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Arg | Gly | Glu | Lys | Leu | Leu | Gly | Ser | Leu | Gly | Gly | Met | Phe | Ser | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Trp | Lys | Pro | Lys | Lys | Thr | Arg | Pro | Ile | Asn | Gly | Pro | Val | Val | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Asp | Asp | Ser | Pro | Thr | Arg | Arg | Val | Asn | His | Leu | Glu | Lys | Arg | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Leu | Gly | Leu | Asn | Ser | Ala | Pro | Arg | Gly | Gln | Ser | Arg | Thr | Arg | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Leu | Pro | Glu | Ser | Ala | Asp | Ala | Tyr | Gln | Arg | Val | Glu | Met | Glu | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Lys | Gln | Asp | Asp | Gly | Leu | Ser | Asp | Leu | Ser | Asp | Ile | Leu | Gly | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Lys | Asn | Met | Ala | Val | Asp | Met | Gly | Ser | Glu | Ile | Glu | Lys | Gln | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Gly | Leu | Asp | His | Leu | His | Asp | Asp | Val | Asp | Glu | Leu | Asn | Phe | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Gln | Gln | Ser | Asn | Gln | Arg | Gly | Arg | Arg | Leu | Leu | Gly | Lys |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 247 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..247  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568601  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Asn | Pro | Phe | Gly | Gly | Glu | Arg | Val | Gln | Lys | Gly | Asp | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Lys | Gln | Ser | Leu | Phe | Ser | Asn | Ser | Lys | Tyr | Gln | Tyr | Lys | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |



Asn Phe Arg Asp Ser Gly Gly Ile Glu Asn Gln Ser Val Gln Glu Leu  
35 40 45  
Glu Gly Tyr Ala Val Tyr Lys Ala Glu Glu Thr Thr Lys Ser Val Gln  
50 55 60  
Gly Cys Leu Lys Val Ala Glu Asp Ile Arg Ser Asp Ala Thr Arg Thr  
65 70 75 80  
Leu Val Met Leu His Asp Gln Gly Glu Gln Ile Thr Arg Thr His His  
85 90 95  
Lys Ala Val Glu Ile Asp His Asp Leu Ser Arg Gly Glu Lys Leu Leu  
100 105 110  
Gly Ser Leu Gly Gly Met Phe Ser Lys Thr Trp Lys Pro Lys Lys Thr  
115 120 125  
Arg Pro Ile Asn Gly Pro Val Thr Arg Asp Asp Ser Pro Thr Arg  
130 135 140  
Arg Val Asn His Leu Glu Lys Arg Glu Lys Leu Gly Leu Asn Ser Ala  
145 150 155 160  
Pro Arg Gly Gln Ser Arg Thr Arg Glu Pro Leu Pro Glu Ser Ala Asp  
165 170 175  
Ala Tyr Gln Arg Val Glu Met Glu Lys Ala Lys Gln Asp Asp Gly Leu  
180 185 190  
Ser Asp Leu Ser Asp Ile Leu Gly Glu Leu Lys Asn Met Ala Val Asp  
195 200 205  
Met Gly Ser Glu Ile Glu Lys Gln Asn Lys Gly Leu Asp His Leu His  
210 215 220  
Asp Asp Val Asp Glu Leu Asn Phe Arg Val Gln Gln Ser Asn Gln Arg  
225 230 235 240  
Gly Arg Arg Leu Leu Gly Lys  
245

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatttttttag ggtttcaagt gaaaagagta atagcgcggc ggaGCcatgg ttctcaagac | 60  |
| tgagcttttg cgattcagtg gccagaaaat ttaccttgt agagggatca gatttatccg   | 120 |
| atcggaactct caggtgtttt tgtttctcaa ctccaaatgt aagaggtatt tccacaacaa | 180 |
| gttgaagcca tctaagcttt gctggactgc tatgtaccga aagcagcaca agaaggacgc  | 240 |
| agcacaagag gctgtgaaga gaaggagacg tgcaactaag aagccttact caaggtcgat  | 300 |
| tgtcggtgct actttggagg ttattcagaa gaagcgagca gagaagcctg aagttcgtga  | 360 |
| tgccgctaga gaagctgccc tacgtgagat caaggagaga atcaagaaga ccaaggacga  | 420 |
| gaagaaggca aagaaggtcg agtatgcac aaagcaacag aagtcacaag tgaaggga     | 480 |
| tatccccaag agtgctgcac ccaaggctgc taagatgggt ggtggtggag gcagacgttg  | 540 |
| aatggagcta tagagtagcc cactcttctc tcttcaacta tctttctttc ttgktttgac  | 600 |
| attgktttgt tttgtcagcc attttttagt tttgcaccag atctaataata ttcagtttat | 660 |
| gaaaactttt tgtttggc                                                |     |

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1568603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr  
1 5 10 15  
Pro Gly Arg Gly Ile Arg Phe Ile Arg Ser Asp Ser Gln Val Phe Leu  
20 25 30  
Phe Leu Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Lys Leu Lys Pro  
35 40 45  
Ser Lys Leu Cys Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp  
50 55 60  
Ala Ala Gln Glu Ala Val Lys Arg Arg Arg Arg Ala Thr Lys Lys Pro  
65 70 75 80  
Tyr Ser Arg Ser Ile Val Gly Ala Thr Leu Glu Val Ile Gln Lys Lys  
85 90 95  
Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu  
100 105 110  
Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala  
115 120 125  
Lys Lys Val Glu Tyr Ala Ser Lys Lys Gln Gln Lys Ser Gln Val Lys Gly  
130 135 140  
Asn Ile Pro Lys Ser Ala Ala Pro Lys Ala Ala Lys Met Gly Gly Gly  
145 150 155 160  
Gly Gly Arg Arg

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1568604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys  
1 5 10 15  
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly  
20 25 30  
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val  
35 40 45  
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile  
50 55 60  
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Tyr Ala Ser  
65 70 75 80  
Lys Gln Gln Lys Ser Gln Val Lys Gly Asn Ile Pro Lys Ser Ala Ala  
85 90 95  
Pro Lys Ala Ala Lys Met Gly Gly Gly Gly Gly Arg Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1568605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaacttaatc acacacaagg agagaagaga gaaagagaga aagagagaca gagataatgg  | 60  |
| cgtacagtg cgtgtttccta caccagagcg cattggcttc atcagccgca cgtatcatcat | 120 |
| cttctctctc atcccagcgt cacgtgtcgc tctccaaacc tggttcagatc atctgtaaag | 180 |
| cacaagctgg agacaagagg tggttcaagg gagccaggaa atttgtcgag agcgcagcCa  | 240 |
| cttctttcag tgttgcttga gtgaaagcaa cacaacgtaa caatgctctg cttgctttct  | 300 |
| tcatttgtct cttgtaaaaa atggaaaatg aaactgagct ttg                    |     |

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1568606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asn Leu Ile Thr His Lys Glu Arg Arg Glu Lys Glu Arg Lys Arg Asp |  |
| 1 5 10 15                                                       |  |
| Arg Asp Asn Gly Val Gln Cys Val Phe Pro Thr Pro Glu Arg Ile Gly |  |
| 20 25 30                                                        |  |
| Phe Ile Ser Arg Thr Ile Ile Ile Phe Leu Leu Ile Pro Ala Ser Arg |  |
| 35 40 45                                                        |  |
| Val Ala Leu Gln Thr Cys Ser Asp His Leu                         |  |
| 50 55                                                           |  |

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1568607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Tyr Ser Ala Cys Phe Leu His Gln Ser Ala Leu Ala Ser Ser |  |
| 1 5 10 15                                                       |  |
| Ala Ala Arg Ser Ser Ser Ser Ser Ser Gln Arg His Val Ser Leu     |  |
| 20 25 30                                                        |  |
| Ser Lys Pro Val Gln Ile Ile Cys Lys Ala Gln Ala Gly Asp Lys Arg |  |
| 35 40 45                                                        |  |
| Trp Phe Lys Gly Ala Arg Lys Phe Val Glu Ser Ala Ala Thr Ser Phe |  |
| 50 55 60                                                        |  |
| Ser Val Ala                                                     |  |
| 65                                                              |  |

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1001 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1001

(D) OTHER INFORMATION: / Ceres Seq. ID 1568614

00000000-00000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| ctcacacaca  | caccaacgca  | aacctccaaa  | acagggccgg  | ggcgattcat | tcacaatctc | 60  |
| ggcgattctc  | tcttcggtct  | cgagtcgctg  | agatccatca  | gtaaaaggtc | tgcaaaatgg | 120 |
| ttgctcaggg  | attcactgtg  | gatcttaaaa  | agccccttgt  | atttcagggt | ggtcatcttg | 180 |
| gagaagatta  | tgaggaatgg  | gttcaccaac  | ctatcgcgac  | caaggaaggc | cctcggtttt | 240 |
| ttcagagtga  | cttttgggag  | ttottgacac  | ttacagtttg  | gtgggcagtt | cctgtcattt | 300 |
| ggttgccagt  | tgtagtctgg  | tgcataatcaa | ggtcagtaag  | tatgggatgt | tcacttccag | 360 |
| aaatcgtccc  | aattgtttgc  | atgggaatat  | tcactctggac | atTTTTtgaa | tacgttcttc | 420 |
| accggttcgt  | tttccacata  | aaaacgaaga  | gttactgggg  | aaacactgca | cactatctta | 480 |
| ttcacgggatg | ccatcataag  | cacccgatgg  | accaccttcg  | gctcgtcttt | cctcctactg | 540 |
| caacagcgat  | tttatgcttt  | ccgttcttga  | acattgcggc  | tatctcaact | ccttcaaccg | 600 |
| cacctgcatt  | gtttgggtga  | ggcatgctcg  | gatatgtgat  | gtacgatgtc | actcattatt | 660 |
| accttcacca  | tgcccaacct  | actagaccag  | tgacaaaaaa  | tctcaagaag | taccatttga | 720 |
| atcatcactt  | caggattcag  | gacaaaggat  | ttggtatAac  | ttcgtcgtta | tgggacatag | 780 |
| tctttggggac | acttcccaacc | acaaaagccc  | ccagaaaaga  | gcaatagtag | taaaaggcaa | 840 |
| aaactaaaaa  | gatgtttgta  | atacatTTaa  | tttaattctta | agttattaat | catccttctg | 900 |
| aattttgaga  | tgtttaatct  | gaggtttcat  | ttggatcact  | gtcttttgta | gtttgtaaat | 960 |
| caatacttca  | caatccta    | ataatatttt  | tctgcgaaag  | t          |            |     |

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1568615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Gln | Gly | Phe | Thr | Val | Asp | Leu | Lys | Lys | Pro | Leu | Val | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Val | Gly | His | Leu | Gly | Glu | Asp | Tyr | Glu | Glu | Trp | Val | His | Gln | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Thr | Lys | Glu | Gly | Pro | Arg | Phe | Phe | Gln | Ser | Asp | Phe | Trp | Glu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Phe | Leu | Thr | Leu | Thr | Val | Trp | Trp | Ala | Val | Pro | Val | Ile | Trp | Leu | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Val | Val | Trp | Cys | Ile | Ser | Arg | Ser | Val | Ser | Met | Gly | Cys | Ser | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Glu | Ile | Val | Pro | Ile | Val | Val | Met | Gly | Ile | Phe | Ile | Trp | Thr | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Glu | Tyr | Val | Leu | His | Arg | Phe | Val | Phe | His | Ile | Lys | Thr | Lys | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Trp | Gly | Asn | Thr | Ala | His | Tyr | Leu | Ile | His | Gly | Cys | His | His | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Pro | Met | Asp | His | Leu | Arg | Leu | Val | Phe | Pro | Pro | Thr | Ala | Thr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Leu | Cys | Phe | Pro | Phe | Trp | Asn | Ile | Ala | Ala | Ile | Ser | Thr | Pro | Ser |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Ala | Pro | Ala | Leu | Phe | Gly | Gly | Gly | Met | Leu | Gly | Tyr | Val | Met | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Val | Thr | His | Tyr | Tyr | Leu | His | His | Ala | Gln | Pro | Thr | Arg | Pro | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Lys | Asn | Leu | Lys | Lys | Tyr | His | Leu | Asn | His | His | Phe | Arg | Ile | Gln |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Lys | Gly | Phe | Gly | Ile | Thr | Ser | Ser | Leu | Trp | Asp | Ile | Val | Phe | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Leu | Pro | Thr | Thr | Lys | Ala | Pro | Arg | Lys | Glu | Gln |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:991:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 161 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..161  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568616  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

Met Gly Cys Ser Leu Pro Glu Ile Val Pro Ile Val Val Met Gly Ile  
1                  5                  10                  15  
Phe Ile Trp Thr Phe Phe Glu Tyr Val Leu His Arg Phe Val Phe His  
                  20                  25                  30  
Ile Lys Thr Lys Ser Tyr Trp Gly Asn Thr Ala His Tyr Leu Ile His  
                  35                  40                  45  
Gly Cys His His Lys His Pro Met Asp His Leu Arg Leu Val Phe Pro  
50                  55                  60  
Pro Thr Ala Thr Ala Ile Leu Cys Phe Pro Phe Trp Asn Ile Ala Ala  
65                  70                  75                  80  
Ile Ser Thr Pro Ser Thr Ala Pro Ala Leu Phe Gly Gly Gly Met Leu  
                  85                  90                  95  
Gly Tyr Val Met Tyr Asp Val Thr His Tyr Tyr Leu His His Ala Gln  
                  100                  105                  110  
Pro Thr Arg Pro Val Thr Lys Asn Leu Lys Lys Tyr His Leu Asn His  
                  115                  120                  125  
His Phe Arg Ile Gln Asp Lys Gly Phe Gly Ile Thr Ser Ser Leu Trp  
130                  135                  140  
Asp Ile Val Phe Gly Thr Leu Pro Thr Thr Lys Ala Pro Arg Lys Glu  
145                  150                  155                  160  
Gln

- (2) INFORMATION FOR SEQ ID NO:992:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 148 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..148  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1568617  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

Met Gly Ile Phe Ile Trp Thr Phe Phe Glu Tyr Val Leu His Arg Phe  
1                  5                  10                  15  
Val Phe His Ile Lys Thr Lys Ser Tyr Trp Gly Asn Thr Ala His Tyr  
                  20                  25                  30  
Leu Ile His Gly Cys His His Lys His Pro Met Asp His Leu Arg Leu  
35                  40                  45  
Val Phe Pro Pro Thr Ala Thr Ala Ile Leu Cys Phe Pro Phe Trp Asn  
50                  55                  60  
Ile Ala Ala Ile Ser Thr Pro Ser Thr Ala Pro Ala Leu Phe Gly Gly  
65                  70                  75                  80  
Gly Met Leu Gly Tyr Val Met Tyr Asp Val Thr His Tyr Tyr Leu His  
                  85                  90                  95  
His Ala Gln Pro Thr Arg Pro Val Thr Lys Asn Leu Lys Lys Tyr His  
100                  105                  110  
Leu Asn His His Phe Arg Ile Gln Asp Lys Gly Phe Gly Ile Thr Ser  
115                  120                  125

Ser Leu Trp Asp Ile Val Phe Gly Thr Leu Pro Thr Thr Lys Ala Pro  
130 135 140  
Arg Lys Glu Gln  
145

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| gagtttcaat | ggcggcaatt | ttttctctct  | tccttttctt | cattctcttc | atcgtctctc  | 60   |
| ttctcatcat | cttatctttc | atcgtaacgc  | caagatccgt | cacgatcccc | atcaagtttc  | 120  |
| gccacgtctt | catcaccggt | ggatcaagcg  | gaatcggtct | cgctctcgct | caccgtgccg  | 180  |
| tctccgaagg | cgctaaagtc | tccatcctcg  | ctcgttcaac | tgaaaagctc | gccgaagcca  | 240  |
| aacgatccat | ccagctagct | accggtgtcg  | aggtcgccac | gttctctgcg | gacgttcgcg  | 300  |
| attacgacgc | cgtttcgaaa | gcgattgatg  | aatcgggacc | gacgatgtg  | ttgattgtta  | 360  |
| atcaaggcgt | gtttattggg | aaagagattg  | agaaacagag | tcctgaggag | gttaagttaa  | 420  |
| tgattgatgt | gaatctgact | gggagcttca  | atgtgattaa | ggcggcttta | cctgctatga  | 480  |
| aagctaggga | aagtcgtggt | tctgcttcca  | tttctcttgt | gtcctctcaa | gctggtcagg  | 540  |
| caggtatata | tggttacact | gcataattcag | cgagcaagtt | tgggcttcag | ggtttagcgc  | 600  |
| aagcattgca | gcaagaagtt | atttctgatg  | acattcatgt | gactctcttg | tttcctcctg  | 660  |
| acactgatac | acccgggttt | gaacaagaac  | tgaagaagag | gccagaacta | acttcaatca  | 720  |
| tagccgcata | atcgggttca | atgaaaacca  | aggaagtggc | caagatatgt | tttgatggta  | 780  |
| tcaaagcagg | aaaatttaca | gtgacatgcc  | attttattgg | cttcttacta | tcaattgcta  | 840  |
| gcaccggcat | gtccctcag  | ggatcgtttt  | Ggcttgcgct | cattgaagtt | atattcgggtg | 900  |
| gtctaataag | attcgtcagc | ttggttttcc  | aatggcaatg | gtacaaaacc | atagaaaagt  | 960  |
| ggagcaaaga | aaaacaagta | aatagtaagt  | tagcttaggt | tattttgtac | aatgggtacta | 1020 |
| atactatatg | atcagtctct | tgtacagtga  | acaggctcat | gtgtttgtag | ttccaacttc  | 1080 |
| ggcttctctg | ttttcaattt | gaataaattg  | tg         |            |             |      |

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Met | Ala | Ala | Ile | Phe | Ser | Leu | Phe | Leu | Phe | Phe | Ile | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Val | Ser | Leu | Leu | Ile | Ile | Leu | Ser | Phe | Ile | Val | Arg | Pro | Arg | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Val | Thr | Ile | Pro | Ile | Lys | Phe | Arg | His | Val | Phe | Ile | Thr | Gly | Gly | Ser |
|     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |     |     |
| Ser | Gly | Ile | Gly | Leu | Ala | Leu | Ala | His | Arg | Ala | Val | Ser | Glu | Gly | Ala |
|     | 50  |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |     |
| Lys | Val | Ser | Ile | Leu | Ala | Arg | Ser | Thr | Glu | Lys | Leu | Ala | Glu | Ala | Lys |
| 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |     |
| Arg | Ser | Ile | Gln | Leu | Ala | Thr | Gly | Val | Glu | Val | Ala | Thr | Phe | Ser | Ala |
|     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |     |
| Asp | Val | Arg | Asp | Tyr | Asp | Ala | Val | Ser | Lys | Ala | Ile | Asp | Glu | Ser | Gly |
|     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |

Pro Ile Asp Val Leu Ile Val Asn Gln Gly Val Phe Ile Gly Lys Glu  
115 120 125  
Ile Glu Lys Gln Ser Pro Glu Val Lys Phe Met Ile Asp Val Asn  
130 135 140  
Leu Thr Gly Ser Phe Asn Val Ile Lys Ala Ala Leu Pro Ala Met Lys  
145 150 155 160  
Ala Arg Glu Ser Arg Gly Ser Ala Ser Ile Ser Leu Val Ser Ser Gln  
165 170 175  
Ala Gly Gln Ala Gly Ile Tyr Gly Tyr Thr Ala Tyr Ser Ala Ser Lys  
180 185 190  
Phe Gly Leu Gln Gly Leu Ala Gln Ala Leu Gln Gln Glu Val Ile Ser  
195 200 205  
Asp Asp Ile His Val Thr Leu Phe Pro Pro Asp Thr Asp Thr Pro  
210 215 220  
Gly Phe Glu Gln Glu Leu Lys Lys Arg Pro Glu Leu Thr Ser Ile Ile  
225 230 235 240  
Ala Ala Ser Ser Gly Ser Met Lys Thr Lys Glu Val Ala Lys Ile Cys  
245 250 255  
Phe Asp Gly Ile Lys Ala Gly Lys Phe Thr Val Thr Cys His Phe Ile  
260 265 270  
Gly Phe Leu Ser Ile Ala Ser Thr Gly Met Ser Pro Gln Gly Ser  
275 280 285  
Phe Trp Leu Ala Leu Ile Glu Val Ile Phe Gly Gly Leu Ile Arg Phe  
290 295 300  
Val Ser Leu Val Phe Gln Trp Gln Trp Tyr Lys Thr Ile Glu Lys Trp  
305 310 315 320  
Ser Lys Glu Lys Gln Val Asn Ser Lys Leu Ala  
325 330

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..329
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Met Ala Ala Ile Phe Ser Leu Phe Leu Phe Phe Ile Leu Phe Ile Val  
1 5 10 15  
Ser Leu Leu Ile Ile Leu Ser Phe Ile Val Arg Pro Arg Ser Val Thr  
20 25 30  
Ile Pro Ile Lys Phe Arg His Val Phe Ile Thr Gly Gly Ser Ser Gly  
35 40 45  
Ile Gly Leu Ala Leu Ala His Arg Ala Val Ser Glu Gly Ala Lys Val  
50 55 60  
Ser Ile Leu Ala Arg Ser Thr Glu Lys Leu Ala Glu Ala Lys Arg Ser  
65 70 75 80  
Ile Gln Leu Ala Thr Gly Val Glu Val Ala Thr Phe Ser Ala Asp Val  
85 90 95  
Arg Asp Tyr Asp Ala Val Ser Lys Ala Ile Asp Glu Ser Gly Pro Ile  
100 105 110  
Asp Val Leu Ile Val Asn Gln Gly Val Phe Ile Gly Lys Glu Ile Glu  
115 120 125  
Lys Gln Ser Pro Glu Glu Val Lys Phe Met Ile Asp Val Asn Leu Thr  
130 135 140  
Gly Ser Phe Asn Val Ile Lys Ala Ala Leu Pro Ala Met Lys Ala Arg  
145 150 155 160  
Glu Ser Arg Gly Ser Ala Ser Ile Ser Leu Val Ser Ser Gln Ala Gly

SEQUENCE LISTING

165 170 175  
Gln Ala Gly Ile Tyr Gly Tyr Thr Ala Tyr Ser Ala Ser Lys Phe Gly  
180 185 190  
Leu Gln Gly Leu Ala Gln Ala Leu Gln Gln Glu Val Ile Ser Asp Asp  
195 200 205  
Ile His Val Thr Leu Leu Phe Pro Pro Asp Thr Asp Thr Pro Gly Phe  
210 215 220  
Glu Gln Glu Leu Lys Lys Arg Pro Glu Leu Thr Ser Ile Ile Ala Ala  
225 230 235 240  
Ser Ser Gly Ser Met Lys Thr Lys Glu Val Ala Lys Ile Cys Phe Asp  
245 250 255  
Gly Ile Lys Ala Gly Lys Phe Thr Val Thr Cys His Phe Ile Gly Phe  
260 265 270  
Leu Leu Ser Ile Ala Ser Thr Gly Met Ser Pro Gln Gly Ser Phe Trp  
275 280 285  
Leu Ala Leu Ile Glu Val Ile Phe Gly Gly Leu Ile Arg Phe Val Ser  
290 295 300  
Leu Val Phe Gln Trp Gln Trp Tyr Lys Thr Ile Glu Lys Trp Ser Lys  
305 310 315 320  
Glu Lys Gln Val Asn Ser Lys Leu Ala  
325

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1568638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

Met Ile Asp Val Asn Leu Thr Gly Ser Phe Asn Val Ile Lys Ala Ala  
1 5 10 15  
Leu Pro Ala Met Lys Ala Arg Glu Ser Arg Gly Ser Ala Ser Ile Ser  
20 25 30  
Leu Val Ser Ser Gln Ala Gly Gln Ala Gly Ile Tyr Gly Tyr Thr Ala  
35 40 45  
Tyr Ser Ala Ser Lys Phe Gly Leu Gln Gly Leu Ala Gln Ala Leu Gln  
50 55 60  
Gln Glu Val Ile Ser Asp Asp Ile His Val Thr Leu Leu Phe Pro Pro  
65 70 75 80  
Asp Thr Asp Thr Pro Gly Phe Glu Gln Glu Leu Lys Lys Arg Pro Glu  
85 90 95  
Leu Thr Ser Ile Ile Ala Ala Ser Ser Gly Ser Met Lys Thr Lys Glu  
100 105 110  
Val Ala Lys Ile Cys Phe Asp Gly Ile Lys Ala Gly Lys Phe Thr Val  
115 120 125  
Thr Cys His Phe Ile Gly Phe Leu Leu Ser Ile Ala Ser Thr Gly Met  
130 135 140  
Ser Pro Gln Gly Ser Phe Trp Leu Ala Leu Ile Glu Val Ile Phe Gly  
145 150 155 160  
Gly Leu Ile Arg Phe Val Ser Leu Val Phe Gln Trp Gln Trp Tyr Lys  
165 170 175  
Thr Ile Glu Lys Trp Ser Lys Glu Lys Gln Val Asn Ser Lys Leu Ala  
180 185 190

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1267
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568645
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

```
aaacaaaWWY WWaWccaaag acgagccaga gccacctcta acaccatcgg cgacttctcc 60
tctactcct ccgtcgccga cgtgttcgat ttacaacgat tcggtggcta atcggttgta 120
gatttagaat taaagggttaa aggagacgac gacgagagat gccgtcaaac ggagatctcg 180
accgtcagat cgaacagcta atggagtgtg agccggttagg tgaagcagac gtgaagatcc 240
tttgcgatca agctaaagcg attctcgttg aggaatataa tgttcaaccg gttaagtgtc 300
cggttacggg atgcggcgat atccatggac agttttatga cctaattgag ctatttcgta 360
ttggtggtaa tgctcctgat actaattacc tcttcattgg agattatgta gatcgtggct 420
actattctgt agaaacagtc tctctattgg tggcattgaa ggtgcgttac agggacagac 480
ttacgatcct gcgaggggaat catgagagcc gtcagattac acaagtctat ggtttttatg 540
acgaatgctt gaggaaatac ggaaatgcaa atgtgtggaa gtattttacg gaccttttcg 600
attatctccc tctaacagca ctcatagaga gtcagggttt ctggttgcat ggaggccttt 660
caccttctct ggatactctt gacaatatcc gaagcttgga tcgaatacaa gaggttccac 720
acgaaggacc aatgtgcgat ctactctggg ctgatcccga cgcgttgtgt ggatggggaa 780
tatctcctcg tgggtcgtgtg tacacgtttg gacaggacat tgctactcag ttcaatcata 840
acaatggact gagtctgata tcaagagcgc atcaacttgt aatggaaggc tataattggg 900
gtcaggaaaa gaacgtagtg acagtgttta gtgcaccaa ctactgttac agatgtggaa 960
acatggccgc aattcttgag attggagaaa agatggaaca gaacttcctt caattcgatc 1020
cagcacctag acaagtcgaa cccgatacca caccgaagac ccctgattat tttttgtgat 1080
ttcatttttt ttcttccaaa gtttggtttg tgctgtatca ttgtagatgt gtctctgttt 1140
tattttgttt ttctcgagtct ctagatggaa tgtgatacca aagacgaaaa acccatcatt 1200
ttttgttgta tgttgatact gaaacaggtt tgtagaagcc tcttcttatt atagaaaatg 1260
tcttttg
```

- (2) INFORMATION FOR SEQ ID NO:998:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 306 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..306
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1568646
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```
Met Pro Ser Asn Gly Asp Leu Asp Arg Gln Ile Glu Gln Leu Met Glu
1 5 10 15
Cys Lys Pro Leu Gly Glu Ala Asp Val Lys Ile Leu Cys Asp Gln Ala
 20 25 30
Lys Ala Ile Leu Val Glu Glu Tyr Asn Val Gln Pro Val Lys Cys Pro
 35 40 45
Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Ile Glu
 50 55 60
Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu Phe Met
65 70 75 80
Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser Leu
 85 90 95
Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile Leu Arg
 100 105 110
Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
 115 120 125
Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr Phe Thr
```

130 135 140  
Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln Val  
145 150 155 160  
Phe Cys Leu His Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn  
165 170 175  
Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met  
180 185 190  
Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile  
195 200 205  
Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala Thr Gln  
210 215 220  
Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu  
225 230 235 240  
Val Met Glu Gly Tyr Asn Trp Cys Gln Glu Lys Asn Val Val Thr Val  
245 250 255  
Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile  
260 265 270  
Leu Glu Ile Gly Glu Lys Met Glu Gln Asn Phe Leu Gln Phe Asp Pro  
275 280 285  
Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr  
290 295 300  
Phe Leu  
305

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1568647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

Met Glu Cys Lys Pro Leu Gly Glu Ala Asp Val Lys Ile Leu Cys Asp  
1 5 10 15  
Gln Ala Lys Ala Ile Leu Val Glu Glu Tyr Asn Val Gln Pro Val Lys  
20 25 30  
Cys Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu  
35 40 45  
Ile Glu Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu  
50 55 60  
Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val  
65 70 75 80  
Ser Leu Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile  
85 90 95  
Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe  
100 105 110  
Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr  
115 120 125  
Phe Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser  
130 135 140  
Gln Val Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu  
145 150 155 160  
Asp Asn Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly  
165 170 175  
Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp  
180 185 190  
Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala  
195 200 205

Thr Gln Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His  
210 215 220  
Gln Leu Val Met Glu Gly Tyr Asn Trp Cys Gln Glu Lys Asn Val Val  
225 230 235 240  
Thr Val Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala  
245 250 255  
Ala Ile Leu Glu Ile Gly Glu Lys Met Glu Gln Asn Phe Leu Gln Phe  
260 265 270  
Asp Pro Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro  
275 280 285  
Asp Tyr Phe Leu  
290

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1568648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser  
1 5 10 15  
Leu Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile Leu  
20 25 30  
Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr  
35 40 45  
Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr Phe  
50 55 60  
Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln  
65 70 75 80  
Val Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp  
85 90 95  
Asn Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro  
100 105 110  
Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly  
115 120 125  
Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala Thr  
130 135 140  
Gln Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln  
145 150 155 160  
Leu Val Met Glu Gly Tyr Asn Trp Cys Gln Glu Lys Asn Val Val Thr  
165 170 175  
Val Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala  
180 185 190  
Ile Leu Glu Ile Gly Glu Lys Met Glu Gln Asn Phe Leu Gln Phe Asp  
195 200 205  
Pro Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp  
210 215 220  
Tyr Phe Leu  
225

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1354

(D) OTHER INFORMATION: / Ceres Seq. ID 1568657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acacaacaac aacacatcca ctcgaatttt ctattttcga ataacaaaaac cgatcggcgg | 60   |
| agacatgacg gcggcacaag ggaactctaa cgagactctg ttttcttctt acaagatggg  | 120  |
| aagattcgat ctctctcatc gagtgtttct ggcgcgatg acgcggtgca gggcggtgaa   | 180  |
| cggagtacca aacgcggcgt tggcagagta ttatgctcaa cggaccactc ccggcggttt  | 240  |
| tctcatctcc gaaggcacca tgggtctctcc cggatocgca Gggttccac atgtgcctgg  | 300  |
| aatctattca gatgaacaag tagaagcatg gaagcaagtt gtggaagcag ttcacgctaa  | 360  |
| gggaggtttc atcttttgtc aattatggca tgttggacgt gcttctcatg cagtgtatca  | 420  |
| acctaattga ggtacaccaa tatcgtcaac gaacaaacca atctcggaaa acagggtggc  | 480  |
| agttttgttg ccgcatggtt ccacgtgaa gtaccogaaa cctcgggctt tagaagcttc   | 540  |
| cgagatacct cgggtgtgtg aggtattattg cctttctgct ttgaatgcga ttcgagctgg | 600  |
| tttcgatggg attgagatcc acggggcgca tggttacctc attgatcagt ttttgaaaga  | 660  |
| cgggatcaat gaccgtactg accaatacgg aggatccatt gaaaaccgtt gtagattctt  | 720  |
| gaaacaagta gtggaagtg tagtttcagc cataggagct agtaaagttg gtgtgagggt   | 780  |
| atctccagct atagatcact tggacgcaac tgattctaac ccattatcac tcgggctagc  | 840  |
| cgtggttgat atgctcaata agttacaaga tgtaaatggc ttgaagctcg cttaccttca  | 900  |
| cgttacacaa cctcgtacc acgcctacgg gcaaacagag tcgggaaggc aagggagtga   | 960  |
| tgaggaagaa gctaagctaa tgaagagctt gagaatggct tataaaggaa cctttatgtc  | 1020 |
| cagttggagga ttcaataagg aactaggcat gcaagctgtt caacaagggt atgctgattt | 1080 |
| ggtttcatat ggcaggcttt ttatcgcaaa cccggatttg gtttcgcggt tcaagattga  | 1140 |
| tggaaagttg aataaatata atcgggaagac gttttacact caagatccag ttgttggtta | 1200 |
| cacggattat cctttcttgg ctcccttttc ccgcctctga gtttgataat cggaggagaa  | 1260 |
| aatgtattga tgttgtataa agacaatata ttaatatgta aaatgacaat gttattgtta  | 1320 |
| tccacttaat gaatagtc atgtatcttatt gttt                              |      |

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1568658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| His Asn Asn Asn Thr Ser Thr Arg Ile Phe Tyr Phe Arg Ile Thr Lys |  |
| 1 5 10 15                                                       |  |
| Pro Ile Gly Gly Asp Met Thr Ala Ala Gln Gly Asn Ser Asn Glu Thr |  |
| 20 25 30                                                        |  |
| Leu Phe Ser Ser Tyr Lys Met Gly Arg Phe Asp Leu Ser His Arg Val |  |
| 35 40 45                                                        |  |
| Val Leu Ala Pro Met Thr Arg Cys Arg Ala Leu Asn Gly Val Pro Asn |  |
| 50 55 60                                                        |  |
| Ala Ala Leu Ala Glu Tyr Tyr Ala Gln Arg Thr Thr Pro Gly Gly Phe |  |
| 65 70 75 80                                                     |  |
| Leu Ile Ser Glu Gly Thr Met Val Ser Pro Gly Ser Ala Gly Phe Pro |  |
| 85 90 95                                                        |  |
| His Val Pro Gly Ile Tyr Ser Asp Glu Gln Val Glu Ala Trp Lys Gln |  |
| 100 105 110                                                     |  |
| Val Val Glu Ala Val His Ala Lys Gly Gly Phe Ile Phe Cys Gln Leu |  |
| 115 120 125                                                     |  |
| Trp His Val Gly Arg Ala Ser His Ala Val Tyr Gln Pro Asn Gly Gly |  |
| 130 135 140                                                     |  |
| Ser Pro Ile Ser Ser Thr Asn Lys Pro Ile Ser Glu Asn Arg Trp Arg |  |
| 145 150 155 160                                                 |  |
| Val Leu Leu Pro Asp Gly Ser His Val Lys Tyr Pro Lys Pro Arg Ala |  |

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165 170 175
Leu Glu Ala Ser Glu Ile Pro Arg Val Val Glu Asp Tyr Cys Leu Ser
180 185 190
Ala Leu Asn Ala Ile Arg Ala Gly Phe Asp Gly Ile Glu Ile His Gly
195 200 205
Ala His Gly Tyr Leu Ile Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp
210 215 220
Arg Thr Asp Gln Tyr Gly Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu
225 230 235
Lys Gln Val Val Glu Gly Val Val Ser Ala Ile Gly Ala Ser Lys Val
245 250 255
Gly Val Arg Val Ser Pro Ala Ile Asp His Leu Asp Ala Thr Asp Ser
260 265 270
Asn Pro Leu Ser Leu Gly Leu Ala Val Val Asp Met Leu Asn Lys Leu
275 280 285
Gln Asp Val Asn Gly Leu Lys Leu Ala Tyr Leu His Val Thr Gln Pro
290 295 300
Arg Tyr His Ala Tyr Gly Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp
305 310 315
Glu Glu Glu Ala Lys Leu Met Lys Ser Leu Arg Met Ala Tyr Lys Gly
325 330 335
Thr Phe Met Ser Ser Gly Gly Phe Asn Lys Glu Leu Gly Met Gln Ala
340 345 350
Val Gln Gln Gly Asp Ala Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile
355 360 365
Ala Asn Pro Asp Leu Val Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn
370 375 380
Lys Tyr Asn Arg Lys Thr Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr
385 390 395
Thr Asp Tyr Pro Phe Leu Ala Pro Phe Ser Arg Leu
405 410

```

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1568659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

```

Met Thr Ala Ala Gln Gly Asn Ser Asn Glu Thr Leu Phe Ser Ser Tyr
1 5 10 15
Lys Met Gly Arg Phe Asp Leu Ser His Arg Val Val Leu Ala Pro Met
20 25 30
Thr Arg Cys Arg Ala Leu Asn Gly Val Pro Asn Ala Ala Leu Ala Glu
35 40 45
Tyr Tyr Ala Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Ser Glu Gly
50 55 60
Thr Met Val Ser Pro Gly Ser Ala Gly Phe Pro His Val Pro Gly Ile
65 70 75 80
Tyr Ser Asp Glu Gln Val Glu Ala Trp Lys Gln Val Val Glu Ala Val
85 90 95
His Ala Lys Gly Gly Phe Ile Phe Cys Gln Leu Trp His Val Gly Arg
100 105 110
Ala Ser His Ala Val Tyr Gln Pro Asn Gly Gly Ser Pro Ile Ser Ser
115 120 125
Thr Asn Lys Pro Ile Ser Glu Asn Arg Trp Arg Val Leu Leu Pro Asp
130 135 140

```

SEQUENCE = 1568659

Gly Ser His Val Lys Tyr Pro Lys Pro Arg Ala Leu Glu Ala Ser Glu  
145 150 155 160  
Ile Pro Arg Val Val Glu Asp Tyr Cys Leu Ser Ala Leu Asn Ala Ile  
165 170 175  
Arg Ala Gly Phe Asp Gly Ile Glu Ile His Gly Ala His Gly Tyr Leu  
180 185 190  
Ile Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp Arg Thr Asp Gln Tyr  
195 200 205  
Gly Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu Lys Gln Val Val Glu  
210 215 220  
Gly Val Val Ser Ala Ile Gly Ala Ser Lys Val Gly Val Arg Val Ser  
225 230 235 240  
Pro Ala Ile Asp His Leu Asp Ala Thr Asp Ser Asn Pro Leu Ser Leu  
245 250 255  
Gly Leu Ala Val Val Asp Met Leu Asn Lys Leu Gln Asp Val Asn Gly  
260 265 270  
Leu Lys Leu Ala Tyr Leu His Val Thr Gln Pro Arg Tyr His Ala Tyr  
275 280 285  
Gly Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp Glu Glu Glu Ala Lys  
290 295 300  
Leu Met Lys Ser Leu Arg Met Ala Tyr Lys Gly Thr Phe Met Ser Ser  
305 310 315 320  
Gly Gly Phe Asn Lys Glu Leu Gly Met Gln Ala Val Gln Gln Gly Asp  
325 330 335  
Ala Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile Ala Asn Pro Asp Leu  
340 345 350  
Val Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn Lys Tyr Asn Arg Lys  
355 360 365  
Thr Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe  
370 375 380  
Leu Ala Pro Phe Ser Arg Leu  
385 390

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1568660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

Met Gly Arg Phe Asp Leu Ser His Arg Val Val Leu Ala Pro Met Thr  
1 5 10 15  
Arg Cys Arg Ala Leu Asn Gly Val Pro Asn Ala Ala Leu Ala Glu Tyr  
20 25 30  
Tyr Ala Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Ser Glu Gly Thr  
35 40 45  
Met Val Ser Pro Gly Ser Ala Gly Phe Pro His Val Pro Gly Ile Tyr  
50 55 60  
Ser Asp Glu Gln Val Glu Ala Trp Lys Gln Val Val Glu Ala Val His  
65 70 75 80  
Ala Lys Gly Gly Phe Ile Phe Cys Gln Leu Trp His Val Gly Arg Ala  
85 90 95  
Ser His Ala Val Tyr Gln Pro Asn Gly Gly Ser Pro Ile Ser Ser Thr  
100 105 110  
Asn Lys Pro Ile Ser Glu Asn Arg Trp Arg Val Leu Leu Pro Asp Gly  
115 120 125  
Ser His Val Lys Tyr Pro Lys Pro Arg Ala Leu Glu Ala Ser Glu Ile

1568660

130 135 140  
Pro Arg Val Val Glu Asp Tyr Cys Leu Ser Ala Leu Asn Ala Ile Arg  
145 150 155 160  
Ala Gly Phe Asp Gly Ile Glu Ile His Gly Ala His Gly Tyr Leu Ile  
165 170 175  
Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp Arg Thr Asp Gln Tyr Gly  
180 185 190  
Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu Lys Gln Val Val Glu Gly  
195 200 205  
Val Val Ser Ala Ile Gly Ala Ser Lys Val Gly Val Arg Val Ser Pro  
210 215 220  
Ala Ile Asp His Leu Asp Ala Thr Asp Ser Asn Pro Leu Ser Leu Gly  
225 230 235 240  
Leu Ala Val Val Asp Met Leu Asn Lys Leu Gln Asp Val Asn Gly Leu  
245 250 255  
Lys Leu Ala Tyr Leu His Val Thr Gln Pro Arg Tyr His Ala Tyr Gly  
260 265 270  
Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp Glu Glu Glu Ala Lys Leu  
275 280 285  
Met Lys Ser Leu Arg Met Ala Tyr Lys Gly Thr Phe Met Ser Ser Gly  
290 295 300  
Gly Phe Asn Lys Glu Leu Gly Met Gln Ala Val Gln Gln Gly Asp Ala  
305 310 315 320  
Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile Ala Asn Pro Asp Leu Val  
325 330 335  
Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn Lys Tyr Asn Arg Lys Thr  
340 345 350  
Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu  
355 360 365  
Ala Pro Phe Ser Arg Leu  
370

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acaacccttt ccacaagaag ttataaacca atacatagaa gaaaacttcc aacctcaaaa  | 60   |
| aatgatgaag ggtgccaaagt tttcatctct tcttgtgott ttctttattt ttccgatcgc | 120  |
| atttgctcaa ctgagagtcg ggttttatag tcaatcatgc cctcaagccg agactatcgt  | 180  |
| acgcaatctg gtgcgccaac ggtttggtgt taccccaacc gttaccgccg ctttgctccg  | 240  |
| tatgcatttc cagcactgtt tcgttaaggg ctgtgacgct tctctcctca ttgattcaac  | 300  |
| caattccgag aaaactgctg gaccaaaccg aagcgctcagg gaatttgacc tgatagaccg | 360  |
| gatcaaggct cagctagaag ctgcatgccc ttccacagtc tcatgtgctg acatcgtcac  | 420  |
| attggccaca cgtgactcgg tggccttagc cggaggCcca agctacagca tccccacggg  | 480  |
| aaggcgtagc ggtagggtct caaacaatct tgatgtaacc ttaccgggtc caacgatctc  | 540  |
| cgtctctgga gccgtgagtt tattcacgaa caaagggatg aacacggttc atgcagtagc  | 600  |
| tcttttggtt gcacacactg ttggtcaagg aaatttgtgt ctcttttagt acagaatcac  | 660  |
| tagcttccaa ggaactggac gacccgaccc gtccatggac cccgcttttg ttaccagcct  | 720  |
| aaggaacaca tgcagaaata gcgcgacggc ggcactagac cagtgcagtc cattgagatt  | 780  |
| cgacaaccag ttcttcaagc aaatccgtaa aaggagagga gtgttgcaag ttgaccaacg  | 840  |
| cctcgcattc gaccacaaaa ctctgtgggat tgtggctcgg tatgctaata acaacgcctt | 900  |
| cttcaagcgt cagttcgtta gagcaatggt gaagatggga gccgttgatg tgcttactgg  | 960  |
| tcgtaacggt gagatcagaa ggaactgcag aagattcaac taatgaacta cagaagcgtg  | 1020 |
| gatataatat tacatttgat acaatatatt tcaaattctt tttatatatt tactaattca  | 1080 |

tttttgggtt tgggtgggggt tttcttgcac aaataaggct tttcttaaat tggatgggtt 1140  
cgattttcga gaaagattac tatgtactat attgttggtc tgcatttggg ggaatgtatct 1200  
taagtttaca aataatttgt ggc

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1568670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Pro | Phe | Pro | Gln | Glu | Val | Ile | Asn | Gln | Tyr | Ile | Glu | Glu | Asn | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Pro | Gln | Lys | Met | Met | Lys | Gly | Ala | Lys | Phe | Ser | Ser | Leu | Leu | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Phe | Phe | Ile | Phe | Pro | Ile | Ala | Phe | Ala | Gln | Leu | Arg | Val | Gly | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Ser | Gln | Ser | Cys | Pro | Gln | Ala | Glu | Thr | Ile | Val | Arg | Asn | Leu | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Gln | Arg | Phe | Gly | Val | Thr | Pro | Thr | Val | Thr | Ala | Ala | Leu | Leu | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Met | His | Phe | His | Asp | Cys | Phe | Val | Lys | Gly | Cys | Asp | Ala | Ser | Leu | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ile | Asp | Ser | Thr | Asn | Ser | Glu | Lys | Thr | Ala | Gly | Pro | Asn | Gly | Ser | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Arg | Glu | Phe | Asp | Leu | Ile | Asp | Arg | Ile | Lys | Ala | Gln | Leu | Glu | Ala | Ala |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Cys | Pro | Ser | Thr | Val | Ser | Cys | Ala | Asp | Ile | Val | Thr | Leu | Ala | Thr | Arg |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asp | Ser | Val | Ala | Leu | Ala | Gly | Gly | Pro | Ser | Tyr | Ser | Ile | Pro | Thr | Gly |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Arg | Arg | Asp | Gly | Arg | Val | Ser | Asn | Asn | Leu | Asp | Val | Thr | Leu | Pro | Gly |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Pro | Thr | Ile | Ser | Val | Ser | Gly | Ala | Val | Ser | Leu | Phe | Thr | Asn | Lys | Gly |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Met | Asn | Thr | Phe | Asp | Ala | Val | Ala | Leu | Leu | Gly | Ala | His | Thr | Val | Gly |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Gln | Gly | Asn | Cys | Gly | Leu | Phe | Ser | Asp | Arg | Ile | Thr | Ser | Phe | Gln | Gly |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Thr | Gly | Arg | Pro | Asp | Pro | Ser | Met | Asp | Pro | Ala | Leu | Val | Thr | Ser | Leu |  |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |  |
| Arg | Asn | Thr | Cys | Arg | Asn | Ser | Ala | Thr | Ala | Ala | Leu | Asp | Gln | Ser | Ser |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |  |
| Pro | Leu | Arg | Phe | Asp | Asn | Gln | Phe | Phe | Lys | Gln | Ile | Arg | Lys | Arg | Arg |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |
| Gly | Val | Leu | Gln | Val | Asp | Gln | Arg | Leu | Ala | Ser | Asp | Pro | Gln | Thr | Arg |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gly | Ile | Val | Ala | Arg | Tyr | Ala | Asn | Asn | Asn | Ala | Phe | Phe | Lys | Arg | Gln |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Phe | Val | Arg | Ala | Met | Val | Lys | Met | Gly | Ala | Val | Asp | Val | Leu | Thr | Gly |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Arg | Asn | Gly | Glu | Ile | Arg | Arg | Asn | Cys | Arg | Arg | Phe | Asn |     |     |     |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..313  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568671  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

Met Met Lys Gly Ala Lys Phe Ser Ser Leu Leu Val Leu Phe Phe Ile  
1 5 10 15  
Phe Pro Ile Ala Phe Ala Gln Leu Arg Val Gly Phe Tyr Ser Gln Ser  
20 25 30  
Cys Pro Gln Ala Glu Thr Ile Val Arg Asn Leu Val Arg Gln Arg Phe  
35 40 45  
Gly Val Thr Pro Thr Val Thr Ala Ala Leu Leu Arg Met His Phe His  
50 55 60  
Asp Cys Phe Val Lys Gly Cys Asp Ala Ser Leu Leu Ile Asp Ser Thr  
65 70 75 80  
Asn Ser Glu Lys Thr Ala Gly Pro Asn Gly Ser Val Arg Glu Phe Asp  
85 90 95  
Leu Ile Asp Arg Ile Lys Ala Gln Leu Glu Ala Ala Cys Pro Ser Thr  
100 105 110  
Val Ser Cys Ala Asp Ile Val Thr Leu Ala Thr Arg Asp Ser Val Ala  
115 120 125  
Leu Ala Gly Gly Pro Ser Tyr Ser Ile Pro Thr Gly Arg Arg Asp Gly  
130 135 140  
Arg Val Ser Asn Asn Leu Asp Val Thr Leu Pro Gly Pro Thr Ile Ser  
145 150 155 160  
Val Ser Gly Ala Val Ser Leu Phe Thr Asn Lys Gly Met Asn Thr Phe  
165 170 175  
Asp Ala Val Ala Leu Leu Gly Ala His Thr Val Gly Gln Gly Asn Cys  
180 185 190  
Gly Leu Phe Ser Asp Arg Ile Thr Ser Phe Gln Gly Thr Gly Arg Pro  
195 200 205  
Asp Pro Ser Met Asp Pro Ala Leu Val Thr Ser Leu Arg Asn Thr Cys  
210 215 220  
Arg Asn Ser Ala Thr Ala Ala Leu Asp Gln Ser Ser Pro Leu Arg Phe  
225 230 235 240  
Asp Asn Gln Phe Phe Lys Gln Ile Arg Lys Arg Arg Gly Val Leu Gln  
245 250 255  
Val Asp Gln Arg Leu Ala Ser Asp Pro Gln Thr Arg Gly Ile Val Ala  
260 265 270  
Arg Tyr Ala Asn Asn Asn Ala Phe Phe Lys Arg Gln Phe Val Arg Ala  
275 280 285  
Met Val Lys Met Gly Ala Val Asp Val Leu Thr Gly Arg Asn Gly Glu  
290 295 300  
Ile Arg Arg Asn Cys Arg Arg Phe Asn  
305 310

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 312 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..312  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1568672  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

Met Lys Gly Ala Lys Phe Ser Ser Leu Leu Val Leu Phe Phe Ile Phe

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|                 |                 |                 |                 |
|-----------------|-----------------|-----------------|-----------------|
| 1               | 5               | 10              | 15              |
| Pro Ile Ala Phe | Ala Gln Leu Arg | Val Gly Phe Tyr | Ser Gln Ser Cys |
| 20              | 25              | 30              |                 |
| Pro Gln Ala Glu | Thr Ile Val Arg | Asn Leu Val Arg | Gln Arg Phe Gly |
| 35              | 40              | 45              |                 |
| Val Thr Pro Thr | Val Thr Ala Ala | Leu Leu Arg Met | His Phe His Asp |
| 50              | 55              | 60              |                 |
| Cys Phe Val Lys | Gly Cys Asp Ala | Ser Leu Leu Ile | Asp Ser Thr Asn |
| 65              | 70              | 75              | 80              |
| Ser Glu Lys Thr | Ala Gly Pro Asn | Gly Ser Val Arg | Glu Phe Asp Leu |
| 85              | 90              | 95              |                 |
| Ile Asp Arg Ile | Lys Ala Gln Leu | Glu Ala Ala Cys | Pro Ser Thr Val |
| 100             | 105             | 110             |                 |
| Ser Cys Ala Asp | Ile Val Thr Leu | Ala Thr Arg Asp | Ser Val Ala Leu |
| 115             | 120             | 125             |                 |
| Ala Gly Gly Pro | Ser Tyr Ser Ile | Pro Thr Gly Arg | Arg Asp Gly Arg |
| 130             | 135             | 140             |                 |
| Val Ser Asn Asn | Leu Asp Val Thr | Leu Pro Gly Pro | Thr Ile Ser Val |
| 145             | 150             | 155             | 160             |
| Ser Gly Ala Val | Ser Leu Phe Thr | Asn Lys Gly Met | Asn Thr Phe Asp |
| 165             | 170             | 175             |                 |
| Ala Val Ala Leu | Gly Ala His Thr | Val Gly Gln Gly | Asn Cys Gly     |
| 180             | 185             | 190             |                 |
| Leu Phe Ser Asp | Arg Ile Thr Ser | Phe Gln Gly Thr | Gly Arg Pro Asp |
| 195             | 200             | 205             |                 |
| Pro Ser Met Asp | Pro Ala Leu Val | Thr Ser Leu Arg | Asn Thr Cys Arg |
| 210             | 215             | 220             |                 |
| Asn Ser Ala Thr | Ala Ala Leu Asp | Gln Ser Ser Pro | Leu Arg Phe Asp |
| 225             | 230             | 235             | 240             |
| Asn Gln Phe Phe | Lys Gln Ile Arg | Lys Arg Gly Val | Leu Gln Val     |
| 245             | 250             | 255             |                 |
| Asp Gln Arg Leu | Ala Ser Asp Pro | Gln Thr Arg Gly | Ile Val Ala Arg |
| 260             | 265             | 270             |                 |
| Tyr Ala Asn Asn | Asn Ala Phe Phe | Lys Arg Gln Phe | Val Arg Ala Met |
| 275             | 280             | 285             |                 |
| Val Lys Met Gly | Ala Val Asp Val | Leu Thr Gly Arg | Asn Gly Glu Ile |
| 290             | 295             | 300             |                 |
| Arg Arg Asn Cys | Arg Arg Phe Asn |                 |                 |
| 305             | 310             |                 |                 |

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

|                        |             |            |            |            |     |
|------------------------|-------------|------------|------------|------------|-----|
| aattcactat tAtgggagaa  | agaactaaaa  | acaccaagaa | aataaaaaaa | gagaaagagg | 60  |
| atggagaaaag agttacatga | atccaagggtg | gctacttaca | ccgaaagagg | cattggatca | 120 |
| cacgactcat cgctgaaaa   | ggagaaggaa  | aatctcata  | agcatagagg | attattccac | 180 |
| ctccatcact caaaagatga  | gaaagatgga  | gacaaaaaga | aagaaggatc | aaagagagag | 240 |
| aagatagctg cagcaatggt  | tggtcttggg  | gccactttta | tgaagaagaa | gcacaaaggt | 300 |
| ggtggaaaaa aggaaaaaag  | aggaggagga  | ggaggaaaag | aggaagaagg | aggaggagaa | 360 |
| gaggagggag aagaagaaga  | ggagtcgtct  | tcatcgagg  | aggaagaaga | agaagaagaa | 420 |
| ggaggaggtg gtggtggaga  | tgaagaagag  | ggaggaggca | agtttagtgc | tttcattaca | 480 |
| atgatcgccg aagcctttga  | agaatgaaaa  | tttaatttgt | gatcactttc | ttgtcatttt | 540 |
| tttttttttc aaatttgcta  | tcaaattata  | gcatttgtaa | tgttttatat | gggatgttga | 600 |

attg

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

Met Glu Lys Glu Leu His Glu Ser Lys Val Ala Thr Tyr Thr Glu Arg  
1 5 10 15  
Gly Ile Gly Ser His Asp Ser Ser Pro Glu Lys Glu Lys Glu Lys Ser  
20 25 30  
His Lys His Arg Gly Leu Phe His Leu His His Ser Lys Asp Glu Lys  
35 40 45  
Asp Gly Asp Lys Lys Lys Glu Gly Ser Lys Arg Glu Lys Ile Ala Ala  
50 55 60  
Ala Met Val Gly Leu Gly Ala Thr Phe Met Lys Lys Lys His Lys Gly  
65 70 75 80  
Gly Gly Lys Lys Glu Lys Arg Gly Gly Gly Gly Gly Lys Glu Glu Glu  
85 90 95  
Gly Gly Gly Glu Glu Glu Gly Glu Glu Glu Glu Glu Ser Ser Ser Ser  
100 105 110  
Glu Glu Glu Glu Glu Glu Glu Gly Gly Gly Gly Gly Gly Asp Glu  
115 120 125  
Glu Glu Gly Gly Gly Lys Phe Ser Ala Phe Ile Thr Met Ile Ala Glu  
130 135 140  
Ala Phe Glu Glu  
145

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

Met Val Gly Leu Gly Ala Thr Phe Met Lys Lys Lys His Lys Gly Gly  
1 5 10 15  
Gly Lys Lys Glu Lys Arg Gly Gly Gly Gly Gly Lys Glu Glu Glu Gly  
20 25 30  
Gly Gly Glu Glu Glu Gly Glu Glu Glu Glu Glu Ser Ser Ser Ser Glu  
35 40 45  
Glu Glu Glu Glu Glu Glu Glu Gly Gly Gly Gly Gly Gly Asp Glu Glu  
50 55 60  
Glu Gly Gly Gly Lys Phe Ser Ala Phe Ile Thr Met Ile Ala Glu Ala  
65 70 75 80  
Phe Glu Glu

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..75  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568676  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

Met Lys Lys Lys His Lys Gly Gly Gly Lys Lys Glu Lys Arg Gly Gly  
1 5 10 15  
Gly Gly Gly Lys Glu Glu Glu Gly Gly Glu Glu Glu Glu Glu Glu  
20 25 30  
Glu Glu Glu Ser Ser Ser Ser Glu Glu Glu Glu Glu Glu Glu Gly  
35 40 45  
Gly Gly Gly Gly Gly Asp Glu Glu Glu Gly Gly Gly Lys Phe Ser Ala  
50 55 60  
Phe Ile Thr Met Ile Ala Glu Ala Phe Glu Glu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1013:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1437 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1437  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

tataacggtc aggttgtcgt tgacacttca ttgtctctaa aaagtcgtga ttatagtcac 60  
atcattagcg ttaaaccgct tgctatagct gcaacggaga aggtcgaatt tacagttaaa 120  
ggcatgaatc tccgtcggcg tggcacaagg ttactttgtt ctgttgaagg aaaatacttg 180  
attcaggaaa caacacacga ttgcagcacc agggaggatg acgatttcaa ggacaacaag 240  
agattgttga gtgtgtaaac ttctcttggtg atatgcctat attgagtggt cgaggattca 300  
tggagattga agaccaagga ctacagtagca gcttcttccc tttcttagtg gttgaagatg 360  
acgatgtttg ttctgaaatc cgtataacttg aaaccacatt agagttcact ggaactgatt 420  
ctgctaagca agctatggat ttcatatcatg aaatcggttg gcttcttcac agaagtaaac 480  
ttggggaatc agaccctaat ccaggcggtt tcccattaat acgcttccag tggctaatac 540  
agttctcaat ggatcgagag tgggtgcgctg tgatcagaaa gctattaaac atgttctttg 600  
atggagctgt tgggtgaattt tcttctctct ctaatgccac actgtcagaa ctgtgccttc 660  
ttcacagagc cgtgaggaaa aactctaagc ctatggttga aatgctcttg agatatattc 720  
ccaagcaaca aagaacacgc ttgttttagac ccgatgctgc tgggtccagcc ggcttaacac 780  
ctcttcatat tgcagctggt aaagacggtt cagaagatgt gttggatgag ctaacagaag 840  
atcctgcaat ggtggggatt gaagcgtgga agacatgtcg agacagcaca ggcttTcaca 900  
ccagaagact acgcacttac gcggtcactt ctcatatcat cacttgattc aacgcaagat 960  
caataaaaaag tcaacaactg aagatcatgt tgtgggtcaac atcccagttt ctttctcaga 1020  
cagagagcag aaagaaccaa aatcaggtcc gatggcttca gccttggaga tcacacagat 1080  
tccatgcaag ctctgtgacc ataaactggt gtatgggaca acacgcaggt ctgtagcgta 1140  
cagaccagct atgttgtcaa tgggtggcgat tgctgcggtt tgcgtctgtg tggcacttct 1200  
gtttaagagt tgcccgaag tgctctatgt gtttcaaccg ttcaggtggg agttattgga 1260  
ctatggaaca agctgagtgt aagtctactt tgaaagatct tctaagatat atatatgaat 1320  
gttacttata taaaacccat agaggtgtga tttctatatg taactatatg agtataagat 1380  
atagagacat gttggagaag aagattgttg ttattattgt tggtgtgtgt gttgtgac

(2) INFORMATION FOR SEQ ID NO:1014:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 224 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1568684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ile | Leu | Ser | Gly | Arg | Gly | Phe | Met | Glu | Ile | Glu | Asp | Gln | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Ser | Phe | Phe | Pro | Phe | Leu | Val | Val | Glu | Asp | Asp | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ser | Glu | Ile | Arg | Ile | Leu | Glu | Thr | Thr | Leu | Glu | Phe | Thr | Gly | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | Ala | Lys | Gln | Ala | Met | Asp | Phe | Ile | His | Glu | Ile | Gly | Trp | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | His | Arg | Ser | Lys | Leu | Gly | Glu | Ser | Asp | Pro | Asn | Pro | Gly | Val | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Leu | Ile | Arg | Phe | Gln | Trp | Leu | Ile | Glu | Phe | Ser | Met | Asp | Arg | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Cys | Ala | Val | Ile | Arg | Lys | Leu | Leu | Asn | Met | Phe | Phe | Asp | Gly | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Gly | Glu | Phe | Ser | Ser | Ser | Ser | Asn | Ala | Thr | Leu | Ser | Glu | Leu | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Leu | His | Arg | Ala | Val | Arg | Lys | Asn | Ser | Lys | Pro | Met | Val | Glu | Met |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Leu | Arg | Tyr | Ile | Pro | Lys | Gln | Gln | Arg | Asn | Ser | Leu | Phe | Arg | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ala | Ala | Gly | Pro | Ala | Gly | Leu | Thr | Pro | Leu | His | Ile | Ala | Ala | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Asp | Gly | Ser | Glu | Asp | Val | Leu | Asp | Ala | Leu | Thr | Glu | Asp | Pro | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Val | Gly | Ile | Glu | Ala | Trp | Lys | Thr | Cys | Arg | Asp | Ser | Thr | Gly | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Thr | Arg | Arg | Leu | Arg | Thr | Tyr | Ala | Val | Thr | Ser | His | Thr | Ser | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1568685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Glu | Asp | Gln | Gly | Leu | Ser | Ser | Phe | Phe | Pro | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Val | Val | Glu | Asp | Asp | Asp | Val | Cys | Ser | Glu | Ile | Arg | Ile | Leu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Thr | Leu | Glu | Phe | Thr | Gly | Thr | Asp | Ser | Ala | Lys | Gln | Ala | Met | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | His | Glu | Ile | Gly | Trp | Leu | Leu | His | Arg | Ser | Lys | Leu | Gly | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Pro | Asn | Pro | Gly | Val | Phe | Pro | Leu | Ile | Arg | Phe | Gln | Trp | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Glu | Phe | Ser | Met | Asp | Arg | Glu | Trp | Cys | Ala | Val | Ile | Arg | Lys | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Met | Phe | Phe | Asp | Gly | Ala | Val | Gly | Glu | Phe | Ser | Ser | Ser | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |

Ala Thr Leu Ser Glu Leu Cys Leu Leu His Arg Ala Val Arg Lys Asn  
115 120 125  
Ser Lys Pro Met Val Glu Met Leu Leu Arg Tyr Ile Pro Lys Gln Gln  
130 135 140  
Arg Asn Ser Leu Phe Arg Pro Asp Ala Ala Gly Pro Ala Gly Leu Thr  
145 150 155 160  
Pro Leu His Ile Ala Ala Gly Lys Asp Gly Ser Glu Asp Val Leu Asp  
165 170 175  
Ala Leu Thr Glu Asp Pro Ala Met Val Gly Ile Glu Ala Trp Lys Thr  
180 185 190  
Cys Arg Asp Ser Thr Gly Phe His Thr Arg Arg Leu Arg Thr Tyr Ala  
195 200 205  
Val Thr Ser His Thr Ser Thr  
210 215

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1568686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

Met Asp Phe Ile His Glu Ile Gly Trp Leu Leu His Arg Ser Lys Leu  
1 5 10 15  
Gly Glu Ser Asp Pro Asn Pro Gly Val Phe Pro Leu Ile Arg Phe Gln  
20 25 30  
Trp Leu Ile Glu Phe Ser Met Asp Arg Glu Trp Cys Ala Val Ile Arg  
35 40 45  
Lys Leu Leu Asn Met Phe Phe Asp Gly Ala Val Gly Glu Phe Ser Ser  
50 55 60  
Ser Ser Asn Ala Thr Leu Ser Glu Leu Cys Leu Leu His Arg Ala Val  
65 70 75 80  
Arg Lys Asn Ser Lys Pro Met Val Glu Met Leu Leu Arg Tyr Ile Pro  
85 90 95  
Lys Gln Gln Arg Asn Ser Leu Phe Arg Pro Asp Ala Ala Gly Pro Ala  
100 105 110  
Gly Leu Thr Pro Leu His Ile Ala Ala Gly Lys Asp Gly Ser Glu Asp  
115 120 125  
Val Leu Asp Ala Leu Thr Glu Asp Pro Ala Met Val Gly Ile Glu Ala  
130 135 140  
Trp Lys Thr Cys Arg Asp Ser Thr Gly Phe His Thr Arg Arg Leu Arg  
145 150 155 160  
Thr Tyr Ala Val Thr Ser His Thr Ser Thr  
165 170

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1748 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1748

(D) OTHER INFORMATION: / Ceres Seq. ID 1568715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

aaatgtcatc tccttcatct ctcaggtaaa aaaactgagt cGgagatttg gcgacgtgat

gaatcatttg gtgataatct ctgtgttctt gagctcagtg ttgttatata gaggagaatc 120  
tggaatcaca agtagtttta ttcgatctga atggcctgcg gttgatatac cacttgatca 180  
tcatgttttc aatgtcccaa aaggatataa tgcaccacaa caagtacata taactcaagg 240  
tgattatgat ggtaaagctg ttatcatctc ttgggttaca cctgatgaac ctgggttctag 300  
ccaagtacat tacgggtgcgg ttacagggaa atatgagttt gttgctcaag ggacttacca 360  
taactacacg ttttacaagt ataagtctgg ctttattcat cactgccttg tctctgacct 420  
tgagcatgat acaaaatact attacaagat tgaagcggt gaatcttctc gagagttttg 480  
gtttgttaca ccaccacatg tacatccaga tgcttcctac aagtttggtg ttataggcga 540  
tatgggtcag acattcaact cgttatccac gttggaacat tacatggaga gtggagctca 600  
ggctgtttta tttcttgagg atctttctta tgctgataga tatcagtata atgacgttgg 660  
tgtgagatgg gatagctggg gtcgttttgt ggagcgtagt accgcttate aaccgtggct 720  
ttgggtctga ggaaatcatg aagtagatta catgccatac atgggocgagg tgacaccttt 780  
caggaattac cttcagcgtt acactacgcc ttacttagcc tcaaaaagta gcagtcctct 840  
ttggtacgct gttaggcgtg catctgctca tatcattgtc ctctccagct attcgccttt 900  
tgtgaagtat accccgcaat ggcaactggct tagtgaagag cttacaagag ttgataggga 960  
gaaaacacct tggctaattg ttttgatgca cgtcccaata tacaacagta atgaagcaca 1020  
tttcatggag ggtgaaagca tgcgagcagc ttttgaagag tggtttgtcc aacacaaagt 1080  
tgatgtaatc tttgctgggc atgttcatgc ctacgagaga tctgtaccga tatcaaatgt 1140  
gcggtataac gtgtcaagcg gagatcgta cccagttcca gataagtcag cgcctgttta 1200  
tatcacagtt ggagacggag gaaatcaaga aggtctggct ggaaggttta cggaaccaca 1260  
gccagattat tctgcatttc gggaagctag ctatggccac tctactctgg atataaagaa 1320  
ccgaacacac gctatatacc actggaaccg caatgatgat gggaagaaag tggcaacgga 1380  
tgaatttgta ttacacaacc agtactgggg aaagaacatt cgacggagaa agcttaagaa 1440  
gcattatata aggagtgttg ttgggtggct gatcgccact taattcacta agtctgcctc 1500  
atgctttgta tcaaagtgtg tgaggatatt cttttaactc ggaacttatt acttaatttg 1560  
atgttaaata tctttccgcg ttaagttttc agcaatctgg aatatgaagg gaattatgta 1620  
ttcttatcag tcttttgatg aagtgaggtc tacttctggg attatggatt tgggtgaataa 1680  
tgtattcctt agaacggtgt taaggaattg ttccacatgg gtgtgaattg agaagtccat 1740  
ttgtgttt

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1568716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

Asn Val Ile Ser Phe Ile Ser Gln Val Lys Lys Leu Ser Arg Arg Phe  
1 5 10 15  
Gly Asp Val Met Asn His Leu Val Ile Ile Ser Val Phe Leu Ser Ser  
20 25 30  
Val Leu Leu Tyr Arg Gly Glu Ser Gly Ile Thr Ser Ser Phe Ile Arg  
35 40 45  
Ser Glu Trp Pro Ala Val Asp Ile Pro Leu Asp His His Val Phe Asn  
50 55 60  
Val Pro Lys Gly Tyr Asn Ala Pro Gln Gln Val His Ile Thr Gln Gly  
65 70 75 80  
Asp Tyr Asp Gly Lys Ala Val Ile Ile Ser Trp Val Thr Pro Asp Glu  
85 90 95  
Pro Gly Ser Ser Gln Val His Tyr Gly Ala Val Gln Gly Lys Tyr Glu  
100 105 110  
Phe Val Ala Gln Gly Thr Tyr His Asn Tyr Thr Phe Tyr Lys Tyr Lys  
115 120 125  
Ser Gly Phe Ile His His Cys Leu Val Ser Asp Leu Glu His Asp Thr  
130 135 140  
Lys Tyr Tyr Tyr Lys Ile Glu Ser Gly Glu Ser Ser Arg Glu Phe Trp  
145 150 155 160

Phe Val Thr Pro Pro His Val His Pro Asp Ala Ser Tyr Lys Phe Gly  
165 170 175  
Ile Ile Gly Asp Met Gly Gln Thr Phe Asn Ser Leu Ser Thr Leu Glu  
180 185 190  
His Tyr Met Glu Ser Gly Ala Gln Ala Val Leu Phe Leu Gly Asp Leu  
195 200 205  
Ser Tyr Ala Asp Arg Tyr Gln Tyr Asn Asp Val Gly Val Arg Trp Asp  
210 215 220  
Ser Trp Gly Arg Phe Val Glu Arg Ser Thr Ala Tyr Gln Pro Trp Leu  
225 230 235 240  
Trp Ser Ala Gly Asn His Glu Val Asp Tyr Met Pro Tyr Met Gly Glu  
245 250 255  
Val Thr Pro Phe Arg Asn Tyr Leu Gln Arg Tyr Thr Thr Pro Tyr Leu  
260 265 270  
Ala Ser Lys Ser Ser Ser Pro Leu Trp Tyr Ala Val Arg Arg Ala Ser  
275 280 285  
Ala His Ile Ile Val Leu Ser Ser Tyr Ser Pro Phe Val Lys Tyr Thr  
290 295 300  
Pro Gln Trp His Trp Leu Ser Glu Glu Leu Thr Arg Val Asp Arg Glu  
305 310 315 320  
Lys Thr Pro Trp Leu Ile Val Leu Met His Val Pro Ile Tyr Asn Ser  
325 330 335  
Asn Glu Ala His Phe Met Glu Gly Glu Ser Met Arg Ala Ala Phe Glu  
340 345 350  
Glu Trp Phe Val Gln His Lys Val Asp Val Ile Phe Ala Gly His Val  
355 360 365  
His Ala Tyr Glu Arg Ser Tyr Arg Ile Ser Asn Val Arg Tyr Asn Val  
370 375 380  
Ser Ser Gly Asp Arg Tyr Pro Val Pro Asp Lys Ser Ala Pro Val Tyr  
385 390 395 400  
Ile Thr Val Gly Asp Gly Gly Asn Gln Glu Gly Leu Ala Gly Arg Phe  
405 410 415  
Thr Glu Pro Gln Pro Asp Tyr Ser Ala Phe Arg Glu Ala Ser Tyr Gly  
420 425 430  
His Ser Thr Leu Asp Ile Lys Asn Arg Thr His Ala Ile Tyr His Trp  
435 440 445  
Asn Arg Asn Asp Asp Gly Lys Lys Val Ala Thr Asp Glu Phe Val Leu  
450 455 460  
His Asn Gln Tyr Trp Gly Lys Asn Ile Arg Arg Arg Lys Leu Lys Lys  
465 470 475 480  
His Tyr Ile Arg Ser Val Val Gly Gly Trp Ile Ala Thr  
485 490

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1568717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

Met Asn His Leu Val Ile Ile Ser Val Phe Leu Ser Ser Val Leu Leu  
1 5 10 15  
Tyr Arg Gly Glu Ser Gly Ile Thr Ser Ser Phe Ile Arg Ser Glu Trp  
20 25 30  
Pro Ala Val Asp Ile Pro Leu Asp His His Val Phe Asn Val Pro Lys  
35 40 45  
Gly Tyr Asn Ala Pro Gln Gln Val His Ile Thr Gln Gly Asp Tyr Asp



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Gly Lys Ala Val Ile Ile Ser Trp Val Thr Pro Asp Glu Pro Gly Ser |     |     |
| 65                                                              | 70  | 75  |
| Ser Gln Val His Tyr Gly Ala Val Gln Gly Lys Tyr Glu Phe Val Ala |     |     |
|                                                                 | 85  | 90  |
| Gln Gly Thr Tyr His Asn Tyr Thr Phe Tyr Lys Tyr Lys Ser Gly Phe |     |     |
|                                                                 | 100 | 105 |
| Ile His His Cys Leu Val Ser Asp Leu Glu His Asp Thr Lys Tyr Tyr |     |     |
|                                                                 | 115 | 120 |
| Tyr Lys Ile Glu Ser Gly Glu Ser Ser Arg Glu Phe Trp Phe Val Thr |     |     |
|                                                                 | 130 | 135 |
| Pro Pro His Val His Pro Asp Ala Ser Tyr Lys Phe Gly Ile Ile Gly |     |     |
| 145                                                             | 150 | 155 |
| Asp Met Gly Gln Thr Phe Asn Ser Leu Ser Thr Leu Glu His Tyr Met |     |     |
|                                                                 | 165 | 170 |
| Glu Ser Gly Ala Gln Ala Val Leu Phe Leu Gly Asp Leu Ser Tyr Ala |     |     |
|                                                                 | 180 | 185 |
| Asp Arg Tyr Gln Tyr Asn Asp Val Gly Val Arg Trp Asp Ser Trp Gly |     |     |
|                                                                 | 195 | 200 |
| Arg Phe Val Glu Arg Ser Thr Ala Tyr Gln Pro Trp Leu Trp Ser Ala |     |     |
|                                                                 | 210 | 215 |
| Gly Asn His Glu Val Asp Tyr Met Pro Tyr Met Gly Glu Val Thr Pro |     |     |
| 225                                                             | 230 | 235 |
| Phe Arg Asn Tyr Leu Gln Arg Tyr Thr Thr Pro Tyr Leu Ala Ser Lys |     |     |
|                                                                 | 245 | 250 |
| Ser Ser Ser Pro Leu Trp Tyr Ala Val Arg Arg Ala Ser Ala His Ile |     |     |
|                                                                 | 260 | 265 |
| Ile Val Leu Ser Ser Tyr Ser Pro Phe Val Lys Tyr Thr Pro Gln Trp |     |     |
|                                                                 | 275 | 280 |
| His Trp Leu Ser Glu Glu Leu Thr Arg Val Asp Arg Glu Lys Thr Pro |     |     |
|                                                                 | 290 | 295 |
| Trp Leu Ile Val Leu Met His Val Pro Ile Tyr Asn Ser Asn Glu Ala |     |     |
| 305                                                             | 310 | 315 |
| His Phe Met Glu Gly Glu Ser Met Arg Ala Ala Phe Glu Glu Trp Phe |     |     |
|                                                                 | 325 | 330 |
| Val Gln His Lys Val Asp Val Ile Phe Ala Gly His Val His Ala Tyr |     |     |
|                                                                 | 340 | 345 |
| Glu Arg Ser Tyr Arg Ile Ser Asn Val Arg Tyr Asn Val Ser Ser Gly |     |     |
|                                                                 | 355 | 360 |
| Asp Arg Tyr Pro Val Pro Asp Lys Ser Ala Pro Val Tyr Ile Thr Val |     |     |
|                                                                 | 370 | 375 |
| Gly Asp Gly Gly Asn Gln Glu Gly Leu Ala Gly Arg Phe Thr Glu Pro |     |     |
| 385                                                             | 390 | 395 |
| Gln Pro Asp Tyr Ser Ala Phe Arg Glu Ala Ser Tyr Gly His Ser Thr |     |     |
|                                                                 | 405 | 410 |
| Leu Asp Ile Lys Asn Arg Thr His Ala Ile Tyr His Trp Asn Arg Asn |     |     |
|                                                                 | 420 | 425 |
| Asp Asp Gly Lys Lys Val Ala Thr Asp Glu Phe Val Leu His Asn Gln |     |     |
|                                                                 | 435 | 440 |
| Tyr Trp Gly Lys Asn Ile Arg Arg Arg Lys Leu Lys Lys His Tyr Ile |     |     |
|                                                                 | 450 | 455 |
| Arg Ser Val Val Gly Gly Trp Ile Ala Thr                         |     | 460 |
| 465                                                             | 470 |     |

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..313  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

Met Gly Gln Thr Phe Asn Ser Leu Ser Thr Leu Glu His Tyr Met Glu  
1 5 10 15  
Ser Gly Ala Gln Ala Val Leu Phe Leu Gly Asp Leu Ser Tyr Ala Asp  
20 25 30  
Arg Tyr Gln Tyr Asn Asp Val Gly Val Arg Trp Asp Ser Trp Gly Arg  
35 40 45  
Phe Val Glu Arg Ser Thr Ala Tyr Gln Pro Trp Leu Trp Ser Ala Gly  
50 55 60  
Asn His Glu Val Asp Tyr Met Pro Tyr Met Gly Glu Val Thr Pro Phe  
65 70 75 80  
Arg Asn Tyr Leu Gln Arg Tyr Thr Thr Pro Tyr Leu Ala Ser Lys Ser  
85 90 95  
Ser Ser Pro Leu Trp Tyr Ala Val Arg Arg Ala Ser Ala His Ile Ile  
100 105 110  
Val Leu Ser Ser Tyr Ser Pro Phe Val Lys Tyr Thr Pro Gln Trp His  
115 120 125  
Trp Leu Ser Glu Glu Leu Thr Arg Val Asp Arg Glu Lys Thr Pro Trp  
130 135 140  
Leu Ile Val Leu Met His Val Pro Ile Tyr Asn Ser Asn Glu Ala His  
145 150 155 160  
Phe Met Glu Gly Glu Ser Met Arg Ala Ala Phe Glu Glu Trp Phe Val  
165 170 175  
Gln His Lys Val Asp Val Ile Phe Ala Gly His Val His Ala Tyr Glu  
180 185 190  
Arg Ser Tyr Arg Ile Ser Asn Val Arg Tyr Asn Val Ser Ser Gly Asp  
195 200 205  
Arg Tyr Pro Val Pro Asp Lys Ser Ala Pro Val Tyr Ile Thr Val Gly  
210 215 220  
Asp Gly Gly Asn Gln Glu Gly Leu Ala Gly Arg Phe Thr Glu Pro Gln  
225 230 235 240  
Pro Asp Tyr Ser Ala Phe Arg Glu Ala Ser Tyr Gly His Ser Thr Leu  
245 250 255  
Asp Ile Lys Asn Arg Thr His Ala Ile Tyr His Trp Asn Arg Asn Asp  
260 265 270  
Asp Gly Lys Lys Val Ala Thr Asp Glu Phe Val Leu His Asn Gln Tyr  
275 280 285  
Trp Gly Lys Asn Ile Arg Arg Arg Lys Leu Lys Lys His Tyr Ile Arg  
290 295 300  
Ser Val Val Gly Gly Trp Ile Ala Thr  
305 310

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 596 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..596  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

gaataatttc attctcttat ggcataatggt gctataaaca aacacactta ccacgcttga 60  
tcctacaaca catgaaccat ggcttcttca acccactctt acttcaccac tttagcacta 120  
accctaattct tgatctttcg tctcatacca gaaaccaccg catcacgcca tctgaatgga 180  
aagaatccgg cggttaattgg agttaccact actagcgaga aatacattgt tcctacgccg 240  
ttaccaccgt ttttacgacc ctttttccca cgtttacagt ttgccgctgc accgttcgga 300

gggaatatcc cacaaccacc gttaccttca ccacctccaa catttctacc gtgtctccca 360  
ggtttcaagt ttctctccctt tcagtcccgga aagcctacgc cgccgtaatc gtatatacgt 420  
tgacggcatc aagtctaaaa ctgtaatgaa atattaaact atctacttta atgtattatc 480  
tatctctata tatcaccgtt gatcatctat aaataattga tggtaatatc atggtatgaa 540  
actgtaataa agatcactgg ttagtagtaatt aataaaYtga ataaatacta tgttag

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1568742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

Ile Ile Ser Phe Ser Tyr Gly Ile Trp Cys Tyr Lys Gln Thr His Leu  
1 5 10 15  
Pro Arg Leu Ile Leu Gln His Met Asn His Gly Phe Phe Asn Pro Leu  
20 25 30  
Leu Leu His His Phe Ser Thr Asn Pro Asn Leu Asp Leu Ser Ser His  
35 40 45  
Thr Arg Asn His Arg Ile Thr Pro Ser Glu Trp Lys Glu Ser Gly Gly  
50 55 60  
Asn Trp Ser Tyr His Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1568743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

Met Ala Ser Ser Thr His Ser Tyr Phe Thr Thr Leu Ala Leu Thr Leu  
1 5 10 15  
Ile Leu Ile Phe Arg Leu Ile Pro Glu Thr Thr Ala Ser Arg His Leu  
20 25 30  
Asn Gly Lys Asn Pro Ala Val Ile Gly Val Thr Thr Thr Ser Glu Lys  
35 40 45  
Tyr Ile Val Pro Thr Pro Leu Pro Pro Phe Leu Arg Pro Phe Phe Pro  
50 55 60  
Pro Leu Gln Phe Ala Ala Pro Phe Gly Gly Asn Ile Pro Gln Pro  
65 70 75 80  
Pro Leu Pro Ser Pro Pro Pro Thr Phe Leu Pro Cys Leu Pro Gly Phe  
85 90 95  
Lys Phe Pro Pro Phe Gln Ser Arg Lys Pro Thr Pro Pro  
100 105

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1568754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

Met Ile Pro Phe Ser Asp Arg Cys Ser Leu Ser Val Lys Ser Gln Ser  
1 5 10 15  
Ser Ser Thr Glu Thr Thr Lys Ser Ser Val His Phe Phe Ser Phe Lys  
20 25 30  
Leu Leu Leu His Glu Ser  
35

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1592 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1592

(D) OTHER INFORMATION: / Ceres Seq. ID 1568758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

aagactctct ctgctttcga ccMAaaaacc ttctctctct ctctgggaga tctccatctt 60  
cttcgcttct tcgcttcccc gcctgaaaca attactcgat ctgcgcggcg gaacaagctc 120  
tccgtttctc tttccggcag atcgattctt ccaattcctt attcctttct aggtcttctt 180  
taagaaaccc ttactttctt caaaatctgc atttatggcg attagggtta ccttcaccta 240  
ctccagctat gttgctagga gcattgtctt atccgcggcg actcgtgtcg gtaccggcga 300  
cgttagatca tgcttcgaaa catgggttcg tcccagggtt tgccggccaca atcagatacc 360  
agatattgtt gataaatctc ccggatccaa cacatggggg ccaagctcag gccctcgtgc 420  
tcgaccagct tcatcaatgt atagcaccat tgcgagggaa atcctcgaag aaggctgcaa 480  
gagtcacact gtcttgggta tgatctctct catgaatttg actggagctc cacagttttc 540  
gggtgtgacc ggtctcggga tctctccctt taagacttct tctgtcatcc cgttccttag 600  
gggttccaag tggatgcctt gtagtattcc ggcgacgtta tcaacggata ttgctgaggt 660  
tgatagagga ggaaaggtct gtgatcctaa agtgaagttg gagttgagtg ataaagtctc 720  
gaatggtgga aacggatggg ttaataagct gttgaatatc tgctcggagg atgctaaggc 780  
tgctttcacg gcggttactt tttctctcct tttccgatcg gctttggccg agccaaagtc 840  
tataccttca acatctatgc ttctactctc cgatgtgggt gatcgtgtta tagccgagaa 900  
ggtctcatalc tttttcagga agccagaggt ttcagacata gttatcttca aggctcctcc 960  
tattttggtg gaacatggtt acagttgtgc tgatgttttc ataaaaagga tagttgctag 1020  
cgaaggtgac tgggttgaag tttgtgatgg aaagctctta gtaaatgaca ctgttcaagc 1080  
agaggatttt gtcttagagc caattgacta tgaaatggaa ccaatgtttg tccctgaagg 1140  
ttatgtcttc gtcttaggag acaaccgcaa caaaagcttt gattctcata actgggggtcc 1200  
acttccaata aagaacatca tagggagatc tgtgtttcgc tattggccac caagcaaagt 1260  
gtcagacata atacaccatg aacaagttag ccaaaagaga gctgttgatg tatcttgacc 1320  
aacgcagatg gtatcttagg attaagcaga aaatttgatt agatgagctg tgccatgcca 1380  
accatttttg cgctgaaggc aacagagcaa ttctttcttc ctgtctaggg ttgatggcgg 1440  
acatggaatg cactgggaaa tccatataaa aagaacaaga aaattgatat ttttgctttg 1500  
atataagggt aaactttctt ttttgagtat tt  
1560

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1568759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

Met Ala Ile Arg Val Thr Phe Thr Tyr Ser Ser Tyr Val Ala Arg Ser

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1 5 10 15  
Ile Ala Ser Ser Ala Gly Thr Arg Val Gly Thr Gly Asp Val Arg Ser  
20 25 30  
Cys Phe Glu Thr Trp Val Arg Pro Arg Phe Cys Gly His Asn Gln Ile  
35 40 45  
Pro Asp Ile Val Asp Lys Ser Pro Gly Ser Asn Thr Trp Gly Pro Ser  
50 55 60  
Ser Gly Pro Arg Ala Arg Pro Ala Ser Ser Met Tyr Ser Thr Ile Ala  
65 70 75 80  
Arg Glu Ile Leu Glu Glu Gly Cys Lys Ser Pro Leu Val Leu Gly Met  
85 90 95  
Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val Thr  
100 105 110  
Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe Leu  
115 120 125  
Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser Thr  
130 135 140  
Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys Val  
145 150 155 160  
Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp Val  
165 170 175  
Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe Thr  
180 185 190  
Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro Lys  
195 200 205  
Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp Arg  
210 215 220  
Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val Ser  
225 230 235 240  
Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly Tyr  
245 250 255  
Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly Asp  
260 265 270  
Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val Gln  
275 280 285  
Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro Met  
290 295 300  
Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn Lys  
305 310 315 320  
Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile Ile  
325 330 335  
Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp Ile  
340 345 350  
Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser  
355 360 365

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

Met Tyr Ser Thr Ile Ala Arg Glu Ile Leu Glu Glu Gly Cys Lys Ser  
1 5 10 15  
Pro Leu Val Leu Gly Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro  
20 25 30

Gln Phe Ser Gly Val Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser  
35 40 45  
Ser Val Ile Pro Phe Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile  
50 55 60  
Pro Ala Thr Leu Ser Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys  
65 70 75 80  
Val Cys Asp Pro Lys Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn  
85 90 95  
Gly Gly Asn Gly Trp Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp  
100 105 110  
Ala Lys Ala Ala Phe Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser  
115 120 125  
Ala Leu Ala Glu Pro Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr  
130 135 140  
Leu Asp Val Gly Asp Arg Val Ile Ala Glu Lys Val Ser Tyr Phe Phe  
145 150 155 160  
Arg Lys Pro Glu Val Ser Asp Ile Val Ile Phe Lys Ala Pro Pro Ile  
165 170 175  
Leu Val Glu His Gly Tyr Ser Cys Ala Asp Val Phe Ile Lys Arg Ile  
180 185 190  
Val Ala Ser Glu Gly Asp Trp Val Glu Val Cys Asp Gly Lys Leu Leu  
195 200 205  
Val Asn Asp Thr Val Gln Ala Glu Asp Phe Val Leu Glu Pro Ile Asp  
210 215 220  
Tyr Glu Met Glu Pro Met Phe Val Pro Glu Gly Tyr Val Phe Val Leu  
225 230 235 240  
Gly Asp Asn Arg Asn Lys Ser Phe Asp Ser His Asn Trp Gly Pro Leu  
245 250 255  
Pro Ile Lys Asn Ile Ile Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro  
260 265 270  
Ser Lys Val Ser Asp Ile Ile His His Glu Gln Val Ser Gln Lys Arg  
275 280 285  
Ala Val Asp Val Ser  
290

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1568761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val  
1 5 10 15  
Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe  
20 25 30  
Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser  
35 40 45  
Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys  
50 55 60  
Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp  
65 70 75 80  
Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe  
85 90 95  
Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro  
100 105 110  
Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Arg Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val |     |     |
| 130                                                             | 135 | 140 |
| Ser Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly |     |     |
| 145                                                             | 150 | 155 |
| Tyr Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly |     |     |
| 165                                                             | 170 | 175 |
| Asp Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val |     |     |
| 180                                                             | 185 | 190 |
| Gln Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro |     |     |
| 195                                                             | 200 | 205 |
| Met Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn |     |     |
| 210                                                             | 215 | 220 |
| Lys Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile |     |     |
| 225                                                             | 230 | 235 |
| Ile Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp |     |     |
| 245                                                             | 250 | 255 |
| Ile Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser |     |     |
| 260                                                             | 265 | 270 |

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1568777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctcgttttga taaaaatctc tgaatctctc caagctctct tctcatcaac catggatcct  | 60   |
| tacaagtatc gtccagctag ttcttacaac tctcccttct tcaccaccaa ctctggtgct  | 120  |
| cctgtatgga acaacaactc ctccatgacc gttggaccca gaggtcctat ccttcttgag  | 180  |
| gattaccatc tcgttgagaa gotttgccaat ttcgacaggg aacggattcc agagcgtgtg | 240  |
| gttcatgcc aaggagccag tgctaaagggt ttcttttgagg tcaatcatga tatctctaac | 300  |
| ctcacttggt ctgactttct ccgagctccc ggtgttcaga ctctgtcat tgtccggttc   | 360  |
| tccaccgtta tccatgagcg tggaaagtccc gagaccttga gagaccctcg tggttttgca | 420  |
| gtcaagttct acaccagaga ggggaacttt gatcttggtg gaaacaactt tcctgttttc  | 480  |
| ttcatccgcg atgggatgaa gttccctgac atggtccaag ctcttaagcc gaacccaaaa  | 540  |
| tctcacatcc aagagaactg gagaatcctt gacttcttct cccaccacc tgaaagtttg   | 600  |
| aacatgttca ctttcctctt cgatgatatc ggtatcccac aagattacag gcacatggat  | 660  |
| ggttcagggt tcaacacata catggtgatc aacaaagctg gcaaagctca ctacgtgaag  | 720  |
| ttccattgga aaccaacttg tggagtcaag tctcttttg aagaagatgc aattcgtgtt   | 780  |
| ggaggaacca accacagtca tgcgactcaa gacttgatg actctattgc tgcgtgaaac   | 840  |
| taccctgaat ggaagctctt tatccaaatc attgatcctg ctgatgaaga caagttcgac  | 900  |
| tttgaccgcg tcgatgtaac caagacctgg cctgaagata tcttgctct ccaacctgtt   | 960  |
| ggacgtatgg tgttgaaaca gaacattgac aacttctttg cagagaatga gcaacttgcc  | 1020 |
| ttctgtcctg caattattgt tccagggata cactactcag acgacaagct gcttcaaacc  | 1080 |
| cgtgtcttct cctatgccga tactcagaga caccgtcttg gaccaaacta ccttcagcta  | 1140 |
| ccagGtcaat gctccaaaat gtgctcacca caacaaccac catgagggg              |      |

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1568778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Val | Leu | Ile | Lys | Ile | Ser | Glu | Ser | Leu | Gln | Ala | Leu | Phe | Ser | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Met | Asp | Pro | Tyr | Lys | Tyr | Arg | Pro | Ala | Ser | Ser | Tyr | Asn | Ser | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Phe | Thr | Thr | Asn | Ser | Gly | Ala | Pro | Val | Trp | Asn | Asn | Asn | Ser | Ser |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Met | Thr | Val | Gly | Pro | Arg | Gly | Pro | Ile | Leu | Leu | Glu | Asp | Tyr | His | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Glu | Lys | Leu | Ala | Asn | Phe | Asp | Arg | Glu | Arg | Ile | Pro | Glu | Arg | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Val | His | Ala | Arg | Gly | Ala | Ser | Ala | Lys | Gly | Phe | Phe | Glu | Val | Thr | His |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | Ile | Ser | Asn | Leu | Thr | Cys | Ala | Asp | Phe | Leu | Arg | Ala | Pro | Gly | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Thr | Pro | Val | Ile | Val | Arg | Phe | Ser | Thr | Val | Ile | His | Glu | Arg | Gly |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ser | Pro | Glu | Thr | Leu | Arg | Asp | Pro | Arg | Gly | Phe | Ala | Val | Lys | Phe | Tyr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Thr | Arg | Glu | Gly | Asn | Phe | Asp | Leu | Val | Gly | Asn | Asn | Phe | Pro | Val | Phe |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Phe | Ile | Arg | Asp | Gly | Met | Lys | Phe | Pro | Asp | Met | Val | His | Ala | Leu | Lys |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Pro | Asn | Pro | Lys | Ser | His | Ile | Gln | Glu | Asn | Trp | Arg | Ile | Leu | Asp | Phe |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Phe | Ser | His | His | Pro | Glu | Ser | Leu | Asn | Met | Phe | Thr | Phe | Leu | Phe | Asp |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Asp | Ile | Gly | Ile | Pro | Gln | Asp | Tyr | Arg | His | Met | Asp | Gly | Ser | Gly | Val |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asn | Thr | Tyr | Met | Leu | Ile | Asn | Lys | Ala | Gly | Lys | Ala | His | Tyr | Val | Lys |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Phe | His | Trp | Lys | Pro | Thr | Cys | Gly | Val | Lys | Ser | Leu | Leu | Glu | Glu | Asp |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Ile | Arg | Val | Gly | Gly | Thr | Asn | His | Ser | His | Ala | Thr | Gln | Asp | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Tyr | Asp | Ser | Ile | Ala | Ala | Gly | Asn | Tyr | Pro | Glu | Trp | Lys | Leu | Phe | Ile |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gln | Ile | Ile | Asp | Pro | Ala | Asp | Glu | Asp | Lys | Phe | Asp | Phe | Asp | Pro | Leu |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Asp | Val | Thr | Lys | Thr | Trp | Pro | Glu | Asp | Ile | Leu | Pro | Leu | Gln | Pro | Val |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gly | Arg | Met | Val | Leu | Asn | Lys | Asn | Ile | Asp | Asn | Phe | Phe | Ala | Glu | Asn |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Glu | Gln | Leu | Ala | Phe | Cys | Pro | Ala | Ile | Ile | Val | Pro | Gly | Ile | His | Tyr |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Ser | Asp | Asp | Lys | Leu | Leu | Gln | Thr | Arg | Val | Phe | Ser | Tyr | Ala | Asp | Thr |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Gln | Arg | His | Arg | Leu | Gly | Pro | Asn | Tyr | Leu | Gln | Leu | Pro | Gly | Gln | Cys |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Ser | Lys | Met | Cys | Ser | Pro | Gln | Gln | Pro | Pro |     |     |     |     |     |     |  |
| 385 |     |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1568779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Pro | Tyr | Lys | Tyr | Arg | Pro | Ala | Ser | Ser | Tyr | Asn | Ser | Pro | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Thr | Thr | Asn | Ser | Gly | Ala | Pro | Val | Trp | Asn | Asn | Asn | Ser | Ser | Met |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Val | Gly | Pro | Arg | Gly | Pro | Ile | Leu | Leu | Glu | Asp | Tyr | His | Leu | Val |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Lys | Leu | Ala | Asn | Phe | Asp | Arg | Glu | Arg | Ile | Pro | Glu | Arg | Val | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Ala | Arg | Gly | Ala | Ser | Ala | Lys | Gly | Phe | Phe | Glu | Val | Thr | His | Asp |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Ile | Ser | Asn | Leu | Thr | Cys | Ala | Asp | Phe | Leu | Arg | Ala | Pro | Gly | Val | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Thr | Pro | Val | Ile | Val | Arg | Phe | Ser | Thr | Val | Ile | His | Glu | Arg | Gly | Ser |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Glu | Thr | Leu | Arg | Asp | Pro | Arg | Gly | Phe | Ala | Val | Lys | Phe | Tyr | Thr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg | Glu | Gly | Asn | Phe | Asp | Leu | Val | Gly | Asn | Asn | Phe | Pro | Val | Phe | Phe |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Arg | Asp | Gly | Met | Lys | Phe | Pro | Asp | Met | Val | His | Ala | Leu | Lys | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Asn | Pro | Lys | Ser | His | Ile | Gln | Glu | Asn | Trp | Arg | Ile | Leu | Asp | Phe | Phe |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ser | His | His | Pro | Glu | Ser | Leu | Asn | Met | Phe | Thr | Phe | Leu | Phe | Asp | Asp |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ile | Gly | Ile | Pro | Gln | Asp | Tyr | Arg | His | Met | Asp | Gly | Ser | Gly | Val | Asn |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |
| Thr | Tyr | Met | Leu | Ile | Asn | Lys | Ala | Gly | Lys | Ala | His | Tyr | Val | Lys | Phe |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| His | Trp | Lys | Pro | Thr | Cys | Gly | Val | Lys | Ser | Leu | Leu | Glu | Glu | Asp | Ala |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ile | Arg | Val | Gly | Gly | Thr | Asn | His | Ser | His | Ala | Thr | Gln | Asp | Leu | Tyr |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Asp | Ser | Ile | Ala | Ala | Gly | Asn | Tyr | Pro | Glu | Trp | Lys | Leu | Phe | Ile | Gln |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ile | Ile | Asp | Pro | Ala | Asp | Glu | Asp | Lys | Phe | Asp | Phe | Asp | Pro | Leu | Asp |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |  |
| Val | Thr | Lys | Thr | Trp | Pro | Glu | Asp | Ile | Leu | Pro | Leu | Gln | Pro | Val | Gly |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Arg | Met | Val | Leu | Asn | Lys | Asn | Ile | Asp | Asn | Phe | Phe | Ala | Glu | Asn | Glu |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gln | Leu | Ala | Phe | Cys | Pro | Ala | Ile | Ile | Val | Pro | Gly | Ile | His | Tyr | Ser |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Asp | Asp | Lys | Leu | Leu | Gln | Thr | Arg | Val | Phe | Ser | Tyr | Ala | Asp | Thr | Gln |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Arg | His | Arg | Leu | Gly | Pro | Asn | Tyr | Leu | Gln | Leu | Pro | Gly | Gln | Cys | Ser |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Lys | Met | Cys | Ser | Pro | Gln | Gln | Pro | Pro |     |     |     |     |     |     |     |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..346  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Gly | Pro | Arg | Gly | Pro | Ile | Leu | Leu | Glu | Asp | Tyr | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Glu | Lys | Leu | Ala | Asn | Phe | Asp | Arg | Glu | Arg | Ile | Pro | Glu | Arg | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | His | Ala | Arg | Gly | Ala | Ser | Ala | Lys | Gly | Phe | Phe | Glu | Val | Thr | His |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Asp | Ile | Ser | Asn | Leu | Thr | Cys | Ala | Asp | Phe | Leu | Arg | Ala | Pro | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Thr | Pro | Val | Ile | Val | Arg | Phe | Ser | Thr | Val | Ile | His | Glu | Arg | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Pro | Glu | Thr | Leu | Arg | Asp | Pro | Arg | Gly | Phe | Ala | Val | Lys | Phe | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Arg | Glu | Gly | Asn | Phe | Asp | Leu | Val | Gly | Asn | Asn | Phe | Pro | Val | Phe |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Phe | Ile | Arg | Asp | Gly | Met | Lys | Phe | Pro | Asp | Met | Val | His | Ala | Leu | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Asn | Pro | Lys | Ser | His | Ile | Gln | Glu | Asn | Trp | Arg | Ile | Leu | Asp | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | His | His | Pro | Glu | Ser | Leu | Asn | Met | Phe | Thr | Phe | Leu | Phe | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Ile | Gly | Ile | Pro | Gln | Asp | Tyr | Arg | His | Met | Asp | Gly | Ser | Gly | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Thr | Tyr | Met | Leu | Ile | Asn | Lys | Ala | Gly | Lys | Ala | His | Tyr | Val | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | His | Trp | Lys | Pro | Thr | Cys | Gly | Val | Lys | Ser | Leu | Leu | Glu | Glu | Asp |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Ile | Arg | Val | Gly | Gly | Thr | Asn | His | Ser | His | Ala | Thr | Gln | Asp | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Asp | Ser | Ile | Ala | Ala | Gly | Asn | Tyr | Pro | Glu | Trp | Lys | Leu | Phe | Ile |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Ile | Ile | Asp | Pro | Ala | Asp | Glu | Asp | Lys | Phe | Asp | Phe | Asp | Pro | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Val | Thr | Lys | Thr | Trp | Pro | Glu | Asp | Ile | Leu | Pro | Leu | Gln | Pro | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Arg | Met | Val | Leu | Asn | Lys | Asn | Ile | Asp | Asn | Phe | Phe | Ala | Glu | Asn |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Glu | Gln | Leu | Ala | Phe | Cys | Pro | Ala | Ile | Ile | Val | Pro | Gly | Ile | His | Tyr |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ser | Asp | Asp | Lys | Leu | Leu | Gln | Thr | Arg | Val | Phe | Ser | Tyr | Ala | Asp | Thr |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Arg | His | Arg | Leu | Gly | Pro | Asn | Tyr | Leu | Gln | Leu | Pro | Gly | Gln | Cys |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ser | Lys | Met | Cys | Ser | Pro | Gln | Gln | Pro | Pro |     |     |     |     |     |     |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1466  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

tgtagttagg tcaatggaac agacaaagga tgattctgat tttgaggatg attttgaaac

gaagaagatg gagactgata catcagctca agaggcaagg aatggtaaag acatacaagg 120  
gattcagtgagg gaagggttta agtatactac agacgagttt cgtgacacta ggttgaaaca 180  
ttatgataaac tttgttaata tcttaaggcc tagctctcga gaaaagcttg ataaggaaca 240  
tgggcaagta gttgagaaaag gaaagaactt ttatgacttc caattcaata caaggcttgt 300  
cacttccact attgtgcatt ttcagttggg agtactgtct gagcagccag cagcataacg 360  
atatggcttc ggaatttggg atgggagaca tctaagcatg atgtatatct aatgcaaaat 420  
tattcactca tgcactggtc atctctactc cagagaggga aagaagtagt taatgtcgcc 480  
agatcagtta cccccactca gaaactacct ggattgtttt ctgagccact ctctagggtg 540  
caagtttagca gcatggcagt caaagaaaat ctgatccttt taggaggggt cgacggggag 600  
cttctctgca agtggtgtaa tcagocctggg gttgcttttt gcacaagatt atcaacggaa 660  
gataatgccca tcacacacag ttgatataata ccgagaccca agtggctccc ttaggcttat 720  
aaccgcaaat aacgactgta aaatccgggt attcgatgct cagagcttta cagctgtcag 780  
tgaattttact tttgattggg ctgtcaataa tacctcagtt agcccggatg ggaagctact 840  
cgctgtactc ggggacagta cagaatgctt gatctctgat tcccattctg aaaaagtatt 900  
ttcaagcctc agaggccaca aagactactc atttgcattc gcttggcacc cgaatggctc 960  
aatcttagca acgggaaacc aagacacgac atgccgtctc tgggacattc gtaacccgctc 1020  
agaatcattc gctgtcctga aaggaaacat gggagccatc agaggactga agttcacacc 1080  
agaagggcggt tttcttgcaa tggctgagcc tgcagacttt gttcacatct tgcacacgca 1140  
gtccgggttt ctacagtccc aagagattga tctgtttgga gaaatagccg ggatctcctt 1200  
cagccccgac tcagaggcac tatatgttgg ggtcgcagac cgcacttatg gaagcttgat 1260  
ggagtataag aggagtaagg ataactcata tatggactcc ttttactgag aaaaggtaaa 1320  
tggaaagttaa aaagcatcta atatgttgc acaagttggg ttttacccta ttagtgtgta 1380  
tatgtagaca gaattggtag tttctttggg tatgtatggt gtatgtaacc cataatatat 1440  
cttgccaaac ttttaagtatg ttttgt

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

Val Val Arg Ser Met Glu Gln Thr Lys Asp Asp Ser Asp Phe Glu Asp  
1 5 10 15  
Asp Phe Glu Thr Lys Lys Met Glu Thr Asp Thr Ser Ala Gln Glu Ala  
20 25 30  
Arg Asn Gly Lys Asp Ile Gln Gly Ile Gln Trp Glu Gly Phe Lys Tyr  
35 40 45  
Thr Thr Asp Glu Phe Arg Asp Thr Arg Leu Lys His Tyr Asp Asn Phe  
50 55 60  
Val Asn Ile Leu Arg Pro Ser Ser Arg Glu Lys Leu Asp Lys Glu His  
65 70 75 80  
Gly Gln Val Val Glu Lys Gly Lys Asn Phe Tyr Asp Phe Gln Phe Asn  
85 90 95  
Thr Arg Leu Val Thr Ser Thr Ile Val His Phe Gln Leu Gly Val Leu  
100 105 110  
Ser Glu Gln Pro Ala Ala  
115

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1568783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Thr | Lys | Asp | Asp | Ser | Asp | Phe | Glu | Asp | Asp | Phe | Glu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Met | Glu | Thr | Asp | Thr | Ser | Ala | Gln | Glu | Ala | Arg | Asn | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ile | Gln | Gly | Ile | Gln | Trp | Glu | Gly | Phe | Lys | Tyr | Thr | Thr | Asp | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Arg | Asp | Thr | Arg | Leu | Lys | His | Tyr | Asp | Asn | Phe | Val | Asn | Ile | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Pro | Ser | Ser | Arg | Glu | Lys | Leu | Asp | Lys | Glu | His | Gly | Gln | Val | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Lys | Gly | Lys | Asn | Phe | Tyr | Asp | Phe | Gln | Phe | Asn | Thr | Arg | Leu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Ser | Thr | Ile | Val | His | Phe | Gln | Leu | Gly | Val | Leu | Ser | Glu | Gln | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1568784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ser | His | Thr | Val | Asp | Ile | Tyr | Arg | Asp | Pro | Ser | Gly | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Leu | Ile | Thr | Ala | Asn | Asn | Asp | Cys | Lys | Ile | Arg | Val | Phe | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ser | Phe | Thr | Arg | Val | Ser | Glu | Phe | Thr | Phe | Asp | Trp | Ser | Val | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Thr | Ser | Val | Ser | Pro | Asp | Gly | Lys | Leu | Leu | Ala | Val | Leu | Gly | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Glu | Cys | Leu | Ile | Ser | Asp | Ser | His | Ser | Glu | Lys | Val | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Leu | Arg | Gly | His | Lys | Asp | Tyr | Ser | Phe | Ala | Ser | Ala | Trp | His | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gly | Leu | Ile | Leu | Ala | Thr | Gly | Asn | Gln | Asp | Thr | Thr | Cys | Arg | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Asp | Ile | Arg | Asn | Pro | Ser | Glu | Ser | Phe | Ala | Val | Leu | Lys | Gly | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Gly | Ala | Ile | Arg | Gly | Leu | Lys | Phe | Thr | Pro | Glu | Gly | Arg | Phe | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Met | Ala | Glu | Pro | Ala | Asp | Phe | Val | His | Ile | Phe | Asp | Thr | Gln | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Phe | Leu | Gln | Ser | Gln | Glu | Ile | Asp | Leu | Phe | Gly | Glu | Ile | Ala | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ser | Phe | Ser | Pro | Asp | Ser | Glu | Ala | Leu | Tyr | Val | Gly | Val | Ala | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Thr | Tyr | Gly | Ser | Leu | Met | Glu | Tyr | Lys | Arg | Ser | Lys | Asp | Asn | His |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Met | Asp | Ser | Phe | Tyr |     |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568803  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| ctatccgatt | cgtctctctc | acgccctcac | gtttctccac  | ctcatcctca | aactaaccac | 60   |
| aagacctctt | ttttagagta | accaatcaca | gagagataga  | gagagagaac | agagtcaatg | 120  |
| tcaatggcgt | ctatagcttc | ttcttcttcc | accaccctac  | tctcttcctc | taggggtctt | 180  |
| cttccttcaa | agtcttctct | tttatctcct | accgtctctg  | tccccagaac | cctacactct | 240  |
| tcctcggcat | catcctcttc | tctctgttcc | gggtttctcc  | gtctcgggtc | cctcaccacc | 300  |
| agccgctccg | cctcacgccg | gaacttcgcc | gtcaaggctc  | aggctgatga | tttaccactg | 360  |
| gtcggtaata | aggcgctga  | ttttgaagca | gaggcagttt  | ttgatcaaga | gttcataaag | 420  |
| gtgaagctct | ctgagtacat | tggcaaaaag | tatgttatcc  | tattcttcta | ccctttggac | 480  |
| ttcacttttg | tctgccccac | tgagattact | gccttcagtg  | accgttatga | agaatttgag | 540  |
| aagctaaaca | ccgaagtatt | aggggtctct | gtcgacagtg  | tggtctcgca | tctcgcgtgg | 600  |
| gtccaaacag | acagaaagtc | gggagggtct | ggtgatctga  | attatcctct | tggttcggat | 660  |
| atcactaaat | ccatttcaaa | atcgtttggg | gtgctcatcc  | ctgatcaggg | cattgcactg | 720  |
| agagggcttt | tcatcataga | caaggaagga | gtcattcagc  | attccaccat | caacaacctc | 780  |
| ggtattggcc | gaagtgttga | tgagacaatg | agaaccctcc  | aggcattaca | gtatgttcaa | 840  |
| gaaaaccggg | atgaagtgtg | Ccctgcggga | tgggaagccag | gggagaaatc | aatgaaacct | 900  |
| gaccccaagc | tcagcaaaga | atacttttca | gctatctaga  | ggctaagatt | gaacacatgt | 960  |
| ttgggtgaaa | ttagcaatca | gagttgtttt | attcatcttt  | tcaaagttgg | agcagagttg | 1020 |
| ttatttttag | ccaaagaacc | tttgtatcta | tctcatcttt  | ctcctgtttc | tgctatgtga | 1080 |
| ttctccttaa | attgaatcaa | aaataaagaa | atccttcttt  | tcttttgcc  |            |      |

(2) INFORMATION FOR SEQ ID NO:1041:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..273  
(D) OTHER INFORMATION: / Ceres Seq. ID 1568804  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Ala | Ser | Ile | Ala | Ser | Ser | Ser | Ser | Thr | Thr | Leu | Leu | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ser | Arg | Val | Leu | Leu | Pro | Ser | Lys | Ser | Ser | Leu | Leu | Ser | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Val | Pro | Arg | Thr | Leu | His | Ser | Ser | Ser | Ala | Ser | Ser | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Cys | Ser | Gly | Phe | Ser | Ser | Leu | Gly | Ser | Leu | Thr | Thr | Ser | Arg | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ala | Ser | Arg | Arg | Asn | Phe | Ala | Val | Lys | Ala | Gln | Ala | Asp | Asp | Leu | Pro |
|     |     |     |     |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Leu | Val | Gly | Asn | Lys | Ala | Pro | Asp | Phe | Glu | Ala | Glu | Ala | Val | Phe | Asp |
|     |     |     |     |     |     |     | 85  |     |     | 90  |     |     |     | 95  |     |
| Gln | Glu | Phe | Ile | Lys | Val | Lys | Leu | Ser | Glu | Tyr | Ile | Gly | Lys | Lys | Tyr |
|     |     |     |     |     |     |     | 100 |     |     | 105 |     |     | 110 |     |     |
| Val | Ile | Leu | Phe | Phe | Tyr | Pro | Leu | Asp | Phe | Thr | Phe | Val | Cys | Pro | Thr |
|     |     |     |     |     |     |     | 115 |     |     | 120 |     |     | 125 |     |     |
| Glu | Ile | Thr | Ala | Phe | Ser | Asp | Arg | Tyr | Glu | Glu | Phe | Glu | Lys | Leu | Asn |
|     |     |     |     |     |     |     | 130 |     |     |     |     |     | 140 |     |     |
| Thr | Glu | Val | Leu | Gly | Val | Ser | Val | Asp | Ser | Val | Phe | Ser | His | Leu | Ala |
|     |     |     |     |     |     |     | 145 |     |     |     |     |     | 150 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 155 |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Val | Gln | Thr | Asp | Arg | Lys | Ser | Gly | Gly | Leu | Gly | Asp | Leu | Asn | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Leu | Val | Ser | Asp | Ile | Thr | Lys | Ser | Ile | Ser | Lys | Ser | Phe | Gly | Val |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Leu | Ile | Pro | Asp | Gln | Gly | Ile | Ala | Leu | Arg | Gly | Leu | Phe | Ile | Ile | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Glu | Gly | Val | Ile | Gln | His | Ser | Thr | Ile | Asn | Asn | Leu | Gly | Ile | Gly |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Arg | Ser | Val | Asp | Glu | Thr | Met | Arg | Thr | Leu | Gln | Ala | Leu | Gln | Tyr | Val |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Glu | Asn | Pro | Asp | Glu | Val | Cys | Pro | Ala | Gly | Trp | Lys | Pro | Gly | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Ser | Met | Lys | Pro | Asp | Pro | Lys | Leu | Ser | Lys | Glu | Tyr | Phe | Ser | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ile | Ala | Ser | Ser | Ser | Ser | Thr | Thr | Leu | Leu | Ser | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Leu | Leu | Pro | Ser | Lys | Ser | Ser | Leu | Leu | Ser | Pro | Thr | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Pro | Arg | Thr | Leu | His | Ser | Ser | Ser | Ala | Ser | Ser | Ser | Ser | Leu | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Phe | Ser | Ser | Leu | Gly | Ser | Leu | Thr | Thr | Ser | Arg | Ser | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Asn | Phe | Ala | Val | Lys | Ala | Gln | Ala | Asp | Asp | Leu | Pro | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Asn | Lys | Ala | Pro | Asp | Phe | Glu | Ala | Glu | Ala | Val | Phe | Asp | Gln | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ile | Lys | Val | Lys | Leu | Ser | Glu | Tyr | Ile | Gly | Lys | Lys | Tyr | Val | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Phe | Phe | Tyr | Pro | Leu | Asp | Phe | Thr | Phe | Val | Cys | Pro | Thr | Glu | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Ala | Phe | Ser | Asp | Arg | Tyr | Glu | Glu | Phe | Glu | Lys | Leu | Asn | Thr | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Leu | Gly | Val | Ser | Val | Asp | Ser | Val | Phe | Ser | His | Leu | Ala | Trp | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Thr | Asp | Arg | Lys | Ser | Gly | Gly | Leu | Gly | Asp | Leu | Asn | Tyr | Pro | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ser | Asp | Ile | Thr | Lys | Ser | Ile | Ser | Lys | Ser | Phe | Gly | Val | Leu | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Asp | Gln | Gly | Ile | Ala | Leu | Arg | Gly | Leu | Phe | Ile | Ile | Asp | Lys | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Val | Ile | Gln | His | Ser | Thr | Ile | Asn | Asn | Leu | Gly | Ile | Gly | Arg | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Asp | Glu | Thr | Met | Arg | Thr | Leu | Gln | Ala | Leu | Gln | Tyr | Val | Gln | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Pro | Asp | Glu | Val | Cys | Pro | Ala | Gly | Trp | Lys | Pro | Gly | Glu | Lys | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Lys | Pro | Asp | Pro | Lys | Leu | Ser | Lys | Glu | Tyr | Phe | Ser | Ala | Ile |     |

- 260 265 270
- (2) INFORMATION FOR SEQ ID NO:1043:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
- (A) NAME/KEY: -
- (B) LOCATION: 1..1510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568826
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

```
aattattttt cccatttctt tctactatctc tctccctaga aaattgccag aagaagaagg 60
ttctccaatt caaaaaaata gaaactcgct accattcatt tcaaaaaatt tcttggttaag 120
ttacgttttt ttcttttttt ttgcttcttt cgttcttatt gtcttagaag acaaaagaga 180
ctagagagga tagaaaaatg gaagcttcaa gcacaagaag cgagaagaag aagaagaaga 240
agacgataca gagagaaaac accgatactc aaaagaaaaa aaagctaccc agtggttggt 300
tttactttaa gaaatctctc ccttgcaaat ctgatgtctc cgatgtccac attccgagat 360
ccaaaaaaga gctagctccc atatccacta agagaacaac aacctcctcc ggccggcggg 420
tcggcggcag gtccggttgt tcaagatcca tagccaatct taaagacgta atccatggaa 480
accaacggca tttagagaag ccgctttgct ctagccctcg ttctatagga agcagcgagt 540
ttctcaatcc cattactcac gatgtaatct ttagcaactc cacctgcgag ctcaagatca 600
ccgccgccgg agcaacagaa ttcgctcgga atcttagacc agggacgcgc gtcaattact 660
cttcttcacg ccgtagccaa acttcgagaa aggcttcttc tttagataga gaaggattag 720
ggtttcacca gagcagaaga gagaatgata gagaagccgc cattaacgga gacaattcct 780
ctgtttcttg ccataaatgc ggcgagaaat ttagcaactc cgaagctgca gaagctcatc 840
atctaaccaa acacgccgtg actgagctaa tgggaaggaga ctcgctcgagg agaatagtGg 900
agataatctg cagaacaagc tgggttaaaga cagagaatca aggagggaga atcgatcgga 960
ttttgaaagt acacaacatg caaaaaacct tagcgagatt cgaagaatac agagatacag 1020
tgaagatcag agcaagcaag ttacaaaaga aacatccgag atgtatcgcc gacggaaacg 1080
agcttctcag gtttcacggc accactgtgg cttgcgcttt ggggataaac gggtcgacga 1140
gtctgtgttc gtcggaagaa tgtgtcggtt gtcggattat acgaaatggg ttctcggcga 1200
aacgggagat gaataacgga attggggttt ttactgcgtc gacgagttag agggcggttg 1260
agtctattgt gattggagat ggtggtggtg gtgatcgga ggcgttgatt gtgtgtcgag 1320
tgattgccgg gagggttcat cggccggtgg agaattgtag ggagatgggt gggttgttga 1380
gtggggttga ttcattggct ggtaaagttg gggtgtacac aaatgttgag gagctctatt 1440
tgctcaattc tcgagctttg cttcctgttt tgtgctaata tgcaaacctt aaatcaaact 1500
tttgaggtcg
```

- (2) INFORMATION FOR SEQ ID NO:1044:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568827
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

```
Met Glu Ala Ser Ser Thr Arg Ser Glu Lys Lys Lys Lys Lys Lys Thr
1 5 10 15
Ile Gln Arg Glu Asn Thr Asp Thr Gln Lys Lys Lys Lys Leu Pro Ser
20 25 30
Val Trp Phe Ser Leu Lys Lys Ser Leu Pro Cys Lys Ser Asp Val Ser
35 40 45
Asp Val His Ile Pro Arg Ser Lys Lys Glu Leu Ala Pro Ile Ser Thr
50 55 60
Lys Arg Thr Thr Thr Ser Ser Gly Gly Gly Val Gly Gly Arg Ser Gly
65 70 75 80
```



Cys Ser Arg Ser Ile Ala Asn Leu Lys Asp Val Ile His Gly Asn Gln  
85 90 95  
Arg His Leu Glu Lys Pro Leu Cys Ser Ser Pro Arg Ser Ile Gly Ser  
100 105 110  
Ser Glu Phe Leu Asn Pro Ile Thr His Asp Val Ile Phe Ser Asn Ser  
115 120 125  
Thr Cys Glu Leu Lys Ile Thr Ala Ala Gly Ala Thr Glu Phe Val Gly  
130 135 140  
Asn Leu Arg Pro Gly Thr Pro Val Asn Tyr Ser Ser Ser Arg Arg Ser  
145 150 155 160  
Gln Thr Ser Arg Lys Ala Ser Ser Leu Asp Arg Glu Gly Leu Gly Phe  
165 170 175  
His Gln Ser Arg Arg Glu Asn Asp Arg Glu Ala Ala Ile Asn Gly Asp  
180 185 190  
Asn Ser Ser Val Ser Cys His Lys Cys Gly Glu Lys Phe Ser Lys Leu  
195 200 205  
Glu Ala Ala Glu Ala His His Leu Thr Lys His Ala Val Thr Glu Leu  
210 215 220  
Met Glu Gly Asp Ser Ser Arg Arg Ile Val Glu Ile Ile Cys Arg Thr  
225 230 235 240  
Ser Trp Leu Lys Thr Glu Asn Gln Gly Gly Arg Ile Asp Arg Ile Leu  
245 250 255  
Lys Val His Asn Met Gln Lys Thr Leu Ala Arg Phe Glu Glu Tyr Arg  
260 265 270  
Asp Thr Val Lys Ile Arg Ala Ser Lys Leu Gln Lys Lys His Pro Arg  
275 280 285  
Cys Ile Ala Asp Gly Asn Glu Leu Leu Arg Phe His Gly Thr Thr Val  
290 295 300  
Ala Cys Ala Leu Gly Ile Asn Gly Ser Thr Ser Leu Cys Ser Ser Glu  
305 310 315 320  
Lys Cys Cys Val Cys Arg Ile Ile Arg Asn Gly Phe Ser Ala Lys Arg  
325 330 335  
Glu Met Asn Asn Gly Ile Gly Val Phe Thr Ala Ser Thr Ser Glu Arg  
340 345 350  
Ala Phe Glu Ser Ile Val Ile Gly Asp Gly Gly Gly Gly Asp Arg Lys  
355 360 365  
Ala Leu Ile Val Cys Arg Val Ile Ala Gly Arg Val His Arg Pro Val  
370 375 380  
Glu Asn Val Glu Glu Met Gly Gly Leu Leu Ser Gly Phe Asp Ser Leu  
385 390 395 400  
Ala Gly Lys Val Gly Leu Tyr Thr Asn Val Glu Glu Leu Tyr Leu Leu  
405 410 415  
Asn Ser Arg Ala Leu Leu Pro Val Leu Cys  
420 425

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1088
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaagathct ataatagtag agatcaaaga cctgagcaaa aactgaaaaa aaaaaaaaaa | 60  |
| aaaaaagact tctcctcaaa aatggcggtt acactaggtg gaagagctcg tcgtctagtc | 120 |
| tctgcaacat caattcatca aaatggttgc ttacacaaac tgcaacaaat tggatcggat | 180 |
| cggtttcagc ttggtgaagc aaaagcaata agattactac ccaggagaac aaacatggtt | 240 |
| caagaattag gaatcaggga agaatttatg gatccaaaca gagaaacaga gacaagttat | 300 |

```
gattttcttg atgaaatgag acacagattt ctgaaattca agagacaaaa gtatctaccg 360
gagatagaaa agtttaaagc tttggccata gctcaatcac caaaggtaat ggtgatagga 420
tgtgcagatt caagggtatg tccatcttat gtactaggat ttcaacctgg tgaagctttt 480
actatccgaa atgtcgccaa tctcgttacc ccggttcaga atggaccaac agaaaccaac 540
tcggctcttg agtttgcggg caccactctt cagggttgaga acattatagt tatgggtcat 600
agcaattgtg gaggaattgc agcacttatg agtcatcaaa accaccaagg gcaacactct 660
agtttagtag aaagggtggg tatgaatggg aaagccgcta agttaagaac acaattagct 720
tcatcacatt tatcctttga tgaacaatgc agaaactgtg agaaggaatc tataaaggat 780
tctgtgatga atttgataac ttattcatgg ataagagata gagtaaagag aggtgaagtc 840
aagattcatg gatgttatta caatttgtca gattgtagtc ttgagaagtg gagattaagt 900
tcagacaaga ctaactatgg attctatatt tcagacagag agatatggag ttgagtaaat 960
attgaacaat cctcatttct aatattcaga tgtatctttg tacatatgaa atgatattta 1020
cacaattgga aaaaaagaaa gaaaaaaaag taatattgta ataacggaat aaaaggtgaa 1080
ttggtYcc
```

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1568860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

```
Lys Arg Xaa Tyr Asn Ser Arg Asp Gln Arg Pro Glu Gln Lys Leu Lys
1 5 10
Lys Lys Lys Lys Lys Lys Asp Phe Ser Ser Lys Met Ala Phe Thr Leu
20 25 30
Gly Gly Arg Ala Arg Arg Leu Val Ser Ala Thr Ser Ile His Gln Asn
35 40 45
Gly Cys Leu His Lys Leu Gln Gln Ile Gly Ser Asp Arg Phe Gln Leu
50 55 60
Gly Glu Ala Lys Ala Ile Arg Leu Leu Pro Arg Arg Thr Asn Met Val
65 70 75 80
Gln Glu Leu Gly Ile Arg Glu Glu Phe Met Asp Pro Asn Arg Glu Thr
85 90 95
Glu Thr Ser Tyr Asp Phe Leu Asp Glu Met Arg His Arg Phe Leu Lys
100 105 110
Phe Lys Arg Gln Lys Tyr Leu Pro Glu Ile Glu Lys Phe Lys Ala Leu
115 120 125
Ala Ile Ala Gln Ser Pro Lys Val Met Val Ile Gly Cys Ala Asp Ser
130 135 140
Arg Val Cys Pro Ser Tyr Val Leu Gly Phe Gln Pro Gly Glu Ala Phe
145 150 155 160
Thr Ile Arg Asn Val Ala Asn Leu Val Thr Pro Val Gln Asn Gly Pro
165 170 175
Thr Glu Thr Asn Ser Ala Leu Glu Phe Ala Val Thr Thr Leu Gln Val
180 185 190
Glu Asn Ile Ile Val Met Gly His Ser Asn Cys Gly Gly Ile Ala Ala
195 200 205
Leu Met Ser His Gln Asn His Gln Gly Gln His Ser Ser Leu Val Glu
210 215 220
Arg Trp Val Met Asn Gly Lys Ala Ala Lys Leu Arg Thr Gln Leu Ala
225 230 235 240
Ser Ser His Leu Ser Phe Asp Glu Gln Cys Arg Asn Cys Glu Lys Glu
245 250 255
Ser Ile Lys Asp Ser Val Met Asn Leu Ile Thr Tyr Ser Trp Ile Arg
260 265 270
Asp Arg Val Lys Arg Gly Glu Val Lys Ile His Gly Cys Tyr Tyr Asn
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 275                                                             | 280 | 285 |
| Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu Ser Ser Asp Lys Thr |     |     |
| 290                                                             | 295 | 300 |
| Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile Trp Ser             |     |     |
| 305                                                             | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1568861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Thr | Leu | Gly | Gly | Arg | Ala | Arg | Arg | Leu | Val | Ser | Ala | Thr |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Ser | Ile | His | Gln | Asn | Gly | Cys | Leu | His | Lys | Leu | Gln | Gln | Ile | Gly | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asp | Arg | Phe | Gln | Leu | Gly | Glu | Ala | Lys | Ala | Ile | Arg | Leu | Leu | Pro | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Arg | Thr | Asn | Met | Val | Gln | Glu | Leu | Gly | Ile | Arg | Glu | Glu | Phe | Met | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Pro | Asn | Arg | Glu | Thr | Glu | Thr | Ser | Tyr | Asp | Phe | Leu | Asp | Glu | Met | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Arg | Phe | Leu | Lys | Phe | Lys | Arg | Gln | Lys | Tyr | Leu | Pro | Glu | Ile | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Phe | Lys | Ala | Leu | Ala | Ile | Ala | Gln | Ser | Pro | Lys | Val | Met | Val | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Cys | Ala | Asp | Ser | Arg | Val | Cys | Pro | Ser | Tyr | Val | Leu | Gly | Phe | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gly | Glu | Ala | Phe | Thr | Ile | Arg | Asn | Val | Ala | Asn | Leu | Val | Thr | Pro |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Gln | Asn | Gly | Pro | Thr | Glu | Thr | Asn | Ser | Ala | Leu | Glu | Phe | Ala | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Thr | Leu | Gln | Val | Glu | Asn | Ile | Ile | Val | Met | Gly | His | Ser | Asn | Cys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Gly | Ile | Ala | Ala | Leu | Met | Ser | His | Gln | Asn | His | Gln | Gly | Gln | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Leu | Val | Glu | Arg | Trp | Val | Met | Asn | Gly | Lys | Ala | Ala | Lys | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Thr | Gln | Leu | Ala | Ser | Ser | His | Leu | Ser | Phe | Asp | Glu | Gln | Cys | Arg |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Asn | Cys | Glu | Lys | Glu | Ser | Ile | Lys | Asp | Ser | Val | Met | Asn | Leu | Ile | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Tyr | Ser | Trp | Ile | Arg | Asp | Arg | Val | Lys | Arg | Gly | Glu | Val | Lys | Ile | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Cys | Tyr | Tyr | Asn | Leu | Ser | Asp | Cys | Ser | Leu | Glu | Lys | Trp | Arg | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ser | Asp | Lys | Thr | Asn | Tyr | Gly | Phe | Tyr | Ile | Ser | Asp | Arg | Glu | Ile |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Trp | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1568862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

Met Val Gln Glu Leu Gly Ile Arg Glu Glu Phe Met Asp Pro Asn Arg  
1 5 10 15  
Glu Thr Glu Thr Ser Tyr Asp Phe Leu Asp Glu Met Arg His Arg Phe  
20 25 30  
Leu Lys Phe Lys Arg Gln Lys Tyr Leu Pro Glu Ile Glu Lys Phe Lys  
35 40 45  
Ala Leu Ala Ile Ala Gln Ser Pro Lys Val Met Val Ile Gly Cys Ala  
50 55 60  
Asp Ser Arg Val Cys Pro Ser Tyr Val Leu Gly Phe Gln Pro Gly Glu  
65 70 75 80  
Ala Phe Thr Ile Arg Asn Val Ala Asn Leu Val Thr Pro Val Gln Asn  
85 90 95  
Gly Pro Thr Glu Thr Asn Ser Ala Leu Glu Phe Ala Val Thr Thr Leu  
100 105 110  
Gln Val Glu Asn Ile Ile Val Met Gly His Ser Asn Cys Gly Gly Ile  
115 120 125  
Ala Ala Leu Met Ser His Gln Asn His Gln Gly Gln His Ser Ser Leu  
130 135 140  
Val Glu Arg Trp Val Met Asn Gly Lys Ala Ala Lys Leu Arg Thr Gln  
145 150 155 160  
Leu Ala Ser Ser His Leu Ser Phe Asp Glu Gln Cys Arg Asn Cys Glu  
165 170 175  
Lys Glu Ser Ile Lys Asp Ser Val Met Asn Leu Ile Thr Tyr Ser Trp  
180 185 190  
Ile Arg Asp Arg Val Lys Arg Gly Glu Val Lys Ile His Gly Cys Tyr  
195 200 205  
Tyr Asn Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu Ser Ser Asp  
210 215 220  
Lys Thr Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile Trp Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1568863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

acaatctgac caattcaatg aaggcaattg gtgttgacat attgactgga tttggcagtg 60  
ttctgggtcc acaaaagggt aaatatggga aggacaatat tattactgca aaagatataa 120  
tcattgccac tggatctgtg ccgtttgtcc cttaaaggaaat tgaagttgat ggaaagactg 180  
tgatcaccag tgaccatgct ttgaaattag agtctgtccc tgagtggatt gcaattgtag 240  
gaagtggtta tattggtctt gagttcagtg atgtttacac agctcttgga agtgaggtaa 300  
cttttataga agcactggat cagctaatagc ctggatttga tcctgagatc agtaagctag 360  
ctcagagggt tttgataaat ccaagaaaga ttgactatca tactggagtc tttgcaagca 420  
aaattactcc ggcaagggt gggaaccag ttctgattga gcttattgat gccaaaacca 480  
aggaacctaa ggatactttg gaggtagatg ctgctcttat tgctactggg agagctccat 540  
tcaccaatgg acttggcttg gaaaatgtca atgttgtgac gcagagaggt ttcataccag 600  
ttgatgagcg aatgcgtgtg atcgatggaa aggggactct ggttccgaac ttgtactgca 660  
ttggtgatgc caatggtaaa ttgatgcttg cacatgcagc cagtgcccaa ggaatttctg 720  
tggtcgagca agtcagcggc agagatcatg tgcttaatac tcttagcatc ccagctgctt 780

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| gctttactca | tcctgAaaat | cagcatgggtg | ggattaacag  | agcctcaagc  | aaaagaaaaa  | 840  |
| ggcgagaagg | aaggatttaa | agttagtgtt  | gtcaagacaa  | gtttcaaggc  | taacacaaaag | 900  |
| gccctagctg | aaaatgaagg | agaaggaata  | gctaagatga  | tataccgacc  | tgacaacggt  | 960  |
| gaaatcttag | gagttcatat | atttggactg  | catgcagctg  | accttatcca  | tgaagcttct  | 1020 |
| aatgcgattg | ctctaggaac | gcgtattcag  | gacataaaaat | tggcagttca  | tgacatcca   | 1080 |
| acactctctg | aggtcctcga | cgaactgttc  | aaagcagcca  | aggttgaaaag | tcattgctacg | 1140 |
| acaaggacag | taagtgaaaa | agtggttgta  | taataagaaa  | ccaaaaactt  | attgggggtgg | 1200 |
| ggagaaacat | cttgaagaaa | gaaaatttgt  | gattgtactt  | tagggagatg  | caaagataaa  | 1260 |
| gctaaacacg | aaccaggaag | atcgaaaagg  | aagaagaaga  | ggaggagatg  | atgagaaaaca | 1320 |
| accttccgta | agtaaagact | tgaaagatat  | atctacaagg  | ccttcttctt  | tctttgagaa  | 1380 |
| tatttctgtt | ggagtcttgt | ctctgctttc  | acgtatattt  | gtttaattgt  | tccatgggtt  | 1440 |
| caattagtgg | agattgtggt | tttggttatt  | gtatgtttgt  | ttgatgtgaa  | cgattttgga  | 1500 |
| tgattcttct | ctttttacta | gtaaaatcac  | ttgtctgtcc  |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1568864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Thr | Asn | Ser | Met | Lys | Ala | Ile | Gly | Val | Asp | Ile | Leu | Thr | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gly | Ser | Val | Leu | Gly | Pro | Gln | Lys | Val | Lys | Tyr | Gly | Lys | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Thr | Ala | Lys | Asp | Ile | Ile | Ile | Ala | Thr | Gly | Ser | Val | Pro | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Pro | Lys | Gly | Ile | Glu | Val | Asp | Gly | Lys | Thr | Val | Ile | Thr | Ser | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| His | Ala | Leu | Lys | Leu | Glu | Ser | Val | Pro | Glu | Trp | Ile | Ala | Ile | Val | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Tyr | Ile | Gly | Leu | Glu | Phe | Ser | Asp | Val | Tyr | Thr | Ala | Leu | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Glu | Val | Thr | Phe | Ile | Glu | Ala | Leu | Asp | Gln | Leu | Met | Pro | Gly | Phe |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Pro | Glu | Ile | Ser | Lys | Leu | Ala | Gln | Arg | Val | Leu | Ile | Asn | Pro | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Ile | Asp | Tyr | His | Thr | Gly | Val | Phe | Ala | Ser | Lys | Ile | Thr | Pro | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Arg | Asp | Gly | Lys | Pro | Val | Leu | Ile | Glu | Leu | Ile | Asp | Ala | Lys | Thr | Lys |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Glu | Pro | Lys | Asp | Thr | Leu | Glu | Val | Asp | Ala | Ala | Leu | Ile | Ala | Thr | Gly |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Ala | Pro | Phe | Thr | Asn | Gly | Leu | Gly | Leu | Glu | Asn | Val | Asn | Val | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Gln | Arg | Gly | Phe | Ile | Pro | Val | Asp | Glu | Arg | Met | Arg | Val | Ile | Asp |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     |     | 205 |     |     |
| Gly | Lys | Gly | Thr | Leu | Val | Pro | Asn | Leu | Tyr | Cys | Ile | Gly | Asp | Ala | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Gly | Lys | Leu | Met | Leu | Ala | His | Ala | Ala | Ser | Ala | Gln | Gly | Ile | Ser | Val |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Glu | Gln | Val | Ser | Gly | Arg | Asp | His | Val | Leu | Asn | His | Leu | Ser | Ile |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Pro | Ala | Ala | Cys | Phe | Thr | His | Pro | Glu | Asn | Gln | His | Gly | Gly | Ile | Asn |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Ala | Ser | Ser | Lys | Arg | Lys | Arg | Arg | Glu | Gly | Arg | Ile |     |     |     |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1568865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

Met Lys Ala Ile Gly Val Asp Ile Leu Thr Gly Phe Gly Ser Val Leu  
1 5 10 15  
Gly Pro Gln Lys Val Lys Tyr Gly Lys Asp Asn Ile Ile Thr Ala Lys  
20 25 30  
Asp Ile Ile Ile Ala Thr Gly Ser Val Pro Phe Val Pro Lys Gly Ile  
35 40 45  
Glu Val Asp Gly Lys Thr Val Ile Thr Ser Asp His Ala Leu Lys Leu  
50 55 60  
Glu Ser Val Pro Glu Trp Ile Ala Ile Val Gly Ser Gly Tyr Ile Gly  
65 70 75 80  
Leu Glu Phe Ser Asp Val Tyr Thr Ala Leu Gly Ser Glu Val Thr Phe  
85 90 95  
Ile Glu Ala Leu Asp Gln Leu Met Pro Gly Phe Asp Pro Glu Ile Ser  
100 105 110  
Lys Leu Ala Gln Arg Val Leu Ile Asn Pro Arg Lys Ile Asp Tyr His  
115 120 125  
Thr Gly Val Phe Ala Ser Lys Ile Thr Pro Ala Arg Asp Gly Lys Pro  
130 135 140  
Val Leu Ile Glu Leu Ile Asp Ala Lys Thr Lys Glu Pro Lys Asp Thr  
145 150 155 160  
Leu Glu Val Asp Ala Ala Leu Ile Ala Thr Gly Arg Ala Pro Phe Thr  
165 170 175  
Asn Gly Leu Gly Leu Glu Asn Val Asn Val Val Thr Gln Arg Gly Phe  
180 185 190  
Ile Pro Val Asp Glu Arg Met Arg Val Ile Asp Gly Lys Gly Thr Leu  
195 200 205  
Val Pro Asn Leu Tyr Cys Ile Gly Asp Ala Asn Gly Lys Leu Met Leu  
210 215 220  
Ala His Ala Ala Ser Ala Gln Gly Ile Ser Val Val Glu Gln Val Ser  
225 230 235 240  
Gly Arg Asp His Val Leu Asn His Leu Ser Ile Pro Ala Ala Cys Phe  
245 250 255  
Thr His Pro Glu Asn Gln His Gly Gly Ile Asn Arg Ala Ser Ser Lys  
260 265 270  
Arg Lys Arg Arg Glu Gly Arg Ile  
275 280

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1568866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

Met Pro Gly Phe Asp Pro Glu Ile Ser Lys Leu Ala Gln Arg Val Leu

1 5 10 15  
Ile Asn Pro Arg Lys Ile Asp Tyr His Thr Gly Val Phe Ala Ser Lys  
20 25 30  
Ile Thr Pro Ala Arg Asp Gly Lys Pro Val Leu Ile Glu Leu Ile Asp  
35 40 45  
Ala Lys Thr Lys Glu Pro Lys Asp Thr Leu Glu Val Asp Ala Ala Leu  
50 55 60  
Ile Ala Thr Gly Arg Ala Pro Phe Thr Asn Gly Leu Gly Leu Glu Asn  
65 70 75 80  
Val Asn Val Val Thr Gln Arg Gly Phe Ile Pro Val Asp Glu Arg Met  
85 90 95  
Arg Val Ile Asp Gly Lys Gly Thr Leu Val Pro Asn Leu Tyr Cys Ile  
100 105 110  
Gly Asp Ala Asn Gly Lys Leu Met Leu Ala His Ala Ser Ala Gln  
115 120 125  
Gly Ile Ser Val Val Glu Gln Val Ser Gly Arg Asp His Val Leu Asn  
130 135 140  
His Leu Ser Ile Pro Ala Ala Cys Phe Thr His Pro Glu Asn Gln His  
145 150 155 160  
Gly Gly Ile Asn Arg Ala Ser Ser Lys Arg Lys Arg Arg Glu Gly Arg  
165 170 175  
Ile

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| actcccatca aagcaaaact atctttctcc ttctcattcc tttttctctc actctcctcc  | 60   |
| attaaagctc tgcactttct caaagagaat gttcatgggt aagatgggtc ttttgggagt  | 120  |
| tgctctgttg tgttttgctg caatggtgtg ctctgttcat ggatatgacg ctggatgggt  | 180  |
| caatgctcat gctactttct atggtggaag tgatgcttca ggaacaatgg gtggagcttg  | 240  |
| tggctacggg aacctctaca gtcaagggtta cgggaccaac acggcggcgt tgagcactgc | 300  |
| tctgttcaac aacggtctta gctgcggggc gtgttttgag atcaagtgtc agagcgacgg  | 360  |
| cgcgtggtgt ttacctggtg ctatcattgt cacagccacc aatttctgtc ctcttaacaa  | 420  |
| cgctcttccc aataacgctg gtggttggtg taaccCtccg cttcatcatt tcgatctctc  | 480  |
| tcagcctgtt tttcaacgca ttgctcagta caaagctggt gttgtccctg tttcttacag  | 540  |
| aagggttccg tgtatgagaa gaggaggtat aagattcaca atcaacggtc actcttactt  | 600  |
| caaccttgtc ttggtgacca atgttggtg tgctggagat gttcattcgg ttgctggttaa  | 660  |
| aggttctagg acaagggtgc aacaaatgtc aagaaactgg ggacagaact ggcaaagcaa  | 720  |
| caatctctta aacggtcaag cattgtcatt taagggtgact gctagtgatg gtcgtaccgt | 780  |
| cgtctctaac aacattgctc cagctagttg gtcctttgga caaaccttca ccggccgtca  | 840  |
| attccgttaa aattgagtca agttcgggtt tatatagttt tagggtttgt gtagtagttg  | 900  |
| gttgaggaaa gagtagagaa agagagaggg ttttaaggctt tttagggttt ttaagtggag | 960  |
| agccttgaaa cttcttcttt gactcttgag ggttaaaatg gagaaaagag cttgttttat  | 1020 |
| aagggtctct ttagtcatgt taaggattag ggttttagta agtgggtgtt gtagtagata  | 1080 |
| gtggtgtgtc ttaagggacc tctatgttcc accaatgggt tcctttgttt tatcactttt  | 1140 |
| ttattttgtt ttatcttctt ttttcaagct tctgtcttgt ggtttaaaaa gcagaagtgg  | 1200 |
| gtaggggcag aggaggaatt tcaccacccg cctatgtgtt tttctttttg ggtcgttttg  | 1260 |
| gtttatgtta tgaagttgta attgtaatgt agatcaacca atgggtttga taagtgtttt  | 1320 |
| gttacc                                                             |      |

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..282
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

Leu Pro Ser Lys Gln Asn Tyr Leu Ser Pro Ser His Ser Phe Phe Ser  
1 5 10 15  
His Ser Pro Pro Leu Lys Leu Cys Thr Phe Ser Lys Arg Met Phe Met  
20 25 30  
Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe Ala Ala Met  
35 40 45  
Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn Ala His Ala  
50 55 60  
Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly Ala Cys  
65 70 75 80  
Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala  
85 90 95  
Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe  
100 105 110  
Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro Gly Ala Ile  
115 120 125  
Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn  
130 135 140  
Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His Phe Asp Leu Ser  
145 150 155 160  
Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly Val Val Pro  
165 170 175  
Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly Ile Arg Phe  
180 185 190  
Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val Thr Asn Val  
195 200 205  
Gly Gly Ala Gly Asp Val His Ser Val Ala Val Lys Gly Ser Arg Thr  
210 215 220  
Arg Trp Gln Gln Met Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn  
225 230 235 240  
Asn Leu Leu Asn Gly Gln Ala Leu Ser Phe Lys Val Thr Ala Ser Asp  
245 250 255  
Gly Arg Thr Val Val Ser Asn Asn Ile Ala Pro Ala Ser Trp Ser Phe  
260 265 270  
Gly Gln Thr Phe Thr Gly Arg Gln Phe Arg  
275 280

(2) INFORMATION FOR SEQ ID NO:1055:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 253 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..253
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1568869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

Met Phe Met Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe  
1 5 10 15  
Ala Ala Met Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn  
20 25 30

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Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly  
35 40 45  
Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn  
50 55 60  
Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly  
65 70 75 80  
Ala Cys Phe Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro  
85 90 95  
Gly Ala Ile Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala  
100 105 110  
Leu Pro Asn Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe  
115 120 125  
Asp Leu Ser Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly  
130 135 140  
Val Val Pro Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly  
145 150 155 160  
Ile Arg Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val  
165 170 175  
Thr Asn Val Gly Gly Ala Gly Asp Val His Ser Val Ala Val Lys Gly  
180 185 190  
Ser Arg Thr Arg Trp Gln Gln Met Ser Arg Asn Trp Gly Gln Asn Trp  
195 200 205  
Gln Ser Asn Asn Leu Leu Asn Gly Gln Ala Leu Ser Phe Lys Val Thr  
210 215 220  
Ala Ser Asp Gly Arg Thr Val Val Ser Asn Asn Ile Ala Pro Ala Ser  
225 230 235 240  
Trp Ser Phe Gly Gln Thr Phe Thr Gly Arg Gln Phe Arg  
245 250

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1568870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

Met Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe Ala Ala  
1 5 10 15  
Met Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn Ala His  
20 25 30  
Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly Ala  
35 40 45  
Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala  
50 55 60  
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys  
65 70 75 80  
Phe Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro Gly Ala  
85 90 95  
Ile Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro  
100 105 110  
Asn Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe Asp Leu  
115 120 125  
Ser Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly Val Val  
130 135 140  
Pro Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly Ile Arg  
145 150 155 160  
Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val Thr Asn

(2) INFORMATION FOR SEO ID NO:1057:

(A) LENGTH: 1270 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1270

(D) OTHER INFORMATION: / Ceres Seq. ID 1568871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| taaaaaagg   | tacaaaagg  | gatgtcacag  | cactaaagcc  | cactataatg | acagctgttc | 60   |
| cagccattct  | tgatcgtgtc | agggatgggtg | tccgcaaaaa  | ggttgatgca | aagggcggat | 120  |
| tgtaaagaa   | attgtttgac | tttgcatatg  | ctcggcgatt  | atctgcaatc | aatggaagtt | 180  |
| ggtttggagc  | ctggggattg | gaaaagcttt  | tgtgggatgt  | gcttggtgtc | aggaaaattc | 240  |
| gtgcagtgtt  | gggaggtcaa | attcgctatt  | tgctctctgg  | tggtgcccc  | ctttctgggt | 300  |
| acactcagag  | attcattaac | atctcgcttg  | gggctccaat  | cggtcaggga | tatgggtcga | 360  |
| cagacacttg  | tgctggtgga | accttctctg  | agtttgagg   | catcatcggt | ggccgagttg | 420  |
| gtgctccact  | tccttgcctc | tttgtaaagc  | tagtagactg  | ggcggaaggt | gggtatctaa | 480  |
| ccagtataaa  | gccaatgccc | cgtggtgaaa  | ttgtaattgg  | tggtcaaat  | atcacgcttg | 540  |
| ggtatttcaa  | aaatgaggag | aaaactaaag  | aagtgtacaa  | ggttgatgaa | aagggaatga | 600  |
| ggtggttcta  | cacaggagac | ataggacgat  | ttcacccctga | tggtgcctc  | gagataatag | 660  |
| accgaaaaaa  | ggatatcgtt | aaacttcagc  | acggagaata  | tgtctccttg | ggcaaagttg | 720  |
| aagctgctct  | aagtataagt | ccctatgttg  | aaaacataat  | agttcatgct | gattcgtttc | 780  |
| acagtactag  | tgtggctctt | tggtgcgctg  | cccaacatac  | agttgaaggt | tgggttccaa | 840  |
| agsaAggaat  | agastttgcc | aacttcgaag  | aactgtgcac  | gaaagagcaa | gccgtgaaag | 900  |
| aagtgtatgc  | ttatcttgtc | aaggcggcta  | aacaatcacg  | attggagaag | tttgagatac | 960  |
| cmgcaaagat  | caaattgttg | gcattctccat | ggacgccaga  | gtcaggatta | gtcacagcag | 1020 |
| ctctaaagct  | taaaagagac | gtaattagga  | gggaattctc  | tgaagatctc | accaagttat | 1080 |
| atgcctaaac  | ttttcttctt | cctttacttt  | gttttatctt  | ttacgtctcg | atgcattcga | 1140 |
| aagacgcaac  | agctgcacaa | aaacttaatt  | ctaagaatag  | tgtatctttt | ctctctgtga | 1200 |
| tgtctgtctt  | ttcgtgcaaa | tgtatggggg  | taactgtgac  | gagactgaaa | gaaagaaaag | 1260 |
| tatcggctctt |            |             |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1058:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1568872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

Lys Lys Gly Thr Lys Gly Asp Val Thr Ala Leu Lys Pro Thr Ile Met  
1 5 10 15  
Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg Lys  
20 25 30

Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe Ala  
35 40 45  
Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala Trp  
50 55 60  
Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile Arg  
65 70 75 80  
Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala Pro  
85 90 95  
Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala Pro  
100 105 110  
Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr Phe  
115 120 125  
Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu Pro  
130 135 140  
Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu Thr  
145 150 155 160  
Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn  
165 170 175  
Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr  
180 185 190  
Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly  
195 200 205  
Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp  
210 215 220  
Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu  
225 230 235 240  
Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala  
245 250 255  
Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His  
260 265 270  
Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe  
275 280 285  
Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr  
290 295 300  
Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa  
305 310 315 320  
Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu  
325 330 335  
Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe  
340 345 350  
Ser Glu Asp Leu Thr Lys Leu Tyr Ala  
355 360

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Met Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg  
1 5 10 15  
Lys Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe  
20 25 30  
Ala Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala  
35 40 45  
Trp Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile

50 55 60  
Arg Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Ser Gly Gly Ala  
65 70 75 80  
Pro Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala  
85 90 95  
Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr  
100 105 110  
Phe Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu  
115 120 125  
Pro Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu  
130 135 140  
Thr Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser  
145 150 155 160  
Asn Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val  
165 170 175  
Tyr Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile  
180 185 190  
Gly Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys  
195 200 205  
Asp Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val  
210 215 220  
Glu Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His  
225 230 235 240  
Ala Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln  
245 250 255  
His Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn  
260 265 270  
Phe Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala  
275 280 285  
Tyr Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile  
290 295 300  
Xaa Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly  
305 310 315 320  
Leu Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu  
325 330 335  
Phe Ser Glu Asp Leu Thr Lys Leu Tyr Ala  
340 345

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1568874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn Ile Thr Leu Gly  
1 5 10 15  
Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr Lys Val Asp Glu  
20 25 30  
Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly Arg Phe His Pro  
35 40 45  
Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp Ile Val Lys Leu  
50 55 60  
Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu Ser  
65 70 75 80  
Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala Asp Ser Phe Tyr  
85 90 95

Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His Thr Val Glu Gly  
100 105 110  
Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe Glu Glu Leu Cys  
115 120 125  
Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr Leu Val Lys Ala  
130 135 140  
Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa Ala Lys Ile Lys  
145 150 155 160  
Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala Ala  
165 170 175  
Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe Ser Glu Asp Leu  
180 185 190  
Thr Lys Leu Tyr Ala  
195

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| gtgtctcaca  | tctctttgtc | ttctccgcct | cctccgatct  | cactccgatc | tctctacgat  | 60   |
| tcattcttct  | atggcttcca | ttgctacttc | tgcttctact  | tctctccaag | ctcgtcctcg  | 120  |
| tcaactgggtg | attggggcta | aacaagttaa | aagctttagc  | tatggaagca | gaagcaatct  | 180  |
| ttcttttaat  | cttcgccagc | ttcctaccgc | cttgactgtt  | tactgcgctg | caaaacctga  | 240  |
| gacagtggac  | aaggtgtgtg | cagttgtcag | aaagcaactc  | tactcaaaag | aggctgacga  | 300  |
| aattaccgct  | gccaccaaat | ttgctgcact | tggtgctgat  | tcccttgata | cggaggagat  | 360  |
| agttatggga  | ttagaggaag | agtttgggat | tgaaatggct  | tcaacgatgt | ttctaaatta  | 420  |
| cctgacttgg  | aagagaagca | tgctcccaaa | ggggcacata  | ccagaagcag | agattgcaaa  | 480  |
| tgatctatcg  | cataacaaga | tgtgtatgca | aggctcatgac | aagatgggtc | gacctatcgc  | 540  |
| tgttgccatt  | gggaacagac | ataacccttc | caaaggcaac  | cctgacgagt | tcaagcgttt  | 600  |
| tgttgtctac  | acgctcgaga | agatttgtgc | tagaatgccg  | agaggtcaag | agaaattcgt  | 660  |
| agcaattgga  | gatctgcaag | gctggggata | ttctaattgt  | gacatccgtg | gctacccttg  | 720  |
| tgctctttcc  | actttgcagg | attgttacco | agagagatta  | gggaaactct | atatagttca  | 780  |
| tgccccctac  | attttcatga | cgcgatggaa | ggtcatttat  | ccttttatcg | acgccaacac  | 840  |
| caagaaaaag  | attgttttcg | tggagaacaa | gaaactcact  | ccaacgctgc | ttgaagacat  | 900  |
| agacgaaagc  | caacttcccg | Gacatctacg | gaggcaaaaT  | tgccacttgt | tcctattcag  | 960  |
| gagacctgat  | tataggtctt | actTaccgGc | ccacctctat  | ttccaaatta | ttacttacta  | 1020 |
| gtattctttt  | ttttatttga | ataaaatgaa | aaacatattg  | agtgtcgcca | aatgcccaaca | 1080 |
| attatatatt  | tactgtcaaa | gaagctaaaa | gatataatat  | tgaaatcacc | ttt         |      |

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Leu | Thr | Ser | Leu | Cys | Leu | Leu | Arg | Leu | Leu | Arg | Ser | His | Ser | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Thr | Ile | His | Ser | Ser | Met | Ala | Ser | Ile | Ala | Thr | Ser | Ala | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |

Thr Ser Leu Gln Ala Arg Pro Arg Gln Leu Val Ile Gly Ala Lys Gln  
35 40 45  
Val Lys Ser Phe Ser Tyr Gly Ser Arg Ser Asn Leu Ser Phe Asn Leu  
50 55 60  
Arg Gln Leu Pro Thr Arg Leu Thr Val Tyr Cys Ala Ala Lys Pro Glu  
65 70 75 80  
Thr Val Asp Lys Val Cys Ala Val Val Arg Lys Gln Leu Ser Leu Lys  
85 90 95  
Glu Ala Asp Glu Ile Thr Ala Ala Thr Lys Phe Ala Ala Leu Gly Ala  
100 105 110  
Asp Ser Leu Asp Thr Val Glu Ile Val Met Gly Leu Glu Glu Phe  
115 120 125  
Gly Ile Glu Met Ala Ser Thr Met Phe Leu Asn Tyr Leu Thr Trp Lys  
130 135 140  
Arg Ser Met Leu Pro Lys Gly His Ile Pro Glu Ala Glu Ile Ala Asn  
145 150 155 160  
Asp Leu Ser His Asn Lys Met Cys Met Gln Gly His Asp Lys Met Gly  
165 170 175  
Arg Pro Ile Ala Val Ala Ile Gly Asn Arg His Asn Pro Ser Lys Gly  
180 185 190  
Asn Pro Asp Glu Phe Lys Arg Phe Val Val Tyr Thr Leu Glu Lys Ile  
195 200 205  
Cys Ala Arg Met Pro Arg Gly Gln Glu Lys Phe Val Ala Ile Gly Asp  
210 215 220  
Leu Gln Gly Trp Gly Tyr Ser Asn Cys Asp Ile Arg Gly Tyr Leu Ala  
225 230 235 240  
Ala Leu Ser Thr Leu Gln Asp Cys Tyr Pro Glu Arg Leu Gly Lys Leu  
245 250 255  
Tyr Ile Val His Ala Pro Tyr Ile Phe Met Thr Ala Trp Lys Val Ile  
260 265 270  
Tyr Pro Phe Ile Asp Ala Asn Thr Lys Lys Lys Ile Val Phe Val Glu  
275 280 285  
Asn Lys Lys Leu Thr Pro Thr Leu Leu Glu Asp Ile Asp Glu Ser Gln  
290 295 300  
Leu Pro Gly His Leu Arg Arg Gln Asn Cys His Leu Phe Leu Phe Arg  
305 310 315 320  
Arg Pro Asp Tyr Arg Ser Tyr Leu Arg Ala His Leu Tyr Phe Gln Ile  
325 330 335  
Ile Thr Tyr

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1568885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Ala Ser Ile Ala Thr Ser Ala Ser Thr Ser Leu Gln Ala Arg Pro  
1 5 10 15  
Arg Gln Leu Val Ile Gly Ala Lys Gln Val Lys Ser Phe Ser Tyr Gly  
20 25 30  
Ser Arg Ser Asn Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu  
35 40 45  
Thr Val Tyr Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala  
50 55 60  
Val Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala

|                     |                 |                     |             |    |  |     |
|---------------------|-----------------|---------------------|-------------|----|--|-----|
| 65                  |                 | 70                  |             | 75 |  | 80  |
| Ala Thr Lys Phe     | Ala Leu Gly Ala | Asp Ser Leu Asp Thr | Val Glu     |    |  |     |
|                     | 85              | 90                  | 95          |    |  |     |
| Ile Val Met Gly     | Leu Glu Glu Phe | Gly Ile Glu Met Ala | Ser Thr     |    |  |     |
|                     | 100             | 105                 | 110         |    |  |     |
| Met Phe Leu Asn Tyr | Leu Thr Trp Lys | Arg Ser Met Leu     | Pro Lys Gly |    |  |     |
|                     | 115             | 120                 | 125         |    |  |     |
| His Ile Pro Glu Ala | Glu Ile Ala Asn | Asp Leu Ser His     | Asn Lys Met |    |  |     |
|                     | 130             | 135                 | 140         |    |  |     |
| Cys Met Gln Gly His | Asp Lys Met Gly | Arg Pro Ile Ala     | Val Ala Ile |    |  |     |
|                     | 145             | 150                 | 155         |    |  | 160 |
| Gly Asn Arg His Asn | Pro Ser Lys Gly | Asn Pro Asp Glu     | Phe Lys Arg |    |  |     |
|                     | 165             | 170                 | 175         |    |  |     |
| Phe Val Val Tyr Thr | Leu Glu Lys Ile | Cys Ala Arg Met     | Pro Arg Gly |    |  |     |
|                     | 180             | 185                 | 190         |    |  |     |
| Gln Glu Lys Phe Val | Ala Ile Gly Asp | Leu Gln Gly Trp     | Gly Tyr Ser |    |  |     |
|                     | 195             | 200                 | 205         |    |  |     |
| Asn Cys Asp Ile Arg | Gly Tyr Leu Ala | Ala Leu Ser Thr     | Leu Gln Asp |    |  |     |
|                     | 210             | 215                 | 220         |    |  |     |
| Cys Tyr Pro Glu Arg | Leu Gly Lys Leu | Tyr Ile Val His     | Ala Pro Tyr |    |  |     |
|                     | 225             | 230                 | 235         |    |  | 240 |
| Ile Phe Met Thr Ala | Trp Lys Val Ile | Tyr Pro Phe Ile     | Asp Ala Asn |    |  |     |
|                     | 245             | 250                 | 255         |    |  |     |
| Thr Lys Lys Lys Ile | Val Phe Val Glu | Asn Lys Lys Leu     | Thr Pro Thr |    |  |     |
|                     | 260             | 265                 | 270         |    |  |     |
| Leu Leu Glu Asp Ile | Asp Glu Ser Gln | Leu Pro Gly His     | Leu Arg Arg |    |  |     |
|                     | 275             | 280                 | 285         |    |  |     |
| Gln Asn Cys His Leu | Phe Leu Phe Arg | Arg Pro Asp Tyr     | Arg Ser Tyr |    |  |     |
|                     | 290             | 295                 | 300         |    |  |     |
| Leu Arg Ala His Leu | Tyr Phe Gln Ile | Ile Thr Tyr         |             |    |  |     |
|                     | 305             | 310                 | 315         |    |  |     |

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Gly Leu Glu Glu Phe Gly Ile Glu Met Ala Ser Thr Met Phe     |             |
| 1                                                               | 5 10 15     |
| Leu Asn Tyr Leu Thr Trp Lys Arg Ser Met Leu Pro Lys Gly His Ile |             |
|                                                                 | 20 25 30    |
| Pro Glu Ala Glu Ile Ala Asn Asp Leu Ser His Asn Lys Met Cys Met |             |
|                                                                 | 35 40 45    |
| Gln Gly His Asp Lys Met Gly Arg Pro Ile Ala Val Ala Ile Gly Asn |             |
|                                                                 | 50 55 60    |
| Arg His Asn Pro Ser Lys Gly Asn Pro Asp Glu Phe Lys Arg Phe Val |             |
| 65                                                              | 70 75 80    |
| Val Tyr Thr Leu Glu Lys Ile Cys Ala Arg Met Pro Arg Gly Gln Glu |             |
|                                                                 | 85 90 95    |
| Lys Phe Val Ala Ile Gly Asp Leu Gln Gly Trp Gly Tyr Ser Asn Cys |             |
|                                                                 | 100 105 110 |
| Asp Ile Arg Gly Tyr Leu Ala Ala Leu Ser Thr Leu Gln Asp Cys Tyr |             |
|                                                                 | 115 120 125 |
| Pro Glu Arg Leu Gly Lys Leu Tyr Ile Val His Ala Pro Tyr Ile Phe |             |
|                                                                 | 130 135 140 |

Met Thr Ala Trp Lys Val Ile Tyr Pro Phe Ile Asp Ala Asn Thr Lys  
145 150 155 160  
Lys Lys Ile Val Phe Val Glu Asn Lys Lys Leu Thr Pro Thr Leu Leu  
165 170 175  
Glu Asp Ile Asp Glu Ser Gln Leu Pro Gly His Leu Arg Arg Gln Asn  
180 185 190  
Cys His Leu Phe Leu Phe Arg Arg Pro Asp Tyr Arg Ser Tyr Leu Arg  
195 200 205  
Ala His Leu Tyr Phe Gln Ile Ile Thr Tyr  
210 215

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1790

(D) OTHER INFORMATION: / Ceres Seq. ID 1568887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| ccttcgcgca  | tcttcggtgc | tataaaacaa  | actcacgact  | agatcatttt | ggagtgagat  | 60   |
| ttacgtttga  | tagactacta | caatgaagga  | gccaacgacg  | gagatagaga | ttgaaacttc  | 120  |
| agctgtcaca  | acgatcctgc | ctctctctct  | tcttcgacg   | gcgtcacctc | atcaggcggt  | 180  |
| ggtggagagg  | ctcaaggatt | atggacagga  | agatgttttc  | tctctctggg | atgaactctc  | 240  |
| accggaagag  | cgagatctcc | tcttcgaga   | tatcgagaat  | ttggatcttc | caaggataga  | 300  |
| tcggtatcat  | agatgtcac  | ttcactcaca  | agggttgcca  | gtggcggcaa | tagaaccggt  | 360  |
| gccggagaat  | tgtgtgtcaa | cgggtggagga | aagaactaag  | gaagacagag | aaaaatggtg  | 420  |
| gaaaatggga  | ttaaaagcta | tctacgaagg  | caaattgggt  | gtggtgcttt | tatctggtgg  | 480  |
| acagggaaaca | agacttggaa | gttcagatcc  | aaaagggtgt  | tataatatcg | gactgccatc  | 540  |
| tgggaaatca  | ctttttcaga | ttcaagctga  | gaggatctta  | tgtgtccaaa | ggcttgcttc  | 600  |
| tcaggcaatg  | agtgaggcaa | gtccaactcg  | cccagttaca  | atacagtgg  | atataatgac  | 660  |
| cagtccattt  | actcatgaac | caacacaaaa  | attcttcgag  | agtcacaagt | attttggcct  | 720  |
| tgaaccagat  | caagtcacct | ttttttcaac  | aaggagctct  | gccttgcat  | tcaaaggatg  | 780  |
| gcaagtttat  | catggagaca | cctttcagcc  | tatccaaggc  | gccggatggg | aacgggggag  | 840  |
| tttatacagc  | tttaaaatct | tcaaggttat  | tagaagatat  | ggcttcgagg | gggattaaat  | 900  |
| atgtggattg  | ctatgggtgt | gacaatgttc  | tggttcgagt  | agctgacct  | acttttctgg  | 960  |
| gatacttcat  | cgacaaaagt | gcagcttcag  | ctgcaaaaagt | agtgcgcaag | gcataatccac | 1020 |
| aggaaaaagt  | tggagtattt | gtaaggagg   | gaaaagggtg  | gcctttgact | gtagttgagt  | 1080 |
| acacagagct  | tgaccagtct | atggcttctg  | caactaatca  | acaaacagga | cgtcttcaat  | 1140 |
| attgctggag  | taacgtgtgc | ttacacatgt  | tcactctgga  | tttccttaac | caagttgcga  | 1200 |
| atgggctgaa  | aaagacagcg | tttaccattt  | ggcgGagaag  | aagataacgt | ctataaatgg  | 1260 |
| cgacatagtg  | ggGGactaaa | actagaacag  | ttcatattcg  | attgctttcc | ttatgctcct  | 1320 |
| tcgactgcac  | tttttgaggt | gttgaggagg  | gaagagtttg  | caccggtgaa | gaacgcaaac  | 1380 |
| gggtcgaaat  | acgacacacc | ggaaagcgca  | agactgttgg  | ttctacgact | gcatacacgt  | 1440 |
| tgggtcatag  | cagctggtgg | atttctaaca  | cattccgttc  | ctttatatgc | gactggtgtg  | 1500 |
| gaagtgtcac  | cattgtgctc | gtacgctgga  | gaaaatctag  | aagcgatttg | tcggggaaga  | 1560 |
| acctttcacg  | caccatgtga | aatctccctc  | taatcttctt  | ctttcttttt | cttatctatt  | 1620 |
| cttgtaattt  | tgtcattgtc | tttgcctttt  | cttttggttt  | ggttcttctt | ttgtgttggt  | 1680 |
| gtttggtctc  | tatatatgaa | ctgtaactgg  | cggaggtggt  | cagtagtctc | ttttcaatgt  | 1740 |
| gttactcttc  | attattgcaa | caatagtga   | gtctccgaaa  | ttttggtggt |             |      |

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

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(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

Met Lys Glu Pro Thr Thr Glu Ile Glu Ile Glu Thr Ser Ala Val Thr  
1 5 10 15  
Thr Ile Leu Pro Pro Pro Leu Pro Pro Thr Ala Ser Pro His Gln Ala  
20 25 30  
Leu Val Glu Arg Leu Lys Asp Tyr Gly Gln Glu Asp Val Phe Ser Leu  
35 40 45  
Trp Asp Glu Leu Ser Pro Glu Glu Arg Asp Leu Leu Leu Arg Asp Ile  
50 55 60  
Glu Asn Leu Asp Leu Pro Arg Ile Asp Arg Ile Ile Arg Cys Ser Leu  
65 70 75 80  
His Ser Gln Gly Leu Pro Val Ala Ala Ile Glu Pro Val Pro Glu Asn  
85 90 95  
Cys Val Ser Thr Val Glu Glu Arg Thr Lys Glu Asp Arg Glu Lys Trp  
100 105 110  
Trp Lys Met Gly Leu Lys Ala Ile Tyr Glu Gly Lys Leu Gly Val Val  
115 120 125  
Leu Leu Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser Ser Asp Pro Lys  
130 135 140  
Gly Cys Tyr Asn Ile Gly Leu Pro Ser Gly Lys Ser Leu Phe Gln Ile  
145 150 155 160  
Gln Ala Glu Arg Ile Leu Cys Val Gln Arg Leu Ala Ser Gln Ala Met  
165 170 175  
Ser Glu Ala Ser Pro Thr Arg Pro Val Thr Ile Gln Trp Tyr Ile Met  
180 185 190  
Thr Ser Pro Phe Thr His Glu Pro Thr Gln Lys Phe Phe Glu Ser His  
195 200 205  
Lys Tyr Phe Gly Leu Glu Pro Asp Gln Val Thr Phe Phe Ser Thr Arg  
210 215 220  
Ser Ser Ala Leu His Phe Lys Gly Trp Gln Val Tyr His Gly Asp Thr  
225 230 235 240  
Phe Gln Pro Ile Gln Gly Ala Gly Trp Glu Arg Gly Ser Leu Tyr Ser  
245 250 255  
Phe Lys Ile Phe Lys Val Ile Arg Arg Tyr Gly Phe Glu Gly Asp  
260 265 270

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1568889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

Met Gly Leu Lys Ala Ile Tyr Glu Gly Lys Leu Gly Val Val Leu Leu  
1 5 10 15  
Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser Ser Asp Pro Lys Gly Cys  
20 25 30  
Tyr Asn Ile Gly Leu Pro Ser Gly Lys Ser Leu Phe Gln Ile Gln Ala  
35 40 45  
Glu Arg Ile Leu Cys Val Gln Arg Leu Ala Ser Gln Ala Met Ser Glu  
50 55 60  
Ala Ser Pro Thr Arg Pro Val Thr Ile Gln Trp Tyr Ile Met Thr Ser  
65 70 75 80  
Pro Phe Thr His Glu Pro Thr Gln Lys Phe Phe Glu Ser His Lys Tyr  
85 90 95

Phe Gly Leu Glu Pro Asp Gln Val Thr Phe Phe Ser Thr Arg Ser Ser  
100 105 110  
Ala Leu His Phe Lys Gly Trp Gln Val Tyr His Gly Asp Thr Phe Gln  
115 120 125  
Pro Ile Gln Gly Ala Gly Trp Glu Arg Gly Ser Leu Tyr Ser Phe Lys  
130 135 140  
Ile Phe Lys Val Ile Arg Arg Tyr Gly Phe Glu Gly Asp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1568890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

Met Asn Gln His Lys Asn Ser Ser Arg Val Thr Ser Ile Leu Ala Leu  
1 5 10 15  
Asn Gln Ile Lys Ser Pro Phe Phe Gln Gln Gly Ala Leu Pro Cys Ile  
20 25 30  
Ser Lys Asp Gly Lys Phe Ile Met Glu Thr Pro Phe Ser Leu Ser Lys  
35 40 45  
Ala Pro Asp Gly Asn Gly Gly Val Tyr Thr Ala Leu Lys Ser Ser Arg  
50 55 60  
Leu Leu Glu Asp Met Ala Ser Arg Gly Ile Lys Tyr Val Asp Cys Tyr  
65 70 75 80  
Gly Val Asp Asn Val Leu Val Arg Val Ala Asp Pro Thr Phe Leu Gly  
85 90 95  
Tyr Phe Ile Asp Lys Ser Ala Ala Ser Ala Ala Lys Val Val Arg Lys  
100 105 110  
Ala Tyr Pro Gln Glu Lys Val Gly Val Phe Val Arg Arg Gly Lys Gly  
115 120 125  
Gly Pro Leu Thr Val Val Glu Tyr Thr Glu Leu Asp Gln Ser Met Ala  
130 135 140  
Ser Ala Thr Asn Gln Gln Thr Gly Arg Leu Gln Tyr Cys Trp Ser Asn  
145 150 155 160  
Val Cys Leu His Met Phe Thr Leu Asp Phe Leu Asn Gln Val Ala Asn  
165 170 175  
Gly Leu Lys Lys Thr Ala Phe Thr Ile Trp Arg Arg Arg Arg Tyr Arg  
180 185 190  
Leu

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1575 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1575

(D) OTHER INFORMATION: / Ceres Seq. ID 1568891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

aaagagcaaaa actatctaata tccatggcgt tctccctcct ctctccaatt cctacctctg 60  
cctctcttttt tttcactctc tccgccatta ccgcttctaa taatgcttcc tcctcctctc 120  
tctcccgtct ttactcttta taccacca aaggacatt acgaaccaga accgcgacct 180

cgtttttccg agcttctggg aacttgagga ttgtttccat ggcggagaat aggcaattgg 240  
tttgtaggat tgggtggcga gcCggCtgct gaattggatg atatggatga aggtgaaatc 300  
cagaggattg gaaatgaaga cgaagacgac gatgaattca tacaagtcca tgctaataat 360  
tcctctgctg ctgcgctga gagatgggat gttttgggtc tcggccaagc catggtagat 420  
ttctctggag ttgtggatga tgagtttcta aagaaacttg gtttaaaaaa gggaacaagg 480  
aaactgatta atcacgagga gaggggtaaa ttattacaag caatggatgg ttgtagctat 540  
aaRgcggcag ctggaggctc attgtccaac actttagttg ctctcgcaag attaggttct 600  
caatccatct gtgaccggcc tttgaatgtg gcaatggctg gcagtattgg aggtgaccct 660  
ctcggtagct tttacgggac taaactacga cgagcaaattg taaattttct ttctgctcca 720  
atcaaggacg gaacaacagg aacagtgata gttctcacia ctctgatgc acaacgtact 780  
atgcttgcat atcaggggaa atcctctgtc gtttaattatg attcttgttt ggctagtttg 840  
atagccaaga caaatgtctt tgttgtggaa ggctatttgc ttgagcttcc tgatactata 900  
agaaccataa caaaagcctg cgaagaagcc cacagaaacg gggcacttgc tgctgtgaca 960  
gcatcagatg tgtcctgcag agagaggcat tatgatgatt tctgggacat tgtggggaac 1020  
tatgcggata ttgtatttgc aaatagcgat gaagcaagag cgttttgcata cttttccgca 1080  
gaggaaaagtc caatttcagc gacaagatac atgagccact ttgttccggt tgtttctggt 1140  
accgatggaa tcaacgggtc atatatggga gtaaaaggag aggccatcta cattcctccg 1200  
tccccatgag tgccagttga tacatgtggt gctggagatg catatgcttc agggatctta 1260  
tacggtatct tgaggggtgt ctctgacttg aaaggaatgg gagatatggc tgcaacgatt 1320  
gcagcaactg tgggtgggtc acaaggaacc aggcctaggg ttcaggacgc ggttgagctg 1380  
gctcgatcac atgccttccg tctcaatggt tctgggtgtc gaacagatgt tgggtcttga 1440  
tgaaacctct ttagcttgtg atttttagct ttttgattca ttctttgtct tcatgtagta 1500  
gtgccttttg caattgactt gtaatcttgt atgtaacatt ttagtatata gtatatgttt 1560  
ccgacaaaagt ttgag

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..385

(D) OTHER INFORMATION: / Ceres Seq. ID 1568892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

Met Asp Glu Gly Ile Gln Arg Ile Gly Asn Glu Asp Glu Asp Asp  
1 5 10 15  
Asp Glu Phe Ile Gln Val His Ala Asn Asn Ser Ser Ala Ala Ser Pro  
20 25 30  
Glu Arg Trp Asp Val Leu Gly Leu Gly Gln Ala Met Val Asp Phe Ser  
35 40 45  
Gly Val Val Asp Asp Glu Phe Leu Lys Lys Leu Gly Leu Lys Lys Gly  
50 55 60  
Thr Arg Lys Leu Ile Asn His Glu Glu Arg Gly Lys Leu Leu Gln Ala  
65 70 75 80  
Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly Gly Ser Leu Ser Asn  
85 90 95  
Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln Ser Ile Cys Asp Arg  
100 105 110  
Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly Gly Asp Pro Leu Gly  
115 120 125  
Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn Val Asn Phe Leu Ser  
130 135 140  
Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val Ile Val Leu Thr Thr  
145 150 155 160  
Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln Gly Thr Ser Ser Val  
165 170 175  
Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile Ala Lys Thr Asn Val  
180 185 190  
Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro Asp Thr Ile Arg Thr

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 195 200 205
Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn Gly Ala Leu Val Ala
 210 215 220
Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg His Tyr Asp Asp Phe
 225 230 235 240
Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val Phe Ala Asn Ser Asp
 245 250 255
Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu Glu Ser Pro Ile Ser
 260 265 270
Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe Val Ser Val Thr Asp
 275 280 285
Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly Glu Ala Ile Tyr Ile
 290 295 300
Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys Gly Ala Gly Asp Ala
 305 310 315 320
Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg Gly Val Ser Asp Leu
 325 330 335
Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala Ala Thr Val Val Gly
 340 345 350
Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala Val Glu Leu Ala Arg
 355 360 365
Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val Arg Thr Asp Val Gly
 370 375 380
Ser
 385

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(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1568893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

```

Met Val Asp Phe Ser Gly Val Val Asp Asp Glu Phe Leu Lys Lys Leu
 1 5 10 15
Gly Leu Lys Lys Gly Thr Arg Lys Leu Ile Asn His Glu Glu Arg Gly
 20 25 30
Lys Leu Leu Gln Ala Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly
 35 40 45
Gly Ser Leu Ser Asn Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln
 50 55 60
Ser Ile Cys Asp Arg Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly
 65 70 75 80
Gly Asp Pro Leu Gly Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn
 85 90 95
Val Asn Phe Leu Ser Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val
 100 105 110
Ile Val Leu Thr Thr Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln
 115 120 125
Gly Thr Ser Ser Val Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile
 130 135 140
Ala Lys Thr Asn Val Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro
 145 150 155 160
Asp Thr Ile Arg Thr Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn
 165 170 175
Gly Ala Leu Val Ala Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg
 180 185 190

```

Sequence: 1071

His Tyr Asp Asp Phe Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val  
195 200 205  
Phe Ala Asn Ser Asp Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu  
210 215 220  
Glu Ser Pro Ile Ser Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe  
225 230 235 240  
Val Ser Val Thr Asp Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly  
245 250 255  
Glu Ala Ile Tyr Ile Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys  
260 265 270  
Gly Ala Gly Asp Ala Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg  
275 280 285  
Gly Val Ser Asp Leu Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala  
290 295 300  
Ala Thr Val Val Gly Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala  
305 310 315 320  
Val Glu Leu Ala Arg Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val  
325 330 335  
Arg Thr Asp Val Gly Ser  
340

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly Gly Ser Leu Ser Asn  
1 5 10 15  
Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln Ser Ile Cys Asp Arg  
20 25 30  
Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly Gly Asp Pro Leu Gly  
35 40 45  
Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn Val Asn Phe Leu Ser  
50 55 60  
Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val Ile Val Leu Thr Thr  
65 70 75 80  
Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln Gly Thr Ser Ser Val  
85 90 95  
Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile Ala Lys Thr Asn Val  
100 105 110  
Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro Asp Thr Ile Arg Thr  
115 120 125  
Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn Gly Ala Leu Val Ala  
130 135 140  
Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg His Tyr Asp Asp Phe  
145 150 155 160  
Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val Phe Ala Asn Ser Asp  
165 170 175  
Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu Glu Ser Pro Ile Ser  
180 185 190  
Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe Val Ser Val Thr Asp  
195 200 205  
Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly Glu Ala Ile Tyr Ile  
210 215 220  
Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys Gly Ala Gly Asp Ala

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(2) INFORMATION FOR SEQ ID NO:1073:

(A) LENGTH: 1374 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (q

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1374

(D) OTHER INFORMATION: / Ceres Seq. ID 1568895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| attagtggta  | attttctgac | ccattgctgc | tctctctcc   | ggagatacaa | aggcgaatct | 60   |
| gaccagtaag  | aaagatggca | gtcgagatgg | cctctcagtc  | tcaggttttg | gtggaagaga | 120  |
| aatcgagtgt  | tagaatcttg | acactaaaca | gaccaaagca  | gctgaatgct | ctgtccttcc | 180  |
| acatgatctc  | togattgctg | caactgttcc | ttgcatttga  | ggaggacct  | agtgtgaaac | 240  |
| ttgtcatcct  | aaagggtcat | gggagagcct | tttgtgctgg  | tggcgatgtt | gcagctgttg | 300  |
| ttcgtgacat  | caatcaaggt | aactggagac | tcggtgccaa  | ttactcttca | tctgaataca | 360  |
| tgctcaacta  | tgttattggc | acatatagca | aagctcaggt  | ttcaactctg | aatggtatcg | 420  |
| tcattgggag  | cggagctggg | gtatccgtcc | atggctgatt  | tcgtattgca | actgagaaca | 480  |
| cggtttttgc  | catgcctgag | acagctctgg | ggctctttcc  | agatgtaggc | gcctcctact | 540  |
| tcttgtcaag  | gctccctggg | ttttttgggg | agtatgttgg  | cctcacacga | gctagattag | 600  |
| atgggtgctga | aatgcttgct | tgtggccttg | caactcattt  | tgttccttca | acgaggttga | 660  |
| ctgcattaga  | agcagatcct | tgcagaatta | attcaaataa  | tccaaacttt | gcctcaacaa | 720  |
| ttctcgatgc  | atacacccag | catccgcgc  | tgaaacagca  | gagtgtttac | cgcaggttag | 780  |
| atgttattga  | tagtggtttc | tcaaggagaa | cagtcgaaga  | aattatattc | gcacttgaga | 840  |
| gagaggccac  | tcaagaagca | gatggttggg | tctcagctac  | cattcaagca | ttgaagaagg | 900  |
| gttcaccagc  | aagccttaaa | atctctctta | gatcgataag  | ggaagggcga | ttgcaggggg | 960  |
| tggggcagtg  | tcttatccgc | gagtatagaa | tgggtgtgtca | tgtgatgaag | ggagaaatca | 1020 |
| gcaaagatth  | tgtggagggg | tgcagagcca | tattggtaga  | caaagataag | aacccaaagt | 1080 |
| gggagccaag  | gcgactggag | gacatgaagg | atagcatggt  | ggagcagtac | ttcgagagag | 1140 |
| tggaacggga  | ggatgatcta | aagcttccgc | caaggataaa  | cttgctctgt | ttagggatcg | 1200 |
| caaagctgtg  | aagtggagaa | ggtgatggag | cactattgtt  | tacgtctgtg | ggaaagaaaa | 1260 |
| aagaaaataa  | atgtaaacac | acttgtgttg | aataggactt  | gcatacatta | cataaatcat | 1320 |
| tattgtattt  | gagaattgac | accaaagcag | cagagcagaa  | ttgtgttaag | attc       |      |

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1568896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Ala Val Glu Met Ala Ser Gln Ser Gln Val Leu Val Glu Glu Lys  
1 5 10 15  
Ser Ser Val Arg Ile Leu Thr Leu Asn Arg Pro Lys Gln Leu Asn Ala

|                                                                 |                                 |     |
|-----------------------------------------------------------------|---------------------------------|-----|
| 20                                                              | 25                              | 30  |
| Leu Ser Phe His Met Ile Ser Arg                                 | Leu Leu Gln Leu Phe Leu Ala Phe |     |
| 35                                                              | 40                              | 45  |
| Glu Glu Asp Pro Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg |                                 |     |
| 50                                                              | 55                              | 60  |
| Ala Phe Cys Ala Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn |                                 |     |
| 65                                                              | 70                              | 75  |
| Gln Gly Asn Trp Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met |                                 |     |
| 85                                                              | 90                              | 95  |
| Leu Asn Tyr Val Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu |                                 |     |
| 100                                                             | 105                             | 110 |
| Asn Gly Ile Val Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg |                                 |     |
| 115                                                             | 120                             | 125 |
| Phe Arg Ile Ala Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala |                                 |     |
| 130                                                             | 135                             | 140 |
| Leu Gly Leu Phe Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu |                                 |     |
| 145                                                             | 150                             | 155 |
| Pro Gly Phe Phe Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp |                                 |     |
| 165                                                             | 170                             | 175 |
| Gly Ala Glu Met Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser |                                 |     |
| 180                                                             | 185                             | 190 |
| Thr Arg Leu Thr Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn |                                 |     |
| 195                                                             | 200                             | 205 |
| Asp Pro Thr Phe Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro |                                 |     |
| 210                                                             | 215                             | 220 |
| Arg Leu Lys Gln Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg |                                 |     |
| 225                                                             | 230                             | 235 |
| Cys Phe Ser Arg Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg |                                 |     |
| 245                                                             | 250                             | 255 |
| Glu Ala Thr Gln Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala |                                 |     |
| 260                                                             | 265                             | 270 |
| Leu Lys Lys Gly Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile |                                 |     |
| 275                                                             | 280                             | 285 |
| Arg Glu Gly Arg Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr |                                 |     |
| 290                                                             | 295                             | 300 |
| Arg Met Val Cys His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val |                                 |     |
| 305                                                             | 310                             | 315 |
| Glu Gly Cys Arg Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp |                                 |     |
| 325                                                             | 330                             | 335 |
| Glu Pro Arg Arg Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr |                                 |     |
| 340                                                             | 345                             | 350 |
| Phe Glu Arg Val Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn |                                 |     |
| 355                                                             | 360                             | 365 |
| Asn Leu Pro Ala Leu Gly Ile Ala Lys Leu                         |                                 |     |
| 370                                                             | 375                             |     |

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Ala Ser Gln Ser Gln Val Leu Val Glu Glu Lys Ser Ser Val Arg |    |    |
| 1                                                               | 5  | 10 |
| Ile Leu Thr Leu Asn Arg Pro Lys Gln Leu Asn Ala Leu Ser Phe His |    |    |
| 20                                                              | 25 | 30 |

Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe Glu Glu Asp Pro  
35 40 45  
Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg Ala Phe Cys Ala  
50 55 60  
Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn Gln Gly Asn Trp  
65 70 75 80  
Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met Leu Asn Tyr Val  
85 90 95  
Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu Asn Gly Ile Val  
100 105 110  
Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg Phe Arg Ile Ala  
115 120 125  
Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala Leu Gly Leu Phe  
130 135 140  
Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu Pro Gly Phe Phe  
145 150 155 160  
Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp Gly Ala Glu Met  
165 170 175  
Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser Thr Arg Leu Thr  
180 185 190  
Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn Asp Pro Thr Phe  
195 200 205  
Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro Arg Leu Lys Gln  
210 215 220  
Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg Cys Phe Ser Arg  
225 230 235 240  
Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg Glu Ala Thr Gln  
245 250 255  
Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala Leu Lys Lys Gly  
260 265 270  
Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile Arg Glu Gly Arg  
275 280 285  
Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr Arg Met Val Cys  
290 295 300  
His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val Glu Gly Cys Arg  
305 310 315 320  
Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp Glu Pro Arg Arg  
325 330 335  
Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr Phe Glu Arg Val  
340 345 350  
Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn Asn Leu Pro Ala  
355 360 365  
Leu Gly Ile Ala Lys Leu  
370

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe Glu Glu Asp Pro  
1 5 10 15  
Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg Ala Phe Cys Ala  
20 25 30  
Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn Gln Gly Asn Trp



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met Leu Asn Tyr Val |     |     |
| 50                                                              | 55  | 60  |
| Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu Asn Gly Ile Val |     |     |
| 65                                                              | 70  | 75  |
| Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg Phe Arg Ile Ala |     |     |
| 85                                                              | 90  | 95  |
| Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala Leu Gly Leu Phe |     |     |
| 100                                                             | 105 | 110 |
| Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu Pro Gly Phe Phe |     |     |
| 115                                                             | 120 | 125 |
| Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp Gly Ala Glu Met |     |     |
| 130                                                             | 135 | 140 |
| Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser Thr Arg Leu Thr |     |     |
| 145                                                             | 150 | 155 |
| Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn Asp Pro Thr Phe |     |     |
| 165                                                             | 170 | 175 |
| Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro Arg Leu Lys Gln |     |     |
| 180                                                             | 185 | 190 |
| Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg Cys Phe Ser Arg |     |     |
| 195                                                             | 200 | 205 |
| Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg Glu Ala Thr Gln |     |     |
| 210                                                             | 215 | 220 |
| Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala Leu Lys Lys Gly |     |     |
| 225                                                             | 230 | 235 |
| Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile Arg Glu Gly Arg |     |     |
| 245                                                             | 250 | 255 |
| Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr Arg Met Val Cys |     |     |
| 260                                                             | 265 | 270 |
| His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val Glu Gly Cys Arg |     |     |
| 275                                                             | 280 | 285 |
| Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp Glu Pro Arg Arg |     |     |
| 290                                                             | 295 | 300 |
| Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr Phe Glu Arg Val |     |     |
| 305                                                             | 310 | 315 |
| Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn Asn Leu Pro Ala |     |     |
| 325                                                             | 330 | 335 |
| Leu Gly Ile Ala Lys Leu                                         |     |     |
| 340                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

|               |             |            |            |            |            |     |
|---------------|-------------|------------|------------|------------|------------|-----|
| aatatagtagtac | caactccatt  | gaatgttaaa | actcagaaga | aagtggagtg | atcatataac | 60  |
| gacaatgaag    | aatctcttta  | acttggtcct | tatgttkttc | tttgcaatgc | caattctttc | 120 |
| actctccgag    | aatccaacca  | atttcagcga | gagttgcgaa | gacgggagtg | gagaaaccgg | 180 |
| ttcaagcttt    | ggcatagggt  | tcgatttggg | tcttgatttt | ggtttatacc | ggaatagctg | 240 |
| cccgaagca     | gagtcctatcg | tctactcgtg | ggtggaaacc | acgggtgtag | aggatccaag | 300 |
| aatggctgct    | tctcttctcc  | gtcttcattt | ccacgactgt | tttgtcaatg | gatgtgatgc | 360 |
| ttcgggtgttg   | ttagatgaca  | cagaaggact | ggttggtgaa | aaaacggcgc | ctcctaattc | 420 |
| aaattctcta    | cgagggttcg  | aagtgattga | ttcgataaag | tctgatattg | aatctgtatg | 480 |
| tccagagacc    | gtctcatgcg  | cagacattct | tgccatggct | gctagagatt | cagtcgttgt | 540 |
| gtcgggtgga    | ccaaggtggg  | aggtggaagt | aggaagaaaa | gacagtagaa | cagcaagcaa | 600 |

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| acaggcagca | acaaatggct  | taccctcacc  | aaactcaacc | gtatcaactc | tcattctctac | 660  |
| tttccagaat | cttggccttt  | cacaaaccga  | catggtcgct | ctttccggtg | gacatacatt  | 720  |
| gggaaaggca | cgggNgcAct  | tcgttttacag | ctcggttgca | gccactgcaa | actggacaac  | 780  |
| cagctaacca | cggagacaac  | cttgagttcc  | tcgagtcact | gcaacagtta | tgctcgactg  | 840  |
| ttggccccag | tgtagggtatc | actcagcttg  | acttggtgac | tccatcaaca | tttgacaacc  | 900  |
| agtactatgt | aaacctcctc  | tcgggtgagg  | gattgcttcc | atcagaccag | gcttttagcgg | 960  |
| ttcaagaccc | agggacaagg  | gcgattgttg  | agacctacgc | aacagatcag | tcggttttct  | 1020 |
| ttgaggattt | taagaacgct  | atgggttaaaa | tgggagggat | atccggtggt | agtaatagcg  | 1080 |
| agattaggaa | gaattgtaga  | atgattaact  | aaaaataaaa | gcccgactta | ttgaatgata  | 1140 |
| tctaattatc | tatataaaaa  | ttaaagaagt  | ccacctacgt |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1568903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Leu | Arg | Arg | Lys | Trp | Ser | Asp | His | Ile | Thr | Thr | Met | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Leu | Phe | Asn | Leu | Phe | Leu | Met | Xaa | Phe | Phe | Ala | Met | Pro | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Ser | Glu | Asn | Pro | Thr | Asn | Phe | Ser | Glu | Ser | Cys | Glu | Asp | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Glu | Thr | Gly | Ser | Ser | Phe | Gly | Ile | Gly | Phe | Asp | Leu | Val | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Gly | Leu | Tyr | Arg | Asn | Ser | Cys | Pro | Glu | Ala | Glu | Ser | Ile | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Ser | Trp | Val | Glu | Thr | Thr | Val | Leu | Glu | Asp | Pro | Arg | Met | Ala | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Leu | Arg | Leu | His | Phe | His | Asp | Cys | Phe | Val | Asn | Gly | Cys | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Val | Leu | Leu | Asp | Asp | Thr | Glu | Gly | Leu | Val | Gly | Glu | Lys | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Pro | Asn | Leu | Asn | Ser | Leu | Arg | Gly | Phe | Glu | Val | Ile | Asp | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Lys | Ser | Asp | Ile | Glu | Ser | Val | Cys | Pro | Glu | Thr | Val | Ser | Cys | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ile | Leu | Ala | Met | Ala | Ala | Arg | Asp | Ser | Val | Val | Val | Ser | Gly | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Arg | Trp | Glu | Val | Glu | Val | Gly | Arg | Lys | Asp | Ser | Arg | Thr | Ala | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gln | Ala | Ala | Thr | Asn | Gly | Leu | Pro | Ser | Pro | Asn | Ser | Thr | Val | Ser |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Thr | Leu | Ile | Ser | Thr | Phe | Gln | Asn | Leu | Gly | Leu | Ser | Gln | Thr | Asp | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Ala | Leu | Ser | Gly | Gly | His | Thr | Leu | Gly | Lys | Ala | Arg | Xaa | His | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Tyr | Ser | Ser | Val | Ala | Ala | Thr | Ala | Asn | Trp | Thr | Thr | Ser |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1568904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Leu | Phe | Asn | Leu | Phe | Leu | Met | Xaa | Phe | Phe | Ala | Met | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Leu | Ser | Leu | Ser | Glu | Asn | Pro | Thr | Asn | Phe | Ser | Glu | Ser | Cys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Gly | Ser | Gly | Glu | Thr | Gly | Ser | Ser | Phe | Gly | Ile | Gly | Phe | Asp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Asp | Phe | Gly | Leu | Tyr | Arg | Asn | Ser | Cys | Pro | Glu | Ala | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Val | Tyr | Ser | Trp | Val | Glu | Thr | Thr | Val | Leu | Glu | Asp | Pro | Arg | Met |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ala | Ser | Leu | Leu | Arg | Leu | His | Phe | His | Asp | Cys | Phe | Val | Asn | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Asp | Ala | Ser | Val | Leu | Leu | Asp | Asp | Thr | Glu | Gly | Leu | Val | Gly | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Thr | Ala | Pro | Pro | Asn | Leu | Asn | Ser | Leu | Arg | Gly | Phe | Glu | Val | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Asp | Ser | Ile | Lys | Ser | Asp | Ile | Glu | Ser | Val | Cys | Pro | Glu | Thr | Val | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Ala | Asp | Ile | Leu | Ala | Met | Ala | Ala | Arg | Asp | Ser | Val | Val | Val | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Gly | Pro | Arg | Trp | Glu | Val | Glu | Val | Gly | Arg | Lys | Asp | Ser | Arg | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Ser | Lys | Gln | Ala | Ala | Thr | Asn | Gly | Leu | Pro | Ser | Pro | Asn | Ser | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ser | Thr | Leu | Ile | Ser | Thr | Phe | Gln | Asn | Leu | Gly | Leu | Ser | Gln | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Met | Val | Ala | Leu | Ser | Gly | Gly | His | Thr | Leu | Gly | Lys | Ala | Arg | Xaa |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Phe | Val | Tyr | Ser | Ser | Val | Ala | Ala | Thr | Ala | Asn | Trp | Thr | Thr | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Phe | Phe | Ala | Met | Pro | Ile | Leu | Ser | Leu | Ser | Glu | Asn | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Asn | Phe | Ser | Glu | Ser | Cys | Glu | Asp | Gly | Ser | Gly | Glu | Thr | Gly | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Ile | Gly | Phe | Asp | Leu | Val | Leu | Asp | Phe | Gly | Leu | Tyr | Arg | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Cys | Pro | Glu | Ala | Glu | Ser | Ile | Val | Tyr | Ser | Trp | Val | Glu | Thr | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Leu | Glu | Asp | Pro | Arg | Met | Ala | Ala | Ser | Leu | Leu | Arg | Leu | His | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Asp | Cys | Phe | Val | Asn | Gly | Cys | Asp | Ala | Ser | Val | Leu | Leu | Asp | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

Thr Glu Gly Leu Val Gly Glu Lys Thr Ala Pro Pro Asn Leu Asn Ser  
100 105 110  
Leu Arg Gly Phe Glu Val Ile Asp Ser Ile Lys Ser Asp Ile Glu Ser  
115 120 125  
Val Cys Pro Glu Thr Val Ser Cys Ala Asp Ile Leu Ala Met Ala Ala  
130 135 140  
Arg Asp Ser Val Val Val Ser Gly Gly Pro Arg Trp Glu Val Glu Val  
145 150 155 160  
Gly Arg Lys Asp Ser Arg Thr Ala Ser Lys Gln Ala Ala Thr Asn Gly  
165 170 175  
Leu Pro Ser Pro Asn Ser Thr Val Ser Thr Leu Ile Ser Thr Phe Gln  
180 185 190  
Asn Leu Gly Leu Ser Gln Thr Asp Met Val Ala Leu Ser Gly Gly His  
195 200 205  
Thr Leu Gly Lys Ala Arg Xaa His Phe Val Tyr Ser Ser Val Ala Ala  
210 215 220  
Thr Ala Asn Trp Thr Thr Ser  
225 230

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| aacttagctc  | ataagcatat | ctaatcggag | ctcggagaaa | tttcggttgt | gaagagaaga | 60   |
| aagatgggga  | atgtgttttg | ttgtgtgcaa | gtggatcaat | caacggtagc | gataaaggaa | 120  |
| acattcggga  | aattcgaaga | tggtcttgag | cctggttgcc | atcttcttcc | atggtgtctt | 180  |
| ggtagtcaag  | ttgctgggta | cctctctcta | agggttcagc | aattggacgt | tcgttgcgag | 240  |
| acaaagacta  | aggacaatgt | gtttgttaat | gttggtgcat | cgattcagta | ccgtgcttta | 300  |
| gctaataagg  | caaatgatgc | gtactacaag | ctcagtaaca | caaggggtca | gattcaagct | 360  |
| tatgtgtttg  | atgttattag | agcgaagtgc | ccgaagttgc | ttcttgatga | tgtctttgag | 420  |
| cagaagaatg  | atattgcgaa | aGctgttgaa | gaggagctcg | agaaggcaat | gtcggcttac | 480  |
| ggttatgaga  | ttgtgcaaac | tctcattgtt | gatatcgagc | ctgatgaaca | tgtcaaacgg | 540  |
| gccatgaacg  | aaatcaacgc | tgctgcaagg | atgagattgg | ctgcaaacga | aaaggcagag | 600  |
| gcagagaaaa  | tcctacagat | taagagagct | gaaggtgaag | ctgagtgcaa | gtacctctct | 660  |
| ggctcttgga  | tcgcccgtca | gaggcaggcg | attgtcgatg | gattacgcga | cagtgttttg | 720  |
| ggtttcgctg  | tgaatgtccc | tgggacaact | gctaaagatg | tgatggacat | ggtgctagtt | 780  |
| acacagtact  | ttgacacaat | gaaggagatt | ggtgctagct | ccaagtcgtc | tgccgtgttc | 840  |
| atacctcatg  | gaccaggagc | ggttcgtgat | gtggcttctc | agattagaga | tggccttctt | 900  |
| caaggctcgt  | ccgcaaacct | gtgaagtga  | ttcactgatt | atgtcctctt | ttcttttgac | 960  |
| tatggtgtga  | ttatcatctt | cttctttctt | ttggattatg | ttcgaactct | tttgttttgg | 1020 |
| ttttcttatt  | tctatttgta | tagacttatt | gggggtttat | aattcatata | gaatattaaa | 1080 |
| acgtgttttag | tactaattat | tattgtacac | gaattatggt | ggtg       |            |      |

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..286
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

```

Met Gly Asn Leu Phe Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala
1 5 10
Ile Lys Glu Thr Phe Gly Lys Phe Glu Asp Val Leu Glu Pro Gly Cys
20 25 30
His Phe Leu Pro Trp Cys Leu Gly Ser Gln Val Ala Gly Tyr Leu Ser
35 40 45
Leu Arg Val Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp
50 55 60
Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala
65 70 75 80
Asn Lys Ala Asn Asp Ala Tyr Tyr Lys Leu Ser Asn Thr Arg Gly Gln
85 90 95
Ile Gln Ala Tyr Val Phe Asp Val Ile Arg Ala Ser Val Pro Lys Leu
100 105 110
Leu Leu Asp Asp Val Phe Glu Gln Lys Asn Asp Ile Ala Lys Ala Val
115 120 125
Glu Glu Glu Leu Glu Lys Ala Met Ser Ala Tyr Gly Tyr Glu Ile Val
130 135 140
Gln Thr Leu Ile Val Asp Ile Glu Pro Asp Glu His Val Lys Arg Ala
145 150 155 160
Met Asn Glu Ile Asn Ala Ala Ala Arg Met Arg Leu Ala Ala Asn Glu
165 170 175
Lys Ala Glu Ala Glu Lys Ile Leu Gln Ile Lys Arg Ala Glu Gly Glu
180 185 190
Ala Glu Ser Lys Tyr Leu Ser Gly Leu Gly Ile Ala Arg Gln Arg Gln
195 200 205
Ala Ile Val Asp Gly Leu Arg Asp Ser Val Leu Gly Phe Ala Val Asn
210 215 220
Val Pro Gly Thr Thr Ala Lys Asp Val Met Asp Met Val Leu Val Thr
225 230 235 240
Gln Tyr Phe Asp Thr Met Lys Glu Ile Gly Ala Ser Ser Lys Ser Ser
245 250 255
Ala Val Phe Ile Pro His Gly Pro Gly Ala Val Arg Asp Val Ala Ser
260 265 270
Gln Ile Arg Asp Gly Leu Leu Gln Gly Ser Ser Ala Asn Leu
275 280 285

```

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

```

Met Ser Ala Tyr Gly Tyr Glu Ile Val Gln Thr Leu Ile Val Asp Ile
1 5 10 15
Glu Pro Asp Glu His Val Lys Arg Ala Met Asn Glu Ile Asn Ala Ala
20 25 30
Ala Arg Met Arg Leu Ala Ala Asn Glu Lys Ala Glu Ala Glu Lys Ile
35 40 45
Leu Gln Ile Lys Arg Ala Glu Gly Glu Ala Glu Ser Lys Tyr Leu Ser
50 55 60
Gly Leu Gly Ile Ala Arg Gln Arg Gln Ala Ile Val Asp Gly Leu Arg
65 70 75 80
Asp Ser Val Leu Gly Phe Ala Val Asn Val Pro Gly Thr Thr Ala Lys
85 90 95
Asp Val Met Asp Met Val Leu Val Thr Gln Tyr Phe Asp Thr Met Lys

```

100 105 110  
Glu Ile Gly Ala Ser Ser Lys Ser Ser Ala Val Phe Ile Pro His Gly  
115 120 125  
Pro Gly Ala Val Arg Asp Val Ala Ser Gln Ile Arg Asp Gly Leu Leu  
130 135 140  
Gln Gly Ser Ser Ala Asn Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

gaaaaagaga gcgagcgatg aacagtatct tctccattga cgatttctcc gatcctttct 60  
gggaaactcc tccgattcct ctcaatcctg actcttctaa gcctgttacg gcggatgaag 120  
ttagccagag tcaaccggaa tggactttcg agatgtttct cgaagagatt tcttcgtcgg 180  
cggtagctc tgagccaact ggtaacaaca acaacgcgat cgtcgggtgtt tcttcggcgc 240  
aatctcttcc ttctgtttcc ggacagaatg atttcgagga tgatagtcga tttcgtgatc 300  
gcgattcggg aaatttgatg tgtgctgctc ccatgacgac gaagacgggtg attgttgatt 360  
ccgatgatta tcgtcgtgtt cttagaaca agcttgagac tgagtgcgct actgttgatt 420  
ctcttcgggt tgggtctgtg aagcctgaag attcgactag ttctccagaa actcaacttc 480  
aaccagttca atccagtcct cttactcaag gagaacttgg tgttacttct tccttaccag 540  
ctgaggtgAa aaaaactggt gtatcaatga agcagggttac tagtggatcg tcgagagaat 600  
attctgatga cgaggacctt gatgaagaga atgaaaccac cggttccttg aagccagagg 660  
acgttaaaaa atctagaagg atgctgtcaa atcgtgagtc agctaggcga tctagaagga 720  
gaaagcagga gcaacaagt gacctcgaaa cacagggtta tgatctaaaa ggtgagcatt 780  
catcacttct taaacaactg agcaacatga atcacaagta tgacgaggct gctgttgga 840  
atagaatact aaaggctgac attgagacat taagagctaa ggtgaaaatg gcggaagaaa 900  
ccgtgaagag agtaacagga atgaatccga tgcttctcgg aagatcaagt ggacataaca 960  
acaacaacag aatgccata actggttaaca acaggatgga ttcttctagc attattccag 1020  
cttatcaacc aactcaaac ctaaaccaca tgtcaaacca aaacatcggg atcccaacca 1080  
ttctacctcc aagactcgga acaatttcg ctgctcctcc atcccaaac agctctccct 1140  
tgcagagaat tagaaatgg caaatcacc atgttactcc aagcgccaac ccgtatggct 1200  
ggaataccga acctcagaac gattcagcat ggccgaaaaa atgcgtggac tgatcaaca 1260  
agaagcgggt ttcgcactat attaatgtct atgcatctgt aatttgtaag tgttattaag 1320  
ttacgaatca tgagaaaaca tcttgtgaaa atacagtctc atggcttata tatatataag 1380  
ctctgtctta t

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

Lys Arg Glu Arg Ala Met Asn Ser Ile Phe Ser Ile Asp Asp Phe Ser  
1 5 10 15  
Asp Pro Phe Trp Glu Thr Pro Pro Ile Pro Leu Asn Pro Asp Ser Ser  
20 25 30  
Lys Pro Val Thr Ala Asp Glu Val Ser Gln Ser Gln Pro Glu Trp Thr  
35 40 45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Glu | Met | Phe | Leu | Glu | Glu | Ile | Ser | Ser | Ser | Ala | Val | Ser | Ser | Glu |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Leu | Gly | Asn | Asn | Asn | Asn | Ala | Ile | Val | Gly | Val | Ser | Ser | Ala | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Pro | Ser | Val | Ser | Gly | Gln | Asn | Asp | Phe | Glu | Asp | Asp | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Arg | Asp | Arg | Asp | Ser | Gly | Asn | Leu | Asp | Cys | Ala | Ala | Pro | Met | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Lys | Thr | Val | Ile | Val | Asp | Ser | Asp | Asp | Tyr | Arg | Arg | Val | Leu | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Lys | Leu | Glu | Thr | Glu | Cys | Ala | Thr | Val | Val | Ser | Leu | Arg | Val | Gly |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Val | Lys | Pro | Glu | Asp | Ser | Thr | Ser | Ser | Pro | Glu | Thr | Gln | Leu | Gln |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Val | Gln | Ser | Ser | Pro | Leu | Thr | Gln | Gly | Glu | Leu | Gly | Val | Thr | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Leu | Pro | Ala | Glu | Val | Lys | Lys | Thr | Gly | Val | Ser | Met | Lys | Gln | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Ser | Gly | Ser | Ser | Arg | Glu | Tyr | Ser | Asp | Asp | Glu | Asp | Leu | Asp | Glu |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Glu | Asn | Glu | Thr | Thr | Gly | Ser | Leu | Lys | Pro | Glu | Asp | Val | Lys | Lys | Ser |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Arg | Arg | Met | Leu | Ser | Asn | Arg | Glu | Ser | Ala | Arg | Arg | Ser | Arg | Arg | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Gln | Glu | Gln | Thr | Ser | Asp | Leu | Glu | Thr | Gln | Val | Asn | Asp | Leu | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Glu | His | Ser | Ser | Leu | Leu | Lys | Gln | Leu | Ser | Asn | Met | Asn | His | Lys |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Asp | Glu | Ala | Ala | Val | Gly | Asn | Arg | Ile | Leu | Lys | Ala | Asp | Ile | Glu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Thr | Leu | Arg | Ala | Lys | Val | Lys | Met | Ala | Glu | Glu | Thr | Val | Lys | Arg | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Gly | Met | Asn | Pro | Met | Leu | Leu | Gly | Arg | Ser | Ser | Gly | His | Asn | Asn |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Asn | Arg | Met | Pro | Ile | Thr | Gly | Asn | Asn | Arg | Met | Asp | Ser | Ser | Ser |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ile | Ile | Pro | Ala | Tyr | Gln | Pro | His | Ser | Asn | Leu | Asn | His | Met | Ser | Asn |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Asn | Ile | Gly | Ile | Pro | Thr | Ile | Leu | Pro | Pro | Arg | Leu | Gly | Asn | Asn |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Phe | Ala | Ala | Pro | Pro | Ser | Gln | Thr | Ser | Ser | Pro | Leu | Gln | Arg | Ile | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Asn | Gly | Gln | Asn | His | His | Val | Thr | Pro | Ser | Ala | Asn | Pro | Tyr | Gly | Trp |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |
| Asn | Thr | Glu | Pro | Gln | Asn | Asp | Ser | Ala | Trp | Pro | Lys | Lys | Cys | Val | Asp |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

Met Asn Ser Ile Phe Ser Ile Asp Asp Phe Ser Asp Pro Phe Trp Glu

```

1 5 10 15
Thr Pro Pro Ile Pro Leu Asn Pro Asp Ser Ser Lys Pro Val Thr Ala
20 25 30
Asp Glu Val Ser Gln Ser Gln Pro Glu Trp Thr Phe Glu Met Phe Leu
35 40 45
Glu Glu Ile Ser Ser Ser Ala Val Ser Ser Glu Pro Leu Gly Asn Asn
50 55 60
Asn Asn Ala Ile Val Gly Val Ser Ser Ala Gln Ser Leu Pro Ser Val
65 70 75
Ser Gly Gln Asn Asp Phe Glu Asp Asp Ser Arg Phe Arg Asp Arg Asp
85 90 95
Ser Gly Asn Leu Asp Cys Ala Ala Pro Met Thr Thr Lys Thr Val Ile
100 105 110
Val Asp Ser Asp Asp Tyr Arg Arg Val Leu Lys Asn Lys Leu Glu Thr
115 120 125
Glu Cys Ala Thr Val Val Ser Leu Arg Val Gly Ser Val Lys Pro Glu
130 135 140
Asp Ser Thr Ser Ser Pro Glu Thr Gln Leu Gln Pro Val Gln Ser Ser
145 150 155
Pro Leu Thr Gln Gly Glu Leu Gly Val Thr Ser Ser Leu Pro Ala Glu
165 170 175
Val Lys Lys Thr Gly Val Ser Met Lys Gln Val Thr Ser Gly Ser Ser
180 185 190
Arg Glu Tyr Ser Asp Asp Glu Asp Leu Asp Glu Glu Asn Glu Thr Thr
195 200 205
Gly Ser Leu Lys Pro Glu Asp Val Lys Lys Ser Arg Arg Met Leu Ser
210 215 220
Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg Lys Lys Gln Glu Gln Thr
225 230 235
Ser Asp Leu Glu Thr Gln Val Asn Asp Leu Lys Gly Glu His Ser Ser
245 250 255
Leu Leu Lys Gln Leu Ser Asn Met Asn His Lys Tyr Asp Glu Ala Ala
260 265 270
Val Gly Asn Arg Ile Leu Lys Ala Asp Ile Glu Thr Leu Arg Ala Lys
275 280 285
Val Lys Met Ala Glu Glu Thr Val Lys Arg Val Thr Gly Met Asn Pro
290 295 300
Met Leu Leu Gly Arg Ser Ser Gly His Asn Asn Asn Arg Met Pro
305 310 315
Ile Thr Gly Asn Asn Arg Met Asp Ser Ser Ser Ile Ile Pro Ala Tyr
325 330 335
Gln Pro His Ser Asn Leu Asn His Met Ser Asn Gln Asn Ile Gly Ile
340 345 350
Pro Thr Ile Leu Pro Pro Arg Leu Gly Asn Asn Phe Ala Ala Pro Pro
355 360 365
Ser Gln Thr Ser Ser Pro Leu Gln Arg Ile Arg Asn Gly Gln Asn His
370 375 380
His Val Thr Pro Ser Ala Asn Pro Tyr Gly Trp Asn Thr Glu Pro Gln
385 390 395 400
Asn Asp Ser Ala Trp Pro Lys Lys Cys Val Asp
405 410

```

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366



(D) OTHER INFORMATION: / Ceres Seq. ID 1568931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Glu | Glu | Ile | Ser | Ser | Ser | Ser | Ala | Val | Ser | Ser | Glu | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Gly | Asn | Asn | Asn | Asn | Ala | Ile | Val | Gly | Val | Ser | Ser | Ala | Gln | Ser | Leu |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Ser | Val | Ser | Gly | Gln | Asn | Asp | Phe | Glu | Asp | Asp | Ser | Arg | Phe | Arg |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Arg | Asp | Ser | Gly | Asn | Leu | Asp | Cys | Ala | Ala | Pro | Met | Thr | Thr | Lys |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Val | Ile | Val | Asp | Ser | Asp | Asp | Tyr | Arg | Arg | Val | Leu | Lys | Asn | Lys |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Glu | Thr | Glu | Cys | Ala | Thr | Val | Val | Ser | Leu | Arg | Val | Gly | Ser | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Pro | Glu | Asp | Ser | Thr | Ser | Ser | Pro | Glu | Thr | Gln | Leu | Gln | Pro | Val |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gln | Ser | Ser | Pro | Leu | Thr | Gln | Gly | Glu | Leu | Gly | Val | Thr | Ser | Ser | Leu |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Pro | Ala | Glu | Val | Lys | Lys | Thr | Gly | Val | Ser | Met | Lys | Gln | Val | Thr | Ser |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Gly | Ser | Ser | Arg | Glu | Tyr | Ser | Asp | Asp | Glu | Asp | Leu | Asp | Glu | Glu | Asn |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Glu | Thr | Thr | Gly | Ser | Leu | Lys | Pro | Glu | Asp | Val | Lys | Lys | Ser | Arg | Arg |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Met | Leu | Ser | Asn | Arg | Glu | Ser | Ala | Arg | Arg | Ser | Arg | Arg | Arg | Lys | Gln |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Glu | Gln | Thr | Ser | Asp | Leu | Glu | Thr | Gln | Val | Asn | Asp | Leu | Lys | Gly | Glu |     |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| His | Ser | Ser | Leu | Leu | Lys | Gln | Leu | Ser | Asn | Met | Asn | His | Lys | Tyr | Asp |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Glu | Ala | Ala | Val | Gly | Asn | Arg | Ile | Leu | Lys | Ala | Asp | Ile | Glu | Thr | Leu |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Arg | Ala | Lys | Val | Lys | Met | Ala | Glu | Glu | Thr | Val | Lys | Arg | Val | Thr | Gly |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |     |
| Met | Asn | Pro | Met | Leu | Leu | Gly | Arg | Ser | Ser | Gly | His | Asn | Asn | Asn | Asn |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Arg | Met | Pro | Ile | Thr | Gly | Asn | Asn | Arg | Met | Asp | Ser | Ser | Ser | Ile | Ile |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Pro | Ala | Tyr | Gln | Pro | His | Ser | Asn | Leu | Asn | His | Met | Ser | Asn | Gln | Asn |     |
|     |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |     |
| Ile | Gly | Ile | Pro | Thr | Ile | Leu | Pro | Pro | Arg | Leu | Gly | Asn | Asn | Phe | Ala |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Ala | Pro | Pro | Ser | Gln | Thr | Ser | Ser | Pro | Leu | Gln | Arg | Ile | Arg | Asn | Gly |     |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |     |
| Gln | Asn | His | His | Val | Thr | Pro | Ser | Ala | Asn | Pro | Tyr | Gly | Trp | Asn | Thr |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Glu | Pro | Gln | Asn | Asp | Ser | Ala | Trp | Pro | Lys | Lys | Cys | Val | Asp |     |     |     |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

gtctctcttc cagaacaatc taacgctttc tcgaacatct tcttcttctt ctttctcgaa

attatttttc cagtgatcaa tttcttctct tctagatttt tacaggaact aattttctgc 120  
tctgaggtat cagatgagta gccgatggaa tcgtacgac tacgttggga atttgccctgg 180  
agatattcgc aagtgtgagg ttgaagatct cttctacaag tatggaccaa ttgtggacat 240  
tgatttgaag attccaccga gacctcctgg ttatgccttt gtcgagtttg aagatcctcg 300  
tgatgcagac gatgcaattt atggacgtga tggttatgat tttgatgggt gtcgacttcg 360  
ggttgagatt gcacatggtg gtcgtagatt ttcaccatca gttgataggt acagcagcag 420  
ctacagtgcg agccgtgcac cttcaagacg ctctgactat cgcgtgcttg tgaccggatt 480  
accgcttctt gcttcgtggc aggaccttaa ggatcacatg cgcaaagctg gagatgtctg 540  
cttctctgaa gttttccctg accgtaaagg catgtctggg gttgtggatt atagcaacta 600  
tgatgatatg aagtacgcaa taaggaaact tgatgccact gaatttcgaa atgctttctc 660  
tagtgcttat atacgggtga gggaatatga gtcgaggagt gtgagtcgaa gccagatga 720  
ttctaaaagc tatagaagca ggagtcggag ccgtggtcca agctgtagct atagtagcaa 780  
gagcaggagt gtgtcacctg ctatgacctt ttccccgcgt tcacggcccc ttagtcgttc 840  
togctcgca tacagctctg tctcaaggct ccaatcaaga tcaaaatcaa gatCAAcAYc 900  
aCgatcaaga tcgaattctc cagtttcacc tgtgatatct ggatgaaaat gaaaactggc 960  
cactggctgt acccgaatcg tctcaagctt ctcaggctcc actgctaata gaatttgatt 1020  
ccgatttggg attattatac tgggtcttct gtatgggacg accaatatgt ctttctagtt 1080  
ttagttgtga acctggaatt ggtctgttat tgtgtcatta aaaagccgga aactctgtct 1140  
cggctgcata ataaagttca tcagacgttg tgttgggtgt ggtgaggttt ttccatacat 1200  
atacatttac att

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met Ser Ser Arg Trp Asn Arg Thr Ile Tyr Val Gly Asn Leu Pro Gly  
1 5 10 15  
Asp Ile Arg Lys Cys Glu Val Glu Asp Leu Phe Tyr Lys Tyr Gly Pro  
20 25 30  
Ile Val Asp Ile Asp Leu Lys Ile Pro Pro Arg Pro Pro Gly Tyr Ala  
35 40 45  
Phe Val Glu Phe Glu Asp Pro Arg Asp Ala Asp Asp Ala Ile Tyr Gly  
50 55 60  
Arg Asp Gly Tyr Asp Phe Asp Gly Cys Arg Leu Arg Val Glu Ile Ala  
65 70 75 80  
His Gly Gly Arg Arg Phe Ser Pro Ser Val Asp Arg Tyr Ser Ser Ser  
85 90 95  
Tyr Ser Ala Ser Arg Ala Pro Ser Arg Arg Ser Asp Tyr Arg Val Leu  
100 105 110  
Val Thr Gly Leu Pro Pro Ser Ala Ser Trp Gln Asp Leu Lys Asp His  
115 120 125  
Met Arg Lys Ala Gly Asp Val Cys Phe Ser Glu Val Phe Pro Asp Arg  
130 135 140  
Lys Gly Met Ser Gly Val Val Asp Tyr Ser Asn Tyr Asp Asp Met Lys  
145 150 155 160  
Tyr Ala Ile Arg Lys Leu Asp Ala Thr Glu Phe Arg Asn Ala Phe Ser  
165 170 175  
Ser Ala Tyr Ile Arg Val Arg Glu Tyr Glu Ser Arg Ser Val Ser Arg  
180 185 190  
Ser Pro Asp Asp Ser Lys Ser Tyr Arg Ser Arg Ser Arg Ser Arg Gly  
195 200 205  
Pro Ser Cys Ser Tyr Ser Ser Lys Ser Arg Ser Val Ser Pro Ala Arg  
210 215 220  
Ser Ile Ser Pro Arg Ser Arg Pro Leu Ser Arg Ser Arg Ser Pro Tyr

(2) INFORMATION FOR SEQ ID NO:1090:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1568946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Ala | Gly | Asp | Val | Cys | Phe | Ser | Glu | Val | Phe | Pro | Asp | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Met | Ser | Gly | Val | Val | Asp | Tyr | Ser | Asn | Tyr | Asp | Asp | Met | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ala | Ile | Arg | Lys | Leu | Asp | Ala | Thr | Glu | Phe | Arg | Asn | Ala | Phe | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Tyr | Ile | Arg | Val | Arg | Glu | Tyr | Glu | Ser | Arg | Ser | Val | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Asp | Asp | Ser | Lys | Ser | Tyr | Arg | Ser | Arg | Ser | Arg | Ser | Arg | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Ser | Cys | Ser | Tyr | Ser | Ser | Lys | Ser | Arg | Ser | Val | Ser | Pro | Ala | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ile | Ser | Pro | Arg | Ser | Arg | Pro | Leu | Ser | Arg | Ser | Arg | Ser | Pro | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Val | Ser | Arg | Ser | Gln | Ser | Arg | Ser | Lys | Ser | Arg | Ser | Thr | Xaa |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ser | Arg | Ser | Asn | Ser | Pro | Val | Ser | Pro | Val | Ile | Ser | Gly |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1204

(D) OTHER INFORMATION: / Ceres Seq. ID 1568962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

| (A1) SEQUENCE ALIGNMENT |             |             |             |            | Position   |     |
|-------------------------|-------------|-------------|-------------|------------|------------|-----|
| atataaaata              | accatatctc  | tcacttcttc  | ttcttctctt  | tcttatcact | attcgctcat | 60  |
| ttcccccttc              | ctgttggtac  | agaagtcgac  | ggcgagtacg  | ttcaaccaa  | aagaaacacc | 120 |
| agtatctgtc              | tcagcaatgg  | agtttttcca  | gaaagcaaaa  | gctattcgaa | tgcgtaacag | 180 |
| tcacaacaag              | tatctaacag  | cagacgacga  | tgaagaaacc  | gtaactcaa  | accgtaacgg | 240 |
| atctacaaaa              | aacggttcgt  | ggaccgtcga  | accggttcgt  | gattcttttc | atggtattcg | 300 |
| tcttaaaaa               | tgttacggta  | agttacttaac | cgttcttaac  | gagcggttct | tgctcggagc | 360 |
| tacggggaag              | aaagtgattc  | agttgaaact  | gagtcgggtt  | gattcttctg | ttgagtgggg | 420 |
| accggttaga              | gaaggatcta  | agattaagct  | taggactaga  | tctggtaact | atttacgagg | 480 |
| taatggtggt              | cttcctcctt  | ggagaaactc  | ggtcacacac  | gacgttcctc | atttgtctgc | 540 |
| tactcaggat              | tcgatttctt  | gggatgttga  | tgttgttgag  | atcttgactg | attccgaatt | 600 |
| ccagacggag              | tctgcgaaag  | cgcgcgcacc  | gaagacgacg  | tctccaccgc | cgcactcgag | 660 |
| accgacgagt              | tcgcgcgttg  | cggctcgact  | tccaaggaCt  | tcgtcttctc | tttcagacag | 720 |
| atccgattta              | gattcggttg  | agctctcgcc  | taaactctgat | ggacgaacca | tatattacca | 780 |
| tgctcgctgac             | gaggaaaggac | acgtggaaga  | tgaacaaccc  | gttggatatg | ctttcacggt | 840 |

```
taaaggaaat agcgtggcgg agctgactca gacattgcga gaagaaacgt gcatggaaga 900
cgctgtggtg tgtactcgta gtccttttaa cggcaagctg ttctctcttc gtttgcaact 960
tcctcctaac aacggaacat tgcatgtcat ttactaccc tccagcgcg gacctctagaa 1020
tcgacccgag acaattagaa atgagtgatt gtttggtgaa gcatatgtta tgagtcattt 1080
tactaccctc cagcgcgagc ctctagaatc gacccgagac aattagaaat gagtgattgt 1140
gtgattgttt ggtgaagcat atgttatgaa ccgtataaga agatagtaag agttggtagt 1200
tggt
```

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1568963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

```
Tyr Lys Ile Thr Ser Leu Thr Ser Ser Ser Ser Ser Tyr His
1 5 10 15
Tyr Ser Leu Ile Ser Pro Ser Leu Leu Gln Lys Ser Thr Ala Ser
 20 25 30
Ser Phe Asn Gln Lys Glu Thr Pro Val Ser Val Ser Ala Met Glu Phe
 35 40 45
Phe Gln Lys Ala Lys Ala Ile Arg Met Arg Asn Ser His Asn Lys Tyr
 50 55 60
Leu Thr Ala Asp Asp Asp Glu Glu Thr Val Thr Gln Asn Arg Asn Gly
 65 70 75 80
Ser Thr Lys Asn Val Arg Trp Thr Val Glu Pro Val Arg Asp Ser Phe
 85 90 95
His Val Ile Arg Leu Lys Ser Cys Tyr Gly Lys Tyr Leu Thr Ala Ser
 100 105 110
Asn Glu Arg Phe Leu Leu Gly Ala Thr Gly Lys Lys Val Ile Gln Leu
 115 120 125
Lys Leu Ser Arg Val Asp Ser Ser Val Glu Trp Glu Pro Val Arg Glu
 130 135 140
Gly Ser Lys Ile Lys Leu Arg Thr Arg Ser Gly Asn Tyr Leu Arg Gly
 145 150 155 160
Asn Gly Gly Leu Pro Pro Trp Arg Asn Ser Val Thr His Asp Val Pro
 165 170 175
His Leu Ser Ala Thr Gln Asp Ser Ile Ser Trp Asp Val Asp Val Val
 180 185 190
Glu Ile Leu Thr Asp Ser Glu Phe Gln Thr Glu Ser Ala Lys Ala Pro
 195 200 205
Pro Pro Lys Thr Thr Ser Pro Pro Pro His Arg Arg Pro Thr Ser Ser
 210 215 220
Pro Leu Ser Ala Glu Ser Pro Arg Thr Ser Ser Ser Leu Ser Asp Arg
 225 230 235 240
Ser Asp Ser Asp Ser Val Glu Ser Pro Pro Lys Ser Asp Gly Arg Thr
 245 250 255
Ile Tyr Tyr His Val Ala Asp Glu Glu Gly His Val Glu Asp Glu Thr
 260 265 270
Thr Val Gly Tyr Ala Phe Thr Phe Lys Gly Asn Ser Val Ala Glu Leu
 275 280 285
Thr Gln Thr Leu Arg Glu Glu Thr Cys Met Glu Asp Ala Val Val Cys
 290 295 300
Thr Arg Ser Pro Leu Asn Gly Lys Leu Phe Pro Leu Arg Leu Gln Leu
 305 310 315 320
Pro Pro Asn Asn Gly Thr Leu His Val Ile Leu Leu Pro Ser Ser Ala
 325 330 335
```

Ser Leu

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

Met Glu Phe Phe Gln Lys Ala Lys Ala Ile Arg Met Arg Asn Ser His  
1 5 10 15  
Asn Lys Tyr Leu Thr Ala Asp Asp Asp Glu Glu Thr Val Thr Gln Asn  
20 25 30  
Arg Asn Gly Ser Thr Lys Asn Val Arg Trp Thr Val Glu Pro Val Arg  
35 40 45  
Asp Ser Phe His Val Ile Arg Leu Lys Ser Cys Tyr Gly Lys Tyr Leu  
50 55 60  
Thr Ala Ser Asn Glu Arg Phe Leu Leu Gly Ala Thr Gly Lys Lys Val  
65 70 75 80  
Ile Gln Leu Lys Leu Ser Arg Val Asp Ser Ser Val Glu Trp Glu Pro  
85 90 95  
Val Arg Glu Gly Ser Lys Ile Lys Leu Arg Thr Arg Ser Gly Asn Tyr  
100 105 110  
Leu Arg Gly Asn Gly Gly Leu Pro Trp Arg Asn Ser Val Thr His  
115 120 125  
Asp Val Pro His Leu Ser Ala Thr Gln Asp Ser Ile Ser Trp Asp Val  
130 135 140  
Asp Val Val Glu Ile Leu Thr Asp Ser Glu Phe Gln Thr Glu Ser Ala  
145 150 155 160  
Lys Ala Pro Pro Pro Lys Thr Thr Ser Pro Pro Pro His Arg Arg Pro  
165 170 175  
Thr Ser Ser Pro Leu Ser Ala Glu Ser Pro Arg Thr Ser Ser Ser Leu  
180 185 190  
Ser Asp Arg Ser Asp Ser Asp Ser Val Glu Ser Pro Pro Lys Ser Asp  
195 200 205  
Gly Arg Thr Ile Tyr Tyr His Val Ala Asp Glu Glu Gly His Val Glu  
210 215 220  
Asp Glu Thr Thr Val Gly Tyr Ala Phe Thr Phe Lys Gly Asn Ser Val  
225 230 235 240  
Ala Glu Leu Thr Gln Thr Leu Arg Glu Glu Thr Cys Met Glu Asp Ala  
245 250 255  
Val Val Cys Thr Arg Ser Pro Leu Asn Gly Lys Leu Phe Pro Leu Arg  
260 265 270  
Leu Gln Leu Pro Pro Asn Asn Gly Thr Leu His Val Ile Leu Leu Pro  
275 280 285  
Ser Ser Ala Ser Leu  
290

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1568965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

Met Arg Asn Ser His Asn Lys Tyr Leu Thr Ala Asp Asp Asp Glu Glu  
1 5 10 15  
Thr Val Thr Gln Asn Arg Asn Gly Ser Thr Lys Asn Val Arg Trp Thr  
20 25 30  
Val Glu Pro Val Arg Asp Ser Phe His Val Ile Arg Leu Lys Ser Cys  
35 40 45  
Tyr Gly Lys Tyr Leu Thr Ala Ser Asn Glu Arg Phe Leu Leu Gly Ala  
50 55 60  
Thr Gly Lys Lys Val Ile Gln Leu Lys Leu Ser Arg Val Asp Ser Ser  
65 70 75 80  
Val Glu Trp Glu Pro Val Arg Glu Gly Ser Lys Ile Lys Leu Arg Thr  
85 90 95  
Arg Ser Gly Asn Tyr Leu Arg Gly Asn Gly Gly Leu Pro Pro Trp Arg  
100 105 110  
Asn Ser Val Thr His Asp Val Pro His Leu Ser Ala Thr Gln Asp Ser  
115 120 125  
Ile Ser Trp Asp Val Asp Val Val Glu Ile Leu Thr Asp Ser Glu Phe  
130 135 140  
Gln Thr Glu Ser Ala Lys Ala Pro Pro Pro Lys Thr Thr Ser Pro Pro  
145 150 155 160  
Pro His Arg Arg Pro Thr Ser Ser Pro Leu Ser Ala Glu Ser Pro Arg  
165 170 175  
Thr Ser Ser Ser Leu Ser Asp Arg Ser Asp Ser Asp Ser Val Glu Ser  
180 185 190  
Pro Pro Lys Ser Asp Gly Arg Thr Ile Tyr Tyr His Val Ala Asp Glu  
195 200 205  
Glu Gly His Val Glu Asp Glu Thr Thr Val Gly Tyr Ala Phe Thr Phe  
210 215 220  
Lys Gly Asn Ser Val Ala Glu Leu Thr Gln Thr Leu Arg Glu Glu Thr  
225 230 235 240  
Cys Met Glu Asp Ala Val Val Cys Thr Arg Ser Pro Leu Asn Gly Lys  
245 250 255  
Leu Phe Pro Leu Arg Leu Gln Leu Pro Asn Asn Gly Thr Leu His  
260 265 270  
Val Ile Leu Leu Pro Ser Ser Ala Ser Leu  
275 280

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1043

(D) OTHER INFORMATION: / Ceres Seq. ID 1568966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

aaaagttggc cactaagtgg tgtaagaata ataaattgtc aatatcaatt gactgattct 60  
tattgttcat atacggacac aaatcttttc gttaagtggag tgttttgatc aaaaaaagtt 120  
gaaaacttta aagccatgcc atcacttttg tctaacgaat ccgatggatc attacgagag 180  
catcttggtg atgttggtgt gctgggttca gaaccaaaga ttcggttaca tgatctgacc 240  
cgagtcgccg atgatggatc tcggatcttg aaaggagtta cgatagatat accaaaaggt 300  
atgatcggtg gtgtgattgg acctagtggg agtggaaggt caacgttttt gagatctctg 360  
aatcgtcttt gggaaccacc ggagtcaact gtgttcttgg acggtgaaga tataaccaac 420  
gttgatgtta ttgctcttcg tcgtagagtt ggaatgcttt ttcagcttcc tgttcttttt 480  
caagggactg ttgcggataa tgtgagatat ggtccgaatt tgagagggga gaaactaagt 540  
gacgaagagg ttataagct gctaagtctt gcagaccttg atgcttcctt tgctaagaag 600

actggtgcag agttatctgt ggggtcaagct caacgagtag cacttgcaag gactctagcc 660  
aacgagcctg aggtgttgct gctcgatgaa ccaacaagtg ctcttgatcc gatatcgaca 720  
gagaacattg aggatgttat agtgaaactg aagaagcaga gagggattac tactgtgatt 780  
gtttctcaca gtatcaagca gattcagaaa gttgctgata tcgtttgcct tgttgctgac 840  
ggagagattg ttgaagttct taaaccaagt gagctttcgc acgCtaccgca tccaatggca 900  
cagaggtttc ttcaactcag ttcttgagac cattttctca ttgatggttc ctgcaagtta 960  
tttgctatatt tgcttgaatc ttaataatct ctttcaagag aggaacaaat gctgggttgaa 1020  
tgtaacaaca cttttcatgg ttt

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1568967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

Met Pro Ser Leu Trp Ser Asn Glu Ser Asp Gly Ser Leu Arg Glu His  
1 5 10 15  
Leu Val Asp Val Val Val Ser Gly Ser Glu Pro Lys Ile Arg Val His  
20 25 30  
Asp Leu Thr Arg Val Ala Asp Asp Gly Ser Arg Ile Leu Lys Gly Val  
35 40 45  
Thr Ile Asp Ile Pro Lys Gly Met Ile Val Gly Val Ile Gly Pro Ser  
50 55 60  
Gly Ser Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn Arg Leu Trp Glu  
65 70 75 80  
Pro Pro Glu Ser Thr Val Phe Leu Asp Gly Glu Asp Ile Thr Asn Val  
85 90 95  
Asp Val Ile Ala Leu Arg Arg Arg Val Gly Met Leu Phe Gln Leu Pro  
100 105 110  
Val Leu Phe Gln Gly Thr Val Ala Asp Asn Val Arg Tyr Gly Pro Asn  
115 120 125  
Leu Arg Gly Glu Lys Leu Ser Asp Glu Glu Val Tyr Lys Leu Leu Ser  
130 135 140  
Leu Ala Asp Leu Asp Ala Ser Phe Ala Lys Lys Thr Gly Ala Glu Leu  
145 150 155 160  
Ser Val Gly Gln Ala Gln Arg Val Ala Leu Ala Arg Thr Leu Ala Asn  
165 170 175  
Glu Pro Glu Val Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro  
180 185 190  
Ile Ser Thr Glu Asn Ile Glu Asp Val Ile Val Lys Leu Lys Lys Gln  
195 200 205  
Arg Gly Ile Thr Thr Val Ile Val Ser His Ser Ile Lys Gln Ile Gln  
210 215 220  
Lys Val Ala Asp Ile Val Cys Leu Val Val Asp Gly Glu Ile Val Glu  
225 230 235 240  
Val Leu Lys Pro Ser Glu Leu Ser His Ala Thr His Pro Met Ala Gln  
245 250 255  
Arg Phe Leu Gln Leu Ser Ser  
260

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1568968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

Met Ile Val Gly Val Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe  
1 5 10 15  
Leu Arg Ser Leu Asn Arg Leu Trp Glu Pro Pro Glu Ser Thr Val Phe  
20 25 30  
Leu Asp Gly Glu Asp Ile Thr Asn Val Asp Val Ile Ala Leu Arg Arg  
35 40 45  
Arg Val Gly Met Leu Phe Gln Leu Pro Val Leu Phe Gln Gly Thr Val  
50 55 60  
Ala Asp Asn Val Arg Tyr Gly Pro Asn Leu Arg Gly Glu Lys Leu Ser  
65 70 75 80  
Asp Glu Glu Val Tyr Lys Leu Leu Ser Leu Ala Asp Leu Asp Ala Ser  
85 90 95  
Phe Ala Lys Lys Thr Gly Ala Glu Leu Ser Val Gly Gln Ala Gln Arg  
100 105 110  
Val Ala Leu Ala Arg Thr Leu Ala Asn Glu Pro Glu Val Leu Leu Leu  
115 120 125  
Asp Glu Pro Thr Ser Ala Leu Asp Pro Ile Ser Thr Glu Asn Ile Glu  
130 135 140  
Asp Val Ile Val Lys Leu Lys Lys Gln Arg Gly Ile Thr Thr Val Ile  
145 150 155 160  
Val Ser His Ser Ile Lys Gln Ile Gln Lys Val Ala Asp Ile Val Cys  
165 170 175  
Leu Val Val Asp Gly Glu Ile Val Glu Val Leu Lys Pro Ser Glu Leu  
180 185 190  
Ser His Ala Thr His Pro Met Ala Gln Arg Phe Leu Gln Leu Ser Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1568969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

Met Leu Phe Gln Leu Pro Val Leu Phe Gln Gly Thr Val Ala Asp Asn  
1 5 10 15  
Val Arg Tyr Gly Pro Asn Leu Arg Gly Glu Lys Leu Ser Asp Glu Glu  
20 25 30  
Val Tyr Lys Leu Leu Ser Leu Ala Asp Leu Asp Ala Ser Phe Ala Lys  
35 40 45  
Lys Thr Gly Ala Glu Leu Ser Val Gly Gln Ala Gln Arg Val Ala Leu  
50 55 60  
Ala Arg Thr Leu Ala Asn Glu Pro Glu Val Leu Leu Asp Glu Pro  
65 70 75 80  
Thr Ser Ala Leu Asp Pro Ile Ser Thr Glu Asn Ile Glu Asp Val Ile  
85 90 95  
Val Lys Leu Lys Lys Gln Arg Gly Ile Thr Thr Val Ile Val Ser His  
100 105 110  
Ser Ile Lys Gln Ile Gln Lys Val Ala Asp Ile Val Cys Leu Val Val  
115 120 125



Asp Gly Glu Ile Val Glu Val Leu Lys Pro Ser Glu Leu Ser His Ala  
130 135 140  
Thr His Pro Met Ala Gln Arg Phe Leu Gln Leu Ser Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

atgctcacca cttcacctct ctctctcttt cttctccact gtaacctccc aattcaaaaa 60  
caattataaa ccaaacttga ttaatatata tttctttatc atcatctctt cgaaatgcaa 120  
gatattcatg atttctccat gaacggaggtt ggtggtgggg gaggaggagg agggagggtt 180  
ttcgggtggag gaatcggcgg cggaggaggtt ggtgatcgaa ggatgagagc tcatcagaac 240  
aatatactta accatcatca atctctcaag tgtcctcggt gtaattctct taacacaaaag 300  
ttctgttact acaacaatta caatctttct cagcctcgtc acttttgcaa gaactgtcgt 360  
cgttactgga ctaaaggtgg tgttctccgt aacgttcccg tcggagggtgg ttgccggaaa 420  
gctaaacgtt cgaaaacaaa acaggttccg tcgtcgatcat cagccgacaa accaacgacg 480  
acgcaagatg atcatcacgt ggaggagaaa tcgagtacag gatctcactc tagcagcgag 540  
agctcttctc tcaccgcttc taactctacc accgtcgccg ccgtctccgt caccgcgggc 600  
gcggaagttg cttcgctcgtt tattccaggt tttgatatgc ctaatatgaa aatttacggt 660  
aacgggatcg agtggctcgac gttacttggg caaggctcat cggccgggtgg tgttttctcg 720  
gagatcgggtg gttttccggc ggtttcagct attgaaacta caccgtttgg attcgggggt 780  
aaattcgtaa atcaagatga tcatctgaag ttagaagggtg aaactgtaca gcagcaacag 840  
tttggagatc gaacggctca ggttgagttt caaggaagat cttcggatcc gaatatggga 900  
tttgaaccgt tggattgggg aagtggcggg ggagatcaaa cactgtttga tttaaccagt 960  
accgttgatc atgcatactg gactcaaagt caatggacgt cgtctgacca agatcagagt 1020  
ggtctctacc ttccttgatt ctgatcatag cttcttcttc ttaacccaaa aatatatatt 1080  
ttatacacat aaggtaaagt tcgatgaagt ggttttttwa attttTattt gatggGtcta 1140  
aaAocgggatt Tattatataa ttatatgact gcttgtaaatt tttttTccca aatatcaaat 1200  
ttacctctct tttttttt

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

Met Gln Asp Ile His Asp Phe Ser Met Asn Gly Val Gly Gly Gly Gly  
1 5 10 15  
Gly Gly Gly Gly Arg Phe Phe Gly Gly Gly Ile Gly Gly Gly Gly Gly  
20 25 30  
Gly Asp Arg Arg Met Arg Ala His Gln Asn Asn Ile Leu Asn His His  
35 40 45  
Gln Ser Leu Lys Cys Pro Arg Cys Asn Ser Leu Asn Thr Lys Phe Cys  
50 55 60  
Tyr Tyr Asn Asn Tyr Asn Leu Ser Gln Pro Arg His Phe Cys Lys Asn  
65 70 75 80  
Cys Arg Arg Tyr Trp Thr Lys Gly Gly Val Leu Arg Asn Val Pro Val  
85 90 95

Gly Gly Gly Cys Arg Lys Ala Lys Arg Ser Lys Thr Lys Gln Val Pro  
100 105 110  
Ser Ser Ser Ser Ala Asp Lys Pro Thr Thr Thr Gln Asp Asp His His  
115 120 125  
Val Glu Glu Lys Ser Ser Thr Gly Ser His Ser Ser Ser Glu Ser Ser  
130 135 140  
Ser Leu Thr Ala Ser Asn Ser Thr Thr Val Ala Ala Val Ser Val Thr  
145 150 155 160  
Ala Ala Ala Glu Val Ala Ser Ser Val Ile Pro Gly Phe Asp Met Pro  
165 170 175  
Asn Met Lys Ile Tyr Gly Asn Gly Ile Glu Trp Ser Thr Leu Leu Gly  
180 185 190  
Gln Gly Ser Ser Ala Gly Gly Val Phe Ser Glu Ile Gly Gly Phe Pro  
195 200 205  
Ala Val Ser Ala Ile Glu Thr Thr Pro Phe Gly Phe Gly Gly Lys Phe  
210 215 220  
Val Asn Gln Asp Asp His Leu Lys Leu Glu Gly Glu Thr Val Gln Gln  
225 230 235 240  
Gln Gln Phe Gly Asp Arg Thr Ala Gln Val Glu Phe Gln Gly Arg Ser  
245 250 255  
Ser Asp Pro Asn Met Gly Phe Glu Pro Leu Asp Trp Gly Ser Gly Gly  
260 265 270  
Gly Asp Gln Thr Leu Phe Asp Leu Thr Ser Thr Val Asp His Ala Tyr  
275 280 285  
Trp Ser Gln Ser Gln Trp Thr Ser Ser Asp Gln Asp Gln Ser Gly Leu  
290 295 300  
Tyr Leu Pro  
305

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..299

(D) OTHER INFORMATION: / Ceres Seq. ID 1568976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

Met Asn Gly Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Arg Phe Phe Gly  
1 5 10 15  
Gly Gly Ile Gly Gly Gly Gly Gly Gly Gly Asp Arg Arg Met Arg Ala His  
20 25 30  
Gln Asn Asn Ile Leu Asn His His Gln Ser Leu Lys Cys Pro Arg Cys  
35 40 45  
Asn Ser Leu Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Asn Leu Ser  
50 55 60  
Gln Pro Arg His Phe Cys Lys Asn Cys Arg Arg Tyr Trp Thr Lys Gly  
65 70 75 80  
Gly Val Leu Arg Asn Val Pro Val Gly Gly Gly Cys Arg Lys Ala Lys  
85 90 95  
Arg Ser Lys Thr Lys Gln Val Pro Ser Ser Ser Ser Ala Asp Lys Pro  
100 105 110  
Thr Thr Thr Gln Asp Asp His His Val Glu Glu Lys Ser Ser Thr Gly  
115 120 125  
Ser His Ser Ser Ser Glu Ser Ser Ser Leu Thr Ala Ser Asn Ser Thr  
130 135 140  
Thr Val Ala Ala Val Ser Val Thr Ala Ala Ala Glu Val Ala Ser Ser  
145 150 155 160  
Val Ile Pro Gly Phe Asp Met Pro Asn Met Lys Ile Tyr Gly Asn Gly

|            |           |     |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|-----------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Arg       | Ala | His        | Gln<br>5   | Asn        | Asn        | Ile        | Leu        | Asn<br>10  | His        | His        | Gln        | Ser        | Leu<br>15  | Lys        |
| Cys        | Pro       | Arg | Cys<br>20  | Asn        | Ser        | Leu        | Asn        | Thr<br>25  | Lys        | Phe        | Cys        | Tyr        | Tyr<br>30  | Asn        | Asn        |
| Tyr        | Asn       | Leu | Ser<br>35  | Gln        | Pro        | Arg        | His<br>40  | Phe        | Cys        | Lys        | Asn        | Cys<br>45  | Arg        | Arg        | Tyr        |
| Trp        | Thr<br>50 | Lys | Gly        | Gly        | Val        | Leu<br>55  | Arg        | Asn        | Val        | Pro        | Val<br>60  | Gly        | Gly        | Gly        | Cys        |
| Arg<br>65  | Lys       | Ala | Lys        | Arg        | Ser<br>70  | Lys        | Thr        | Lys        | Gln        | Val<br>75  | Pro        | Ser        | Ser        | Ser        | Ser<br>80  |
| Ala        | Asp       | Lys | Pro        | Thr<br>85  | Thr        | Thr        | Gln        | Asp<br>90  | Asp        | His        | His        | Val        | Glu        | Glu<br>95  | Lys        |
| Ser        | Ser       | Thr | Gly<br>100 | Ser        | His        | Ser        | Ser        | Ser<br>105 | Glu        | Ser        | Ser        | Ser        | Leu<br>110 | Thr        | Ala        |
| Ser        | Asn       | Ser | Thr<br>115 | Thr        | Val        | Ala        | Ala<br>120 | Val        | Ser        | Val        | Thr        | Ala<br>125 | Ala        | Ala        | Glu        |
| Val<br>130 | Ala       | Ser | Ser        | Val        | Ile        | Pro<br>135 | Gly        | Phe        | Asp        | Met        | Pro<br>140 | Asn        | Met        | Lys        | Ile        |
| Tyr<br>145 | Gly       | Asn | Gly        | Ile<br>150 | Glu        | Trp        | Ser        | Thr        | Leu        | Leu<br>155 | Gly        | Gln        | Gly        | Ser        | Ser<br>160 |
| Ala        | Gly       | Gly | Val        | Phe<br>165 | Ser        | Glu        | Ile        | Gly        | Gly<br>170 | Phe        | Pro        | Ala        | Val        | Ser<br>175 | Ala        |
| Ile        | Glu       | Thr | Thr<br>180 | Pro        | Phe        | Gly        | Phe        | Gly<br>185 | Gly        | Lys        | Phe        | Val        | Asn<br>190 | Gln        | Asp        |
| Asp        | His       | Leu | Lys<br>195 | Leu        | Glu        | Gly        | Glu<br>200 | Thr        | Val        | Gln        | Gln        | Gln<br>205 | Gln        | Phe        | Gly        |
| Asp<br>210 | Arg       | Thr | Ala        | Gln        | Val        | Glu<br>215 | Phe        | Gln        | Gly        | Arg        | Ser        | Ser<br>220 | Asp        | Pro        | Asn        |
| Met<br>225 | Gly       | Phe | Glu        | Pro        | Leu<br>230 | Asp        | Trp        | Gly        | Ser        | Gly<br>235 | Gly        | Gly        | Asp        | Gln        | Thr<br>240 |
| Leu        | Phe       | Asp | Leu        | Thr<br>245 | Ser        | Thr        | Val        | Asp        | His<br>250 | Ala        | Tyr        | Trp        | Ser        | Gln<br>255 | Ser        |

Gln Trp Thr Ser Ser Asp Gln Asp Gln Ser Gly Leu Tyr Leu Pro  
260 265 270

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1484
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

```
acggttcaat ttgatttga taataattct ctttttctct ggaaagtctg aatttttttt 60
tgtttggaag cttggagaaa atattatact cttctcattg aatgatcaat ttacaaatcc 120
tcatttgatc gatcttgatc atttttgaaa aaaaaaatct gaactttgag aaaagtattt 180
gagtttcgat atctgtcggg catggtttga ttgtggctgt tgggtaagac aacaaattag 240
ggtttttgaa tagtttgtgt attgaagatt gtctgaaatg gaagcagcta ttactcagag 300
gattcagtag ccatcatggg ttgattgtag aaaagttgag tgtaagccgc agcgtggttc 360
attgcggtat tctcagcagg ttaaggtaga tagaaggttt agaggtcttt ctttggctcg 420
cttgcaacct gaaagaagaa ttgatcaacg aagagcagtt tctccagcgg tttcctgttc 480
tgataacaat tcctcagcgt tgttgagac tggaaagtgt tatccatttg atgaagatat 540
tctcaagaga aaagcagaag aggttaaacc gtatttgaat ggacgatcta tgtaccttgt 600
cggaatgatg ggttctggga aaacaactgt gggaaagtta atgtccaaag tgctcggtta 660
tacgttcttt gactgcgaca ctttgattga gggcgatgaa tggaaacttct gttgcagaga 720
tatttgttca tcacggagag aattttttta gaggaagga gaccgatgcg cttagaagac 780
tctcttcgag gtatcaagtt gttgtttcca cagggtggag tgtagttata agaccatta 840
actggaagta tatgcataaa ggaactcaga tttggctaga tgtgcctcta gaagcattag 900
cccatagaat cgtgctgtt ggaactgaTt cacgaacct gctacacgat gaatcaggag 960
atgcatactc agtggctttc aaacgtctct cggctatttg ggacgagcgc ggtgaagcat 1020
acacaaacgc aaatgccaga gtctccttag aaaatattgc agcaaagcgt ggctataaaa 1080
atgtctcaga tctcacacca actgaaattt gtatcgaggc cttcgagcaa gttctgagct 1140
ttctagagaa agaagaaact atggagatcc cagacggcga cctctaattt cccagccttc 1200
tgttctccgt ctcttcattt atctgtttta tcaactaaac gaagcaatca ctcacacca 1260
ggccattgag caagttcaga gacaaagaag acctctagtt actggttccg ggtcattgga 1320
gcttacacga gcctaatttt gactggaact atggtttatt gaaagaagat tcaatacatg 1380
tatatataaa atatatactt ttttttttgt ttcagtatca tccttcttct cttttcctta 1440
caataagaat taaggaaaag tagccgtgtt tgtaaacatg ggcc
```

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

```
Met Glu Ala Ala Ile Thr Gln Arg Ile Gln Tyr Pro Ser Trp Val Asp
1 5 10 15
Cys Arg Lys Val Glu Cys Lys Pro Gln Arg Gly Ser Leu Arg Tyr Ser
20 25 30
Gln Gln Val Lys Val Asp Arg Arg Phe Arg Gly Leu Ser Leu Ala Arg
35 40 45
Leu Gln Pro Glu Arg Arg Ile Asp Gln Arg Arg Ala Val Ser Pro Ala
50 55 60
Val Ser Cys Ser Asp Asn Asn Ser Ser Ala Leu Leu Glu Thr Gly Ser
65 70 75 80
```

Val Tyr Pro Phe Asp Glu Asp Ile Leu Lys Arg Lys Ala Glu Glu Val  
85 90 95  
Lys Pro Tyr Leu Asn Gly Arg Ser Met Tyr Leu Val Gly Met Met Gly  
100 105 110  
Ser Gly Lys Thr Thr Val Gly Lys Leu Met Ser Lys Val Leu Gly Tyr  
115 120 125  
Thr Phe Phe Asp Cys Asp Thr Leu Ile Glu Gly Asp Glu Trp Asn Phe  
130 135 140  
Cys Cys Arg Asp Ile Cys Ser Ser Arg Arg Glu Phe Phe  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1568980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

Met Asn Gly Thr Ser Val Ala Glu Ile Phe Val His His Gly Glu Asn  
1 5 10 15  
Phe Phe Arg Gly Lys Glu Thr Asp Ala Leu Lys Lys Leu Ser Ser Arg  
20 25 30  
Tyr Gln Val Val Val Ser Thr Gly Gly Gly Ala Val Ile Arg Pro Ile  
35 40 45  
Asn Trp Lys Tyr Met His Lys Lys Gly Ile Ser Ile Trp Leu Asp Val Pro  
50 55 60  
Leu Glu Ala Leu Ala His Arg Ile Ala Ala Val Gly Thr Asp Ser Arg  
65 70 75 80  
Pro Leu Leu His Asp Glu Ser Gly Asp Ala Tyr Ser Val Ala Phe Lys  
85 90 95  
Arg Leu Ser Ala Ile Trp Asp Glu Arg Gly Glu Ala Tyr Thr Asn Ala  
100 105 110  
Asn Ala Arg Val Ser Leu Glu Asn Ile Ala Ala Lys Arg Gly Tyr Lys  
115 120 125  
Asn Val Ser Asp Leu Thr Pro Thr Glu Ile Cys Ile Glu Ala Phe Glu  
130 135 140  
Gln Val Leu Ser Phe Leu Glu Lys Glu Glu Thr Met Glu Ile Pro Asp  
145 150 155 160  
Gly Asp Leu

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1568981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

Met His Lys Gly Ile Ser Ile Trp Leu Asp Val Pro Leu Glu Ala Leu  
1 5 10 15  
Ala His Arg Ile Ala Ala Val Gly Thr Asp Ser Arg Pro Leu Leu His  
20 25 30  
Asp Glu Ser Gly Asp Ala Tyr Ser Val Ala Phe Lys Arg Leu Ser Ala

35 40 45  
Ile Trp Asp Glu Arg Gly Glu Ala Tyr Thr Asn Ala Asn Ala Arg Val  
50 55 60  
Ser Leu Glu Asn Ile Ala Ala Lys Arg Gly Tyr Lys Asn Val Ser Asp  
65 70 75 80  
Leu Thr Pro Thr Glu Ile Cys Ile Glu Ala Phe Glu Gln Val Leu Ser  
85 90 95  
Phe Leu Glu Lys Glu Glu Thr Met Glu Ile Pro Asp Gly Asp Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

tcccccaattc gtctcctcca acagttttct tcttctcttc ttctttgggt gttccttcca 60  
ccaacggcag aaatcgattt ggcttaaato tccccctcct ttgatctct ctgatcgccg 120  
ccgggaacat tcaatttccc ggtagtcca caaaaaaaaa actctccgtt tttatttttc 180  
cccccttttc accggtggaa gtttccggag atggtgtcac ccgaaaacgc taattggatt 240  
tgtgacttga tcgatgctga ttacggaagt ttacaatoc aaggtcctgg tttctcttgg 300  
cctgttcagc aacctattgg tgtttcttct aactccagt ctggagttga tggctcggct 360  
ggaaactcag aagctagcaa agaacctgga tccaaaaaga gggggagatg tgaatcatcc 420  
tctgccacta gctcgaaagc atgtagagag aagcagcgac gggacagggt gaatgacaag 480  
tttatggaat tgggtgcaat tttggagcct ggaaatcctc ccaaaacaga caaggctgct 540  
atcttggttg atgctgtccg catggtgaca cagctacggg gcgaggccca gaagctgaag 600  
gactccaatt caagtcttca ggacaaaatc aaagagttaa agactgagaa aaacgagctg 660  
cgagatgaga aacagaggct gaagacagag aaagaaaagc tggagcagca gctgaaagcc 720  
attaatgctc ctcaaccaag ttttttccca gccccacct tgatgcctac tgcttttgct 780  
tcagcgcaag gccaaagctc tggaaacaag atggtgccaa tcatcagtta cccaggagtt 840  
gccatgtggc agttcatgcc tctgtcttca gtcgatactt ctcaggatca tgtccttcgt 900  
cctcctggtg cttaatcaag aaaaatcatc aaccgggttg cttcttgctt ccgcttaaaa 960  
gaaaagtctc catttgtttt gctctcctct ctttctcggc tttcttagtc ttatcctttt 1020  
gctttgtcgt gttatcatcg taactgttat ctgttgaaca atgatataac attgtaaaact 1080  
ccaattgCtt cgcgcaatgt tatctattca catgtaaatt taagtagagt ttggcagatc 1140  
gtctctcact ttatgtgttc ttacattaat acatagaatg tggttacttc ctgcgc

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

Met Val Ser Pro Glu Asn Ala Asn Trp Ile Cys Asp Leu Ile Asp Ala  
1 5 10 15  
Asp Tyr Gly Ser Phe Thr Ile Gln Gly Pro Gly Phe Ser Trp Pro Val  
20 25 30  
Gln Gln Pro Ile Gly Val Ser Ser Asn Ser Ser Ala Gly Val Asp Gly  
35 40 45  
Ser Ala Gly Asn Ser Glu Ala Ser Lys Glu Pro Gly Ser Lys Lys Arg  
50 55 60

U.S. PAT. & TM. OFF.

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Cys | Glu | Ser | Ser | Ser | Ala | Thr | Ser | Ser | Lys | Ala | Cys | Arg | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Gln | Arg | Arg | Asp | Arg | Leu | Asn | Asp | Lys | Phe | Met | Glu | Leu | Gly | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Leu | Glu | Pro | Gly | Asn | Pro | Pro | Lys | Thr | Asp | Lys | Ala | Ala | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Asp | Ala | Val | Arg | Met | Val | Thr | Gln | Leu | Arg | Gly | Glu | Ala | Gln | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | Asp | Ser | Asn | Ser | Ser | Leu | Gln | Asp | Lys | Ile | Lys | Glu | Leu | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Glu | Lys | Asn | Glu | Leu | Arg | Asp | Glu | Lys | Gln | Arg | Leu | Lys | Thr | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Glu | Lys | Leu | Glu | Gln | Gln | Leu | Lys | Ala | Ile | Asn | Ala | Pro | Gln | Pro |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Phe | Phe | Pro | Ala | Pro | Pro | Met | Met | Pro | Thr | Ala | Phe | Ala | Ser | Ala |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Gly | Gln | Ala | Pro | Gly | Asn | Lys | Met | Val | Pro | Ile | Ile | Ser | Tyr | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Val | Ala | Met | Trp | Gln | Phe | Met | Pro | Pro | Ala | Ser | Val | Asp | Thr | Ser |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gln | Asp | His | Val | Leu | Arg | Pro | Pro | Val | Ala |     |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Gly | Ala | Ile | Leu | Glu | Pro | Gly | Asn | Pro | Pro | Lys | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Ala | Ile | Leu | Val | Asp | Ala | Val | Arg | Met | Val | Thr | Gln | Leu | Arg |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Glu | Ala | Gln | Lys | Leu | Lys | Asp | Ser | Asn | Ser | Ser | Leu | Gln | Asp | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Lys | Glu | Leu | Lys | Thr | Glu | Lys | Asn | Glu | Leu | Arg | Asp | Glu | Lys | Gln |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Leu | Lys | Thr | Glu | Lys | Glu | Lys | Leu | Glu | Gln | Gln | Leu | Lys | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Ala | Pro | Gln | Pro | Ser | Phe | Phe | Pro | Ala | Pro | Pro | Met | Met | Pro | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Phe | Ala | Ser | Ala | Gln | Gly | Gln | Ala | Pro | Gly | Asn | Lys | Met | Val | Pro |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ile | Ile | Ser | Tyr | Pro | Gly | Val | Ala | Met | Trp | Gln | Phe | Met | Pro | Pro | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Asp | Thr | Ser | Gln | Asp | His | Val | Leu | Arg | Pro | Pro | Val | Ala |     |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

11109-11110

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1569009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Gln | Leu | Arg | Gly | Glu | Ala | Gln | Lys | Leu | Lys | Asp | Ser | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Leu | Gln | Asp | Lys | Ile | Lys | Glu | Leu | Lys | Thr | Glu | Lys | Asn | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Arg | Asp | Glu | Lys | Gln | Arg | Leu | Lys | Thr | Glu | Lys | Glu | Lys | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Gln | Leu | Lys | Ala | Ile | Asn | Ala | Pro | Gln | Pro | Ser | Phe | Phe | Pro | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Pro | Met | Met | Pro | Thr | Ala | Phe | Ala | Ser | Ala | Gln | Gly | Gln | Ala | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Asn | Lys | Met | Val | Pro | Ile | Ile | Ser | Tyr | Pro | Gly | Val | Ala | Met | Trp |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gln | Phe | Met | Pro | Pro | Ala | Ser | Val | Asp | Thr | Ser | Gln | Asp | His | Val | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Pro | Pro | Val | Ala |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1936 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1936

(D) OTHER INFORMATION: / Ceres Seq. ID 1569025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| gaagtatatgt | ttctgtaaca  | acaatggcca  | aaaccagagg | gtcttggtgt  | ctcgtaacg   | 60   |
| ctctaatacgc | tatagctttt  | ttggcgacag  | Cccatttgtg | tgaagctggc  | ttgtctcaga  | 120  |
| aagaacagga  | caaggtctcg  | aaattgcctg  | gtcagaattt | taatgttagt  | tttgctcact  | 180  |
| actctgggtt  | tgttgctact  | aatgagcaat  | tgggaagagc | tctcttttac  | tggttatttg  | 240  |
| aagccgttga  | agatgctaag  | tctaagcctc  | ttgttctctg | gctcaatgga  | ggaccaggat  | 300  |
| gttcatctgt  | tgcataatgt  | gaagcagaag  | agataggacc | atttcacatt  | aaggcagatg  | 360  |
| ggaaaactct  | ttaccttaat  | caatattctt  | ggaaccaagc | tgcaaatatt  | ttgttctctg  | 420  |
| atgcacctgt  | tggagtgtgt  | tattcatact  | caaacacctc | gtctgatttg  | aagagcaatg  | 480  |
| gtgataaaag  | aactgccgaa  | gactcactga  | aatttctgct | gaaatgggtt  | gagcgggttc  | 540  |
| cggaaatacaa | aggaagggac  | ttttatatag  | taggggagag | ctatgcagga  | cattacattc  | 600  |
| ctcagctgag  | tgaagccatt  | gtaaaacata  | accaagggtc | tgacaaaaac  | agtataaatc  | 660  |
| tgaaggggta  | catggttaga  | aatgggctga  | tggacgattt | ccatgacagg  | cttggtcttt  | 720  |
| tccaatatat  | ttggtcgttg  | ggtttttatat | ctgaccaaac | atacagctta  | ctgcaacttc  | 780  |
| aatgcgggtt  | cgaatcggtt  | attcactcct  | ccaaacagtg | taacaagatt  | ctggagatag  | 840  |
| cggacaaaga  | aataggtaac  | atagaccaat  | acagtgtcct | cacccagct   | tgtgttgcca  | 900  |
| atgcttccca  | gtcaaatatg  | ttgctaaaga  | aaagacctat | gactagccgc  | gtgagcgaac  | 960  |
| agtatgatcc  | ttgtacggag  | aaacacacta  | cagtttattt | caatcttcca  | gaggttcaaa  | 1020 |
| aagccctcca  | tgtccacca   | ggacttgcac  | catcaaatg  | ggatacttgc  | agtgatgtcg  | 1080 |
| tgagtgaaca  | ctggaatgac  | tctccttctt  | cggttctaaa | catttaccac  | gagcttatag  | 1140 |
| ctgctgggct  | togtatctgg  | gttttcagtg  | gggacgcaga | tgccggttgta | ccagtcacat  | 1200 |
| caaccgggta  | cagtatcgat  | gcactaaacc  | ttcgtccttt | gggtgcctat  | ggtccttggt  | 1260 |
| acttagatgg  | acaggtggga  | gggtggagtc  | agcagtatgc | tggctctgaac | tttgtagacg  | 1320 |
| tgagaggtgc  | aggccatgaa  | gttccttttg  | acagaccgaa | gcaagctcct  | gcgctcttca  | 1380 |
| aggcttttat  | atctggaact  | ccattgtcca  | cacatgagaa | cagcatcagc  | cgcgacatgt  | 1440 |
| ctgaaactcgt | tagtgactca  | taattgagtt  | tgatttgatg | taatgtgtga  | tttggtattct | 1500 |
| caatcaaaaa  | ctttccacat  | aggccgttga  | aataagaaga | gggaaagaga  | ataaatcagt  | 1560 |
| gttttaagtg  | atacgttcaa  | tgtctcttct  | tcttctgggt | gtttgtttgt  | ttggataaac  | 1620 |
| atttgctgct  | tggaaatctaa | taaaagaagt  | ttctaccatt | tgtagcccat  | acgatccttg  | 1680 |
| aataacaaca  | acataattctt | gtgtaatgag  | aaagtgaagt | ctgatctgtg  | atgtatagga  | 1740 |
| ctgggtatta  | atctggtaac  | ggatataata  | ctggggtaga | aaatagaatt  | tagactagta  | 1800 |



ttgggggtct aaacgaaatt atacagaagc attgggcttg acttggccca tgagacctaa 1860  
gcccataattt taaagaatta ggggtttctt cttcctttgt ctgttcaa tgaagaaacc 1920  
tgtttttttt tatttc

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ile | Val | Ser | Val | Thr | Thr | Met | Ala | Lys | Thr | Arg | Gly | Ser | Cys | Cys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Val | Asn | Ala | Leu | Ile | Ala | Ile | Ala | Phe | Leu | Ala | Thr | Ala | His | Leu |  |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     |     | 30  |     |     |  |
| Cys | Glu | Ala | Gly | Leu | Ser | Gln | Lys | Glu | Gln | Asp | Lys | Val | Ser | Lys | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Pro | Gly | Gln | Asn | Phe | Asn | Val | Ser | Phe | Ala | His | Tyr | Ser | Gly | Phe | Val |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Thr | Asn | Glu | Gln | Leu | Gly | Arg | Ala | Leu | Phe | Tyr | Trp | Leu | Phe | Glu |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ala | Val | Glu | Asp | Ala | Lys | Ser | Lys | Pro | Leu | Val | Leu | Trp | Leu | Asn | Gly |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly | Pro | Gly | Cys | Ser | Ser | Val | Ala | Tyr | Gly | Glu | Ala | Glu | Glu | Ile | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Phe | His | Ile | Lys | Ala | Asp | Gly | Lys | Thr | Leu | Tyr | Leu | Asn | Gln | Tyr |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ser | Trp | Asn | Gln | Ala | Ala | Asn | Ile | Leu | Phe | Leu | Asp | Ala | Pro | Val | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Gly | Tyr | Ser | Tyr | Ser | Asn | Thr | Ser | Ser | Asp | Leu | Lys | Ser | Asn | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Asp | Lys | Arg | Thr | Ala | Glu | Asp | Ser | Leu | Lys | Phe | Leu | Leu | Lys | Trp | Val |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Glu | Arg | Phe | Pro | Glu | Tyr | Lys | Gly | Arg | Asp | Phe | Tyr | Ile | Val | Gly | Glu |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Ser | Tyr | Ala | Gly | His | Tyr | Ile | Pro | Gln | Leu | Ser | Glu | Ala | Ile | Val | Lys |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| His | Asn | Gln | Gly | Ser | Asp | Lys | Asn | Ser | Ile | Asn | Leu | Lys | Gly | Tyr | Met |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Val | Gly | Asn | Gly | Leu | Met | Asp | Asp | Phe | His | Asp | Arg | Leu | Gly | Leu | Phe |  |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Gln | Tyr | Ile | Trp | Ser | Leu | Gly | Phe | Ile | Ser | Asp | Gln | Thr | Tyr | Ser | Leu |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Leu | Gln | Leu | Gln | Cys | Gly | Phe | Glu | Ser | Phe | Ile | His | Ser | Ser | Lys | Gln |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Cys | Asn | Lys | Ile | Leu | Glu | Ile | Ala | Asp | Lys | Glu | Ile | Gly | Asn | Ile | Asp |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gln | Tyr | Ser | Val | Phe | Thr | Pro | Ala | Cys | Val | Ala | Asn | Ala | Ser | Gln | Ser |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |  |
| Asn | Met | Leu | Leu | Lys | Lys | Arg | Pro | Met | Thr | Ser | Arg | Val | Ser | Glu | Gln |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Tyr | Asp | Pro | Cys | Thr | Glu | Lys | His | Thr | Thr | Val | Tyr | Phe | Asn | Leu | Pro |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Glu | Val | Gln | Lys | Ala | Leu | His | Val | Pro | Pro | Gly | Leu | Ala | Pro | Ser | Lys |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Trp | Asp | Thr | Cys | Ser | Asp | Val | Val | Ser | Glu | His | Trp | Asn | Asp | Ser | Pro |  |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |  |

Ser Ser Val Leu Asn Ile Tyr His Glu Leu Ile Ala Ala Gly Leu Arg  
370 375 380  
Ile Trp Val Phe Ser Gly Asp Ala Asp Ala Val Val Pro Val Thr Ser  
385 390 395 400  
Thr Arg Tyr Ser Ile Asp Ala Leu Asn Leu Arg Pro Leu Gly Ala Tyr  
405 410 415  
Gly Pro Trp Tyr Leu Asp Gly Gln Val Gly Gly Trp Ser Gln Gln Tyr  
420 425 430  
Ala Gly Leu Asn Phe Val Thr Val Arg Gly Ala Gly His Glu Val Pro  
435 440 445  
Leu His Arg Pro Lys Gln Ala Leu Ala Leu Phe Lys Ala Phe Ile Ser  
450 455 460  
Gly Thr Pro Leu Ser Thr His Glu Asn Ser Ile Ser Arg Asp Met Ser  
465 470 475 480  
Glu Leu Val Ser Asp Ser  
485

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1569027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

Met Ala Lys Thr Arg Gly Ser Cys Cys Leu Val Asn Ala Leu Ile Ala  
1 5 10 15  
Ile Ala Phe Leu Ala Thr Ala His Leu Cys Glu Ala Gly Leu Ser Gln  
20 25 30  
Lys Glu Gln Asp Lys Val Ser Lys Leu Pro Gly Gln Asn Phe Asn Val  
35 40 45  
Ser Phe Ala His Tyr Ser Gly Phe Val Ala Thr Asn Glu Gln Leu Gly  
50 55 60  
Arg Ala Leu Phe Tyr Trp Leu Phe Glu Ala Val Glu Asp Ala Lys Ser  
65 70 75 80  
Lys Pro Leu Val Leu Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Val  
85 90 95  
Ala Tyr Gly Glu Ala Glu Glu Ile Gly Pro Phe His Ile Lys Ala Asp  
100 105 110  
Gly Lys Thr Leu Tyr Leu Asn Gln Tyr Ser Trp Asn Gln Ala Ala Asn  
115 120 125  
Ile Leu Phe Leu Asp Ala Pro Val Gly Val Gly Tyr Ser Tyr Ser Asn  
130 135 140  
Thr Ser Ser Asp Leu Lys Ser Asn Gly Asp Lys Arg Thr Ala Glu Asp  
145 150 155 160  
Ser Leu Lys Phe Leu Leu Lys Trp Val Glu Arg Phe Pro Glu Tyr Lys  
165 170 175  
Gly Arg Asp Phe Tyr Ile Val Gly Glu Ser Tyr Ala Gly His Tyr Ile  
180 185 190  
Pro Gln Leu Ser Glu Ala Ile Val Lys His Asn Gln Gly Ser Asp Lys  
195 200 205  
Asn Ser Ile Asn Leu Lys Gly Tyr Met Val Gly Asn Gly Leu Met Asp  
210 215 220  
Asp Phe His Asp Arg Leu Gly Leu Phe Gln Tyr Ile Trp Ser Leu Gly  
225 230 235 240  
Phe Ile Ser Asp Gln Thr Tyr Ser Leu Leu Gln Leu Gln Cys Gly Phe  
245 250 255  
Glu Ser Phe Ile His Ser Ser Lys Gln Cys Asn Lys Ile Leu Glu Ile

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 260                                                             | 265 | 270 |
| Ala Asp Lys Glu Ile Gly Asn Ile Asp Gln Tyr Ser Val Phe Thr Pro |     |     |
| 275                                                             | 280 | 285 |
| Ala Cys Val Ala Asn Ala Ser Gln Ser Asn Met Leu Leu Lys Lys Arg |     |     |
| 290                                                             | 295 | 300 |
| Pro Met Thr Ser Arg Val Ser Glu Gln Tyr Asp Pro Cys Thr Glu Lys |     |     |
| 305                                                             | 310 | 315 |
| His Thr Thr Val Tyr Phe Asn Leu Pro Glu Val Gln Lys Ala Leu His |     |     |
| 325                                                             | 330 | 335 |
| Val Pro Pro Gly Leu Ala Pro Ser Lys Trp Asp Thr Cys Ser Asp Val |     |     |
| 340                                                             | 345 | 350 |
| Val Ser Glu His Trp Asn Asp Ser Pro Ser Ser Val Leu Asn Ile Tyr |     |     |
| 355                                                             | 360 | 365 |
| His Glu Leu Ile Ala Ala Gly Leu Arg Ile Trp Val Phe Ser Gly Asp |     |     |
| 370                                                             | 375 | 380 |
| Ala Asp Ala Val Val Pro Val Thr Ser Thr Arg Tyr Ser Ile Asp Ala |     |     |
| 385                                                             | 390 | 395 |
| Leu Asn Leu Arg Pro Leu Gly Ala Tyr Gly Pro Trp Tyr Leu Asp Gly |     |     |
| 405                                                             | 410 | 415 |
| Gln Val Gly Gly Trp Ser Gln Gln Tyr Ala Gly Leu Asn Phe Val Thr |     |     |
| 420                                                             | 425 | 430 |
| Val Arg Gly Ala Gly His Glu Val Pro Leu His Arg Pro Lys Gln Ala |     |     |
| 435                                                             | 440 | 445 |
| Leu Ala Leu Phe Lys Ala Phe Ile Ser Gly Thr Pro Leu Ser Thr His |     |     |
| 450                                                             | 455 | 460 |
| Glu Asn Ser Ile Ser Arg Asp Met Ser Glu Leu Val Ser Asp Ser     |     |     |
| 465                                                             | 470 | 475 |

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1569028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Gly Asn Gly Leu Met Asp Asp Phe His Asp Arg Leu Gly Leu |  |
| 1 5 10 15                                                       |  |
| Phe Gln Tyr Ile Trp Ser Leu Gly Phe Ile Ser Asp Gln Thr Tyr Ser |  |
| 20 25 30                                                        |  |
| Leu Leu Gln Leu Gln Cys Gly Phe Glu Ser Phe Ile His Ser Ser Lys |  |
| 35 40 45                                                        |  |
| Gln Cys Asn Lys Ile Leu Glu Ile Ala Asp Lys Glu Ile Gly Asn Ile |  |
| 50 55 60                                                        |  |
| Asp Gln Tyr Ser Val Phe Thr Pro Ala Cys Val Ala Asn Ala Ser Gln |  |
| 65 70 75 80                                                     |  |
| Ser Asn Met Leu Leu Lys Lys Arg Pro Met Thr Ser Arg Val Ser Glu |  |
| 85 90 95                                                        |  |
| Gln Tyr Asp Pro Cys Thr Glu Lys His Thr Thr Val Tyr Phe Asn Leu |  |
| 100 105 110                                                     |  |
| Pro Glu Val Gln Lys Ala Leu His Val Pro Pro Gly Leu Ala Pro Ser |  |
| 115 120 125                                                     |  |
| Lys Trp Asp Thr Cys Ser Asp Val Val Ser Glu His Trp Asn Asp Ser |  |
| 130 135 140                                                     |  |
| Pro Ser Ser Val Leu Asn Ile Tyr His Glu Leu Ile Ala Ala Gly Leu |  |
| 145 150 155 160                                                 |  |
| Arg Ile Trp Val Phe Ser Gly Asp Ala Asp Ala Val Val Pro Val Thr |  |
| 165 170 175                                                     |  |

Ser Thr Arg Tyr Ser Ile Asp Ala Leu Asn Leu Arg Pro Leu Gly Ala  
180 185 190  
Tyr Gly Pro Trp Tyr Leu Asp Gly Gln Val Gly Gly Trp Ser Gln Gln  
195 200 205  
Tyr Ala Gly Leu Asn Phe Val Thr Val Arg Gly Ala Gly His Glu Val  
210 215 220  
Pro Leu His Arg Pro Lys Gln Ala Leu Ala Leu Phe Lys Ala Phe Ile  
225 230 235 240  
Ser Gly Thr Pro Leu Ser Thr His Glu Asn Ser Ile Ser Arg Asp Met  
245 250 255  
Ser Glu Leu Val Ser Asp Ser  
260

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1666
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ctgattacga ttcaatcctc tccgacgtt ggccctcctgt ttccgtttta ctcgacatcg  | 60   |
| ttccgacgac ttttgacctg gaatcgacgc agtgacttca attcaactat tgcacttggt  | 120  |
| ttgttggcaa tggacaaagg agcacctcct agtatTTTTg tgaatgatgg gtcattcatg  | 180  |
| gaaagattca gacagcttca acaggagaaa gataaagaca aggataagggt tgtccaagtt | 240  |
| gaggattcta agccggtgaa gattatatca aatcccaaac ctgctgctaa taaaatttcc  | 300  |
| attggattaa agcccaatga tgcccagaag aaaggtggta agcttgcttt cagcttgaag  | 360  |
| caaaagtcta agcttcttgc acctcctgtg aagcttggtta cagaagaaga tgaggatgat | 420  |
| gaggatgtta aacatgaaca aggctttgga tccgtaaagc gtcaaaagtt agagcagaga  | 480  |
| gacacacctg taaagtcagc aaaagtatcg gatgttgac caccctccgcc cagtgatcct  | 540  |
| actgtgaaga aagttgctga taaactagca agttttgttg ctaagcatgg aaggccattt  | 600  |
| gagcacatta caggcaaaa gaatcctggg gatacaccat ttaaatttct ttttgacgag   | 660  |
| aactgtgctg actacaagta ctatgtattc aggtctggctg aagaggaaaa attaatTTca | 720  |
| caaaccaagg attctggtgt acttcacagt ggtgatgcag gctcgcgaaac gtccacagca | 780  |
| gcaatccctt tgcaaaagcc agcttatcaa caaacaggat atcagatccc tgcctcagct  | 840  |
| ctctatgata ctctgtgga acctggagct tcttctagat ctgctcaggc atcaattaca   | 900  |
| agacccagcg acagtgaact ctttagtggg ccgaggggtg cagacctct atcaatgatg   | 960  |
| gagttttaca tgaagaaggc tgcccaagaa gagaaaatga gacgtcctag gcagtcaaaa  | 1020 |
| gacgaaatgc ctccaccagc ttcccttcaa ggcccatctg aaacttcctc cacagaccct  | 1080 |
| ggaaagagag gtcacacat gggtgattat atcccacttg aGgagctaga taagttcctt   | 1140 |
| tcaaagtgca atgacgcagc tgcacaaaaa gccacaaagg aggtctgtga gaaagcgaag  | 1200 |
| atccaagcag ataatgttgg acataaaactc ttgtcaaaaa tgggttgga agaaggtgaa  | 1260 |
| ggtataggaa gctccagaaa gggatatgca gaccctataa tggcaggcga tgtaaagaca  | 1320 |
| aacaacttgg gagttggtgc ttccgctcca ggagaagtca agcctgagga tgatatatac  | 1380 |
| gagcagtaca agaagcggat gatgctgggt tacaaaacaca gacccaatcc actgggaaat | 1440 |
| cccaggaagg cgtattacta aggatcaaat caatgtgtta tgcgcaatta ttatctttgg  | 1500 |
| ttcacctcag caccgtctga gctttgcttt tctattataa agaatgttca agctttttaga | 1560 |
| ttactgatat attgaagtgt tggtatgcat tgaattttgcg tttcagtgtg caaatagatc | 1620 |
| tctttgacag acatatcagt tgaaatacaa tggatttggt attgcc                 |      |

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(D) OTHER INFORMATION: / Ceres Seq. ID 1569030

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu<br>1   | Ile        | Thr        | Ile        | Gln<br>5   | Ser        | Ser        | Pro        | Ile        | Val<br>10  | Gly        | Leu        | Leu        | Phe        | Pro<br>15  | Phe        |
| Tyr        | Ser        | Thr        | Ser        | Phe<br>20  | Arg        | Arg        | Leu        | Leu<br>25  | Thr        | Trp        | Asn        | Arg        | Arg        | Ser        | Asp        |
| Phe        | Asn        | Ser        | Thr        | Ile<br>35  | Ala        | Leu        | Gly<br>40  | Leu        | Leu        | Ala        | Met        | Asp<br>45  | Lys        | Gly        | Ala        |
| Pro        | Pro<br>50  | Ser        | Ile        | Phe        | Val<br>55  | Asn        | Asp        | Gly        | Ser        | Phe        | Met<br>60  | Glu        | Arg        | Phe        | Arg        |
| Gln<br>65  | Leu        | Gln        | Gln        | Glu<br>70  | Lys        | Asp        | Lys        | Asp        | Lys        | Asp<br>75  | Lys        | Val        | Val        | Gln        | Val<br>80  |
| Glu        | Asp        | Ser        | Lys        | Pro<br>85  | Val        | Lys        | Ile        | Ile        | Ser<br>90  | Asn        | Pro        | Lys        | Pro        | Ala        | Ala        |
| Asn        | Lys        | Ile        | Ser<br>100 | Ile        | Gly        | Leu        | Lys        | Pro<br>105 | Asn        | Asp        | Ala        | Gln        | Lys<br>110 | Lys        | Gly        |
| Gly        | Lys        | Leu<br>115 | Ala        | Phe        | Ser        | Leu        | Lys<br>120 | Gln        | Lys        | Ser        | Lys        | Leu<br>125 | Leu        | Ala        | Pro        |
| Pro        | Val<br>130 | Lys        | Leu        | Gly        | Thr<br>135 | Glu        | Asp        | Glu        | Asp        | Asp<br>140 | Glu        | Asp        | Val        | Lys        |            |
| His<br>145 | Glu        | Gln        | Gly        | Phe<br>150 | Gly        | Ser        | Val        | Lys        | Arg        | Gln<br>155 | Lys        | Leu        | Glu        | Gln        | Arg<br>160 |
| Asp        | Thr        | Pro        | Val<br>165 | Lys        | Ser        | Ala        | Lys        | Val<br>170 | Ser        | Asp        | Val        | Ala        | Pro        | Pro        | Pro        |
| Pro        | Ser        | Asp        | Pro<br>180 | Thr        | Val        | Lys        | Lys        | Val<br>185 | Ala        | Asp        | Lys        | Leu<br>190 | Ala        | Ser        | Phe        |
| Val        | Ala<br>195 | Lys        | His        | Gly        | Arg        | Pro        | Phe<br>200 | Glu        | His        | Ile        | Thr<br>205 | Arg        | Gln        | Lys        | Asn        |
| Pro        | Gly<br>210 | Asp        | Thr        | Pro        | Phe<br>215 | Lys        | Phe        | Leu        | Phe        | Asp        | Glu<br>220 | Asn        | Cys        | Ala        | Asp        |
| Tyr<br>225 | Lys        | Tyr        | Tyr        | Val<br>230 | Phe        | Arg        | Leu        | Ala        | Glu        | Glu<br>235 | Glu        | Lys        | Leu        | Ile        | Ser<br>240 |
| Gln        | Thr        | Lys        | Asp<br>245 | Ser        | Gly        | Val        | Leu        | His        | Ser<br>250 | Gly        | Asp        | Ala        | Gly        | Ser        | Arg<br>255 |
| Thr        | Ser        | Thr<br>260 | Ala        | Ile        | Pro        | Leu        | Gln<br>265 | Lys        | Pro        | Ala        | Tyr<br>270 | Gln        | Gln        | Thr        |            |
| Gly        | Tyr<br>275 | Gln        | Ile        | Pro        | Ala        | Ser        | Ala<br>280 | Leu        | Tyr        | Asp        | Thr<br>285 | Pro        | Val        | Glu        | Pro        |
| Gly        | Ala<br>290 | Ser        | Ser        | Arg        | Ser        | Ala<br>295 | Gln        | Ala        | Ser        | Ile        | Thr<br>300 | Arg        | Pro        | Ser        | Asp        |
| Ser<br>305 | Asp        | Ser        | Phe        | Ser<br>310 | Gly        | Pro        | Arg        | Gly        | Ala        | Asp<br>315 | Pro        | Leu        | Ser        | Met        | Met<br>320 |
| Glu        | Phe        | Tyr        | Met<br>325 | Lys        | Lys        | Ala        | Ala        | Gln        | Glu<br>330 | Glu        | Lys        | Met        | Arg        | Arg        | Pro<br>335 |
| Arg        | Gln        | Ser<br>340 | Lys        | Asp        | Glu        | Met        | Pro        | Pro<br>345 | Pro        | Ala        | Ser        | Leu        | Gln<br>350 | Gly        | Pro        |
| Ser        | Glu<br>355 | Thr        | Ser        | Ser        | Thr        | Asp        | Pro<br>360 | Gly        | Lys        | Arg        | Gly<br>365 | His        | His        | Met        | Gly        |
| Asp        | Tyr<br>370 | Ile        | Pro        | Leu        | Glu<br>375 | Glu        | Leu        | Asp        | Lys        | Phe        | Leu<br>380 | Ser        | Lys        | Cys        | Asn        |
| Asp<br>385 | Ala        | Ala        | Ala        | Gln<br>390 | Lys        | Ala        | Thr        | Lys        | Glu        | Ala<br>395 | Ala        | Glu        | Lys        | Ala        | Lys<br>400 |
| Ile        | Gln        | Ala        | Asp<br>405 | Asn        | Val        | Gly        | His        | Lys<br>410 | Leu        | Leu        | Ser        | Lys        | Met        | Gly<br>415 | Trp        |
| Lys        | Glu<br>420 | Gly        | Glu        | Gly        | Ile        | Gly        | Ser        | Ser<br>425 | Arg        | Lys        | Gly        | Met        | Ala        | Asp        | Pro        |
| Ile        | Met<br>435 | Ala        | Gly        | Asp        | Val        | Lys        | Thr<br>440 | Asn        | Asn        | Leu        | Gly<br>445 | Val        | Gly        | Ala        | Ser        |
| Ala        | Pro<br>450 | Gly        | Glu        | Val        | Lys<br>455 | Pro        | Glu        | Asp        | Asp        | Ile        | Tyr<br>460 | Glu        | Gln        | Tyr        | Lys        |

(2) INFORMATION FOR SEQ ID NO:1117:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1569031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Lys | Gly | Ala | Pro | Pro | Ser | Ile | Phe | Val | Asn | Asp | Gly | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Arg | Phe | Arg | Gln | Leu | Gln | Gln | Glu | Lys | Asp | Lys | Asp | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Val | Gln | Val | Glu | Asp | Ser | Lys | Pro | Val | Lys | Ile | Ile | Ser | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Lys | Pro | Ala | Ala | Asn | Lys | Ile | Ser | Ile | Gly | Leu | Lys | Pro | Asn | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Gln | Lys | Lys | Gly | Gly | Lys | Leu | Ala | Phe | Ser | Leu | Lys | Gln | Lys | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Leu | Leu | Ala | Pro | Pro | Val | Lys | Leu | Gly | Thr | Glu | Glu | Asp | Glu | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Glu | Asp | Val | Lys | His | Glu | Gln | Gly | Phe | Gly | Ser | Val | Lys | Arg | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Glu | Gln | Arg | Asp | Thr | Pro | Val | Lys | Ser | Ala | Lys | Val | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ala | Pro | Pro | Pro | Pro | Ser | Asp | Pro | Thr | Val | Lys | Lys | Val | Ala | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Lys | Leu | Ala | Ser | Phe | Val | Ala | Lys | His | Gly | Arg | Pro | Phe | Glu | His | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Arg | Gln | Lys | Asn | Pro | Gly | Asp | Thr | Pro | Phe | Lys | Phe | Leu | Phe | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Asn | Cys | Ala | Asp | Tyr | Lys | Tyr | Tyr | Val | Phe | Arg | Leu | Ala | Glu | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Lys | Leu | Ile | Ser | Gln | Thr | Lys | Asp | Ser | Gly | Val | Leu | His | Ser | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Ala | Gly | Ser | Arg | Thr | Ser | Thr | Ala | Ala | Ile | Pro | Leu | Gln | Lys | Pro |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Tyr | Gln | Gln | Thr | Gly | Tyr | Gln | Ile | Pro | Ala | Ser | Ala | Leu | Tyr | Asp |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Pro | Val | Glu | Pro | Gly | Ala | Ser | Ser | Arg | Ser | Ala | Gln | Ala | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Arg | Pro | Ser | Asp | Ser | Asp | Ser | Phe | Ser | Gly | Pro | Arg | Gly | Ala | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Leu | Ser | Met | Met | Glu | Phe | Tyr | Met | Lys | Lys | Ala | Ala | Gln | Glu | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Met | Arg | Arg | Pro | Arg | Gln | Ser | Lys | Asp | Glu | Met | Pro | Pro | Pro | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Leu | Gln | Gly | Pro | Ser | Glu | Thr | Ser | Ser | Thr | Asp | Pro | Gly | Lys | Arg |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | His | His | Met | Gly | Asp | Tyr | Ile | Pro | Leu | Glu | Glu | Leu | Asp | Lys | Phe |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Ser | Lys | Cys | Asn | Asp | Ala | Ala | Ala | Gln | Lys | Ala | Thr | Lys | Glu | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Glu | Lys | Ala | Lys | Ile | Gln | Al  |     |     |     |     |     |     |     |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1 | Glu | Arg | Phe | Arg<br>5 | Gln | Leu | Gln | Gln | Glu<br>10 | Lys | Asp | Lys | Asp | Lys<br>15 | Asp |
| Lys      | Val | Val | Gln | Val      | Glu | Asp | Ser | Lys | Pro       | Val | Lys | Ile | Ile | Ser       | Asn |
|          |     |     | 20  |          |     |     |     | 25  |           |     |     |     | 30  |           |     |
| Pro      | Lys | Pro | Ala | Ala      | Asn | Lys | Ile | Ser | Ile       | Gly | Leu | Lys | Pro | Asn       | Asp |
|          |     |     | 35  |          |     |     | 40  |     |           |     |     | 45  |     |           |     |
| Ala      | Gln | Lys | Lys | Gly      | Gly | Lys | Leu | Ala | Phe       | Ser | Leu | Lys | Gln | Lys       | Ser |
|          |     |     | 50  |          |     | 55  |     |     |           |     | 60  |     |     |           |     |
| Lys      | Leu | Leu | Ala | Pro      | Pro | Val | Lys | Leu | Gly       | Thr | Glu | Glu | Asp | Glu       | Asp |
| 65       |     |     |     |          | 70  |     |     |     |           | 75  |     |     |     | 80        |     |
| Asp      | Glu | Asp | Val | Lys      | His | Glu | Gln | Gly | Phe       | Gly | Ser | Val | Lys | Arg       | Gln |
|          |     |     |     | 85       |     |     |     |     | 90        |     |     |     |     | 95        |     |
| Lys      | Leu | Glu | Gln | Arg      | Asp | Thr | Pro | Val | Lys       | Ser | Ala | Lys | Val | Ser       | Asp |
|          |     |     | 100 |          |     |     |     | 105 |           |     |     |     | 110 |           |     |
| Val      | Ala | Pro | Pro | Pro      | Pro | Ser | Asp | Pro | Thr       | Val | Lys | Lys | Val | Ala       | Asp |
|          |     |     | 115 |          |     |     | 120 |     |           |     |     | 125 |     |           |     |
| Lys      | Leu | Ala | Ser | Phe      | Val | Ala | Lys | His | Gly       | Arg | Pro | Phe | Glu | His       | Ile |
|          |     |     | 130 |          |     | 135 |     |     |           |     | 140 |     |     |           |     |
| Thr      | Arg | Gln | Lys | Asn      | Pro | Gly | Asp | Thr | Pro       | Phe | Lys | Phe | Leu | Phe       | Asp |
| 145      |     |     |     |          | 150 |     |     |     |           | 155 |     |     |     | 160       |     |
| Glu      | Asn | Cys | Ala | Asp      | Tyr | Lys | Tyr | Tyr | Val       | Phe | Arg | Leu | Ala | Glu       | Glu |
|          |     |     |     | 165      |     |     |     |     | 170       |     |     |     |     | 175       |     |
| Glu      | Lys | Leu | Ile | Ser      | Gln | Thr | Lys | Asp | Ser       | Gly | Val | Leu | His | Ser       | Gly |
|          |     |     | 180 |          |     |     |     | 185 |           |     |     | 190 |     |           |     |
| Asp      | Ala | Gly | Ser | Arg      | Thr | Ser | Thr | Ala | Ala       | Ile | Pro | Leu | Gln | Lys       | Pro |
|          |     |     | 195 |          |     |     | 200 |     |           |     |     | 205 |     |           |     |
| Ala      | Tyr | Gln | Gln | Thr      | Gly | Tyr | Gln | Ile | Pro       | Ala | Ser | Ala | Leu | Tyr       | Asp |
|          |     |     | 210 |          |     | 215 |     |     |           |     | 220 |     |     |           |     |
| Thr      | Pro | Val | Glu | Pro      | Gly | Ala | Ser | Ser | Arg       | Ser | Ala | Gln | Ala | Ser       | Ile |
| 225      |     |     |     |          | 230 |     |     |     |           | 235 |     |     |     |           | 240 |
| Thr      | Arg | Pro | Ser | Asp      | Ser | Asp | Ser | Phe | Ser       | Gly | Pro | Arg | Gly | Ala       | Asp |
|          |     |     |     | 245      |     |     |     |     | 250       |     |     |     |     | 255       |     |
| Pro      | Leu | Ser | Met | Met      | Glu | Phe | Tyr | Met | Lys       | Lys | Ala | Ala | Gln | Glu       | Glu |
|          |     |     | 260 |          |     |     |     | 265 |           |     |     | 270 |     |           |     |
| Lys      | Met | Arg | Arg | Pro      | Arg | Gln | Ser | Lys | Asp       | Glu | Met | Pro | Pro | Pro       | Ala |
|          |     |     | 275 |          |     |     | 280 |     |           |     |     | 285 |     |           |     |
| Ser      | Leu | Gln | Gly | Pro      | Ser | Glu | Thr | Ser | Ser       | Thr | Asp | Pro | Gly | Lys       | Arg |
|          |     |     | 290 |          |     | 295 |     |     |           |     | 300 |     |     |           |     |

(2) INFORMATION FOR SEQ ID NO:1119:

(A) LENGTH: 1316 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME/KEY: -

(B) LOCATION: 1..1316

(D) OTHER INFORMATION: / Ceres Seq. ID 1569041

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aaaaaccaa   | attcgcgaga  | gagaagtatg  | tcgaagaCgc  | tgggtgcaacc | ggtagggcaa | 60   |
| aagaggttga  | ctaattgttg  | agtggttcgt  | ctcaaaaagc  | aaggcaatcg  | cttcgagatc | 120  |
| gcttgttaca  | agaataaggt  | cctttcatgg  | cggctctggcg | tggagaagga  | tatagatgaa | 180  |
| gtgctacagt  | cgcatactgt  | ttattcaa    | gtttcgaaag  | gagttcttgc  | aaaatcgaaa | 240  |
| gacttgatga  | agtcggttgg  | atcagatgat  | catacgaaaa  | tatgcatcga  | tattttggag | 300  |
| aaaggagagc  | ttcaagttgc  | tggaaaaagaa | agagaatcac  | agttctcaag  | ccagtttcgg | 360  |
| gatatagcaa  | cgattgttat  | gcagaaaact  | atcaaccctg  | aaacacaacg  | accttatacc | 420  |
| atcagcatgg  | tagagcgctt  | aatgcattgaa | attcattttg  | ctgttgatcc  | tcatagtaat | 480  |
| tccaagaagc  | aggcacttga  | tgtcatccgt  | gagctgcaa   | agcacttccc  | tataaagcgt | 540  |
| tctccaatga  | gactgcgtct  | tactgttcct  | gttcaaaatt  | tcccctcgct  | tctggagaag | 600  |
| ctaaaaaat   | gggatggtag  | tgttgtctcc  | aaagacgaat  | ctggaacaca  | gatgtccact | 660  |
| gtctgcgaga  | tggaaccggg  | cctattccga  | gagtgatgatt | cccatgtgag  | gagtatccag | 720  |
| ggaagactag  | aaatactcgc  | tgtatcagtt  | catgcagaag  | gtgacacaag  | catggatcat | 780  |
| tacgatgagc  | atgatgat    | ggcattgcga  | accacaagc   | cgttgttacc  | tgctgagact | 840  |
| gagactaagg  | atttgaccga  | tcccgctcgtt | gaacttagca  | agaaactgca  | gaagcaagag | 900  |
| ataagtacta  | cagataaacac | aaagcaagaa  | ggtggagaag  | aaaagaaggg  | gaccaagtgc | 960  |
| agcacttgca  | acacgttcgt  | tggagaggct  | aagcaataca  | gagagcactg  | taagagtgat | 1020 |
| tggcaciaaac | acaaccttaa  | togtaagact  | cggaaactcc  | ctcctattag  | tgctgacgaa | 1080 |
| tgcatgtctg  | agattgacat  | ggacgactct  | agagcagatt  | tgaagaacta  | ctctttctga | 1140 |
| aactacaatt  | ttctcctttt  | gtgcttttaa  | ttttgtcaat  | gtgttaaatc  | tcagtatcat | 1200 |
| atgtgagtat  | gaatacacaa  | aacttgtgga  | atgaaaatttt | gcgaaaactt  | taagagtaaa | 1260 |
| aaacttatgtt | taacagacaa  | ccttggaatat | ttggtatttg  | attaataact  | gtgacc     |      |

(2) INFORMATION FOR SEQ ID NO:1120:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1569042



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Gln | Asn | Ser | Arg | Glu | Arg | Ser | Met | Ser | Lys | Thr | Leu | Val | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Val | Gly | Gln | Lys | Arg | Leu | Thr | Asn | Val | Ala | Val | Val | Arg | Leu | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Gln | Gly | Asn | Arg | Phe | Glu | Ile | Ala | Cys | Tyr | Lys | Asn | Lys | Val | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Trp | Arg | Ser | Gly | Val | Glu | Lys | Asp | Ile | Asp | Glu | Val | Leu | Gln | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| His | Thr | Val | Tyr | Ser | Asn | Val | Ser | Lys | Gly | Val | Leu | Ala | Lys | Ser | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Leu | Met | Lys | Ser | Phe | Gly | Ser | Asp | Asp | His | Thr | Lys | Ile | Cys | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Ile | Leu | Glu | Lys | Gly | Glu | Leu | Gln | Val | Ala | Gly | Lys | Glu | Arg | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gln | Phe | Ser | Ser | Gln | Phe | Arg | Asp | Ile | Ala | Thr | Ile | Val | Met | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Thr | Ile | Asn | Pro | Glu | Thr | Gln | Arg | Pro | Tyr | Thr | Ile | Ser | Met | Val |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Glu | Arg | Leu | Met | His | Glu | Ile | His | Phe | Ala | Val | Asp | Pro | His | Ser | Asn |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Lys | Lys | Gln | Ala | Leu | Asp | Val | Ile | Arg | Glu | Leu | Gln | Lys | His | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Pro | Ile | Lys | Arg | Ser | Pro | Met | Arg | Leu | Arg | Leu | Thr | Val | Pro | Val | Gln |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asn | Phe | Pro | Ser | Leu | Leu | Glu | Lys | Leu | Lys | Glu | Trp | Asp | Gly | Ser | Val |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Ser | Lys | Asp | Glu | Ser | Gly | Thr | Gln | Met | Ser | Thr | Val | Cys | Glu | Met |
|     | 210 |     |     |     | 215 |     |     |     |     |     |     | 220 |     |     |     |
| Glu | Pro | Gly | Leu | Phe | Arg | Glu | Cys | Asp | Ser | His | Val | Arg | Ser | Ile | Gln |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Arg | Leu | Glu | Ile | Leu | Ala | Val | Ser | Val | His | Ala | Glu | Gly | Asp | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ser | Met | Asp | His | Tyr | Asp | Glu | His | Asp | Asp | Met | Ala | Leu | Gln | Thr | His |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |     |
| Lys | Pro | Leu | Pro | Ala | Glu | Thr | Glu | Thr | Lys | Asp | Leu | Thr | Asp | Pro |     |
|     | 275 |     |     |     | 280 |     |     |     |     |     |     | 285 |     |     |     |
| Val | Val | Glu | Leu | Ser | Lys | Lys | Leu | Gln | Lys | Gln | Glu | Ile | Ser | Thr | Thr |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Asp | Asn | Thr | Lys | Gln | Glu | Gly | Gly | Glu | Glu | Lys | Lys | Gly | Thr | Lys | Cys |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Thr | Cys | Asn | Thr | Phe | Val | Gly | Glu | Ala | Lys | Gln | Tyr | Arg | Glu | His |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Cys | Lys | Ser | Asp | Trp | His | Lys | His | Asn | Leu | Asn | Arg | Lys | Thr | Arg | Lys |
|     |     | 340 |     |     |     | 345 |     |     |     |     |     |     | 350 |     |     |
| Leu | Pro | Pro | Ile | Ser | Ala | Asp | Glu | Cys | Met | Ser | Glu | Ile | Asp | Met | Asp |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Asp | Ser | Arg | Ala | Asp | Leu | Lys | Asp | Tyr | Ser | Phe |     |     |     |     |     |
| 370 |     |     |     |     | 375 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..370
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

U.S. PAT. & TRADEMARK OFFICE

| Variable             | Mean | Standard deviation | Minimum | Maximum |
|----------------------|------|--------------------|---------|---------|
| Age                  | 34.5 | 10.5               | 20      | 55      |
| Gender               | 0.5  | 0.5                | 0       | 1       |
| Marital status       | 0.5  | 0.5                | 0       | 1       |
| Education            | 12.5 | 1.5                | 10      | 15      |
| Income               | 15.5 | 5.5                | 10      | 25      |
| Health status        | 0.5  | 0.5                | 0       | 1       |
| Smoking status       | 0.5  | 0.5                | 0       | 1       |
| Alcohol consumption  | 0.5  | 0.5                | 0       | 1       |
| Exercise frequency   | 0.5  | 0.5                | 0       | 1       |
| Stress level         | 0.5  | 0.5                | 0       | 1       |
| Sleep quality        | 0.5  | 0.5                | 0       | 1       |
| Work satisfaction    | 0.5  | 0.5                | 0       | 1       |
| Life satisfaction    | 0.5  | 0.5                | 0       | 1       |
| Overall health       | 0.5  | 0.5                | 0       | 1       |
| Depression score     | 0.5  | 0.5                | 0       | 1       |
| Anxiety score        | 0.5  | 0.5                | 0       | 1       |
| Quality of life      | 0.5  | 0.5                | 0       | 1       |
| Physical health      | 0.5  | 0.5                | 0       | 1       |
| Mental health        | 0.5  | 0.5                | 0       | 1       |
| Social health        | 0.5  | 0.5                | 0       | 1       |
| Environmental health | 0.5  | 0.5                | 0       | 1       |
| Overall well-being   | 0.5  | 0.5                | 0       | 1       |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

FEATURE:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1569044

Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Leu Glu Lys Gly Glu Leu Gln Val Ala Gly Lys Glu Arg Glu Ser Gln |     |     |     |
| 20                                                              | 25  | 30  |     |
| Phe Ser Ser Gln Phe Arg Asp Ile Ala Thr Ile Val Met Gln Lys Thr |     |     |     |
| 35                                                              | 40  | 45  |     |
| Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser Met Val Glu Arg |     |     |     |
| 50                                                              | 55  | 60  |     |
| Leu Met His Glu Ile His Phe Ala Val Asp Pro His Ser Asn Ser Lys |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys His Phe Pro Ile |     |     |     |
| 85                                                              | 90  | 95  |     |
| Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro Val Gln Asn Phe |     |     |     |
| 100                                                             | 105 | 110 |     |
| Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly Ser Val Val Ser |     |     |     |
| 115                                                             | 120 | 125 |     |
| Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys Glu Met Glu Pro |     |     |     |
| 130                                                             | 135 | 140 |     |
| Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser Ile Gln Gly Arg |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly Asp Thr Ser Met |     |     |     |
| 165                                                             | 170 | 175 |     |
| Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln Thr His Lys Pro |     |     |     |
| 180                                                             | 185 | 190 |     |
| Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr Asp Pro Val Val |     |     |     |
| 195                                                             | 200 | 205 |     |
| Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser Thr Thr Asp Asn |     |     |     |
| 210                                                             | 215 | 220 |     |
| Thr Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr Lys Cys Ser Thr |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg Glu His Cys Lys |     |     |     |
| 245                                                             | 250 | 255 |     |
| Ser Asp Trp His Lys His Asn Leu Asn Arg Lys Thr Arg Lys Leu Pro |     |     |     |
| 260                                                             | 265 | 270 |     |
| Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp Met Asp Asp Ser |     |     |     |
| 275                                                             | 280 | 285 |     |
| Arg Ala Asp Leu Lys Asp Tyr Ser Phe                             |     |     |     |
| 290                                                             | 295 |     |     |

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaaaaagac gtctcacaca aaaaagctgc tagaggaaga agacgattca cttctttTcc | 60  |
| cgccactttc actatcttct ccggtggtga gcaaagatgt tgtgggtcga caagtacagg | 120 |
| ccgaaatcac tgcacaaggt catagtcat gaagatatcg cccaaaaact caagaaattg  | 180 |
| gtttccgagc aagattgtcc acatttgctc ttttatgggc cgtcaggttc tggtaaagaa | 240 |
| accctaatta tggctcttct caagcagata tatggggcca gtgcagagaa ggtgaaagtg | 300 |
| gagaacaggg catggaaagt tgatgctggg agtagaacta ttgatctgga gctcactaca | 360 |
| ttatcaagca ccaatcatgt ggaacttact ccaagtgatg caggctttca ggacagatat | 420 |
| attgttcagg agataattaa agaaatggcc aagaacagac caattgacac gaaaggaaag | 480 |
| aagggatata aggtgttggt attaaatgag gttgacaagc tctcacgaga agctcaacat | 540 |
| tctctgcgga gaacaatgga gaaatacagc tcatcttgcc gtctcatctt atgctgcaac | 600 |
| agctcttoga aggttaccga agccattaag tctcgttgtc tcaatgtgcg cataaatgca | 660 |
| ccttcgcagg aagagatagt gaaagtgttg gagttcgttg caaagaaaga aagtctgcaa | 720 |

(2) INFORMATION FOR SEQ ID NO:1124:

(A) LENGTH: 354 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1569050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Trp | Val | Asp | Lys | Tyr | Arg | Pro | Lys | Ser | Leu | Asp | Lys | Val | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | His | Glu | Asp | Ile | Ala | Gln | Lys | Leu | Lys | Lys | Leu | Val | Ser | Glu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Cys | Pro | His | Leu | Leu | Phe | Tyr | Gly | Pro | Ser | Gly | Ser | Gly | Lys | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Ile | Met | Ala | Leu | Leu | Lys | Gln | Ile | Tyr | Gly | Ala | Ser | Ala | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Val | Lys | Val | Glu | Asn | Arg | Ala | Trp | Lys | Val | Asp | Ala | Gly | Ser | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ile | Asp | Leu | Glu | Leu | Thr | Thr | Leu | Ser | Ser | Thr | Asn | His | Val | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Pro | Ser | Asp | Ala | Gly | Phe | Gln | Asp | Arg | Tyr | Ile | Val | Gln | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ile | Lys | Glu | Met | Ala | Lys | Asn | Arg | Pro | Ile | Asp | Thr | Lys | Gly | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gly | Tyr | Lys | Val | Leu | Val | Leu | Asn | Glu | Val | Asp | Lys | Leu | Ser | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Gln | His | Ser | Leu | Arg | Arg | Thr | Met | Glu | Lys | Tyr | Ser | Ser | Ser |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Arg | Leu | Ile | Leu | Cys | Cys | Asn | Ser | Ser | Ser | Lys | Val | Thr | Glu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Lys | Ser | Arg | Cys | Leu | Asn | Val | Arg | Ile | Asn | Ala | Pro | Ser | Gln | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Ile | Val | Lys | Val | Leu | Glu | Phe | Val | Ala | Lys | Lys | Glu | Ser | Leu | Gln |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Pro | Gln | Gly | Phe | Ala | Ala | Arg | Ile | Ala | Glu | Lys | Ser | Asn | Arg | Ser |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Leu | Arg | Arg | Ala | Ile | Leu | Ser | Leu | Glu | Thr | Cys | Arg | Val | Gln | Asn | Tyr |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Phe | Thr | Gly | Asn | Gln | Val | Ile | Ser | Pro | Met | Asp | Trp | Glu | Glu | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ala | Glu | Ile | Ala | Thr | Asp | Met | Met | Lys | Glu | Gln | Ser | Pro | Lys | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Phe | Gln | Val | Arg | Gly | Lys | Val | Tyr | Glu | Leu | Leu | Val | Asn | Cys | Ile |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Pro | Glu | Val | Ile | Leu | Lys | Arg | Leu | Leu | His | Glu | Leu | Leu | Lys | Lys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asp | Ser | Glu | Leu | Lys | Leu | Glu | Val | Cys | His | Trp | Ala | Ala | Tyr | Tyr |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 305 |     | 310 |     | 315 |     | 320 |     |     |     |     |     |     |     |     |     |
| Glu | His | Arg | Met | Arg | Leu | Gly | Gln | Lys | Ala | Ile | Phe | His | Ile | Glu | Ala |
|     |     | 325 |     |     |     | 330 |     |     |     |     |     |     |     | 335 |     |
| Phe | Val | Ala | Lys | Phe | Met | Ser | Ile | Tyr | Lys | Asn | Phe | Leu | Ile | Ser | Thr |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     |     | 350 |     |
| Phe | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1569051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Leu | Lys | Gln | Ile | Tyr | Gly | Ala | Ser | Ala | Glu | Lys | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Glu | Asn | Arg | Ala | Trp | Lys | Val | Asp | Ala | Gly | Ser | Arg | Thr | Ile | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Leu | Thr | Thr | Leu | Ser | Ser | Thr | Asn | His | Val | Glu | Leu | Thr | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Ala | Gly | Phe | Gln | Asp | Arg | Tyr | Ile | Val | Gln | Glu | Ile | Ile | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Met | Ala | Lys | Asn | Arg | Pro | Ile | Asp | Thr | Lys | Gly | Lys | Lys | Gly | Tyr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Val | Leu | Val | Leu | Asn | Glu | Val | Asp | Lys | Leu | Ser | Arg | Glu | Ala | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Ser | Leu | Arg | Arg | Thr | Met | Glu | Lys | Tyr | Ser | Ser | Ser | Cys | Arg | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Leu | Cys | Cys | Asn | Ser | Ser | Ser | Lys | Val | Thr | Glu | Ala | Ile | Lys | Ser |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Cys | Leu | Asn | Val | Arg | Ile | Asn | Ala | Pro | Ser | Gln | Glu | Glu | Ile | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Leu | Glu | Phe | Val | Ala | Lys | Lys | Glu | Ser | Leu | Gln | Leu | Pro | Gln |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Phe | Ala | Ala | Arg | Ile | Ala | Glu | Lys | Ser | Asn | Arg | Ser | Leu | Arg | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Ile | Leu | Ser | Leu | Glu | Thr | Cys | Arg | Val | Gln | Asn | Tyr | Pro | Phe | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asn | Gln | Val | Ile | Ser | Pro | Met | Asp | Trp | Glu | Glu | Tyr | Val | Ala | Glu |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Ala | Thr | Asp | Met | Met | Lys | Glu | Gln | Ser | Pro | Lys | Lys | Leu | Phe | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Arg | Gly | Lys | Val | Tyr | Glu | Leu | Leu | Val | Asn | Cys | Ile | Pro | Pro | Glu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Ile | Leu | Lys | Arg | Leu | Leu | His | Glu | Leu | Leu | Lys | Lys | Leu | Asp | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Leu | Lys | Leu | Glu | Val | Cys | His | Trp | Ala | Ala | Tyr | Tyr | Glu | His | Arg |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Met | Arg | Leu | Gly | Gln | Lys | Ala | Ile | Phe | His | Ile | Glu | Ala | Phe | Val | Ala |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Lys | Phe | Met | Ser | Ile | Tyr | Lys | Asn | Phe | Leu | Ile | Ser | Thr | Phe | Gly |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..238  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569052  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

Met Ala Lys Asn Arg Pro Ile Asp Thr Lys Gly Lys Lys Gly Tyr Lys  
1 5 10 15  
Val Leu Val Leu Asn Glu Val Asp Lys Leu Ser Arg Glu Ala Gln His  
20 25 30  
Ser Leu Arg Arg Thr Met Glu Lys Tyr Ser Ser Ser Cys Arg Leu Ile  
35 40 45  
Leu Cys Cys Asn Ser Ser Ser Lys Val Thr Glu Ala Ile Lys Ser Arg  
50 55 60  
Cys Leu Asn Val Arg Ile Asn Ala Pro Ser Gln Glu Glu Ile Val Lys  
65 70 75 80  
Val Leu Glu Phe Val Ala Lys Lys Glu Ser Leu Gln Leu Pro Gln Gly  
85 90 95  
Phe Ala Ala Arg Ile Ala Glu Lys Ser Asn Arg Ser Leu Arg Arg Ala  
100 105 110  
Ile Leu Ser Leu Glu Thr Cys Arg Val Gln Asn Tyr Pro Phe Thr Gly  
115 120 125  
Asn Gln Val Ile Ser Pro Met Asp Trp Glu Glu Tyr Val Ala Glu Ile  
130 135 140  
Ala Thr Asp Met Met Lys Glu Gln Ser Pro Lys Lys Leu Phe Gln Val  
145 150 155 160  
Arg Gly Lys Val Tyr Glu Leu Leu Val Asn Cys Ile Pro Pro Glu Val  
165 170 175  
Ile Leu Lys Arg Leu Leu His Glu Leu Leu Lys Lys Leu Asp Ser Glu  
180 185 190  
Leu Lys Leu Glu Val Cys His Trp Ala Ala Tyr Tyr Glu His Arg Met  
195 200 205  
Arg Leu Gly Gln Lys Ala Ile Phe His Ile Glu Ala Phe Val Ala Lys  
210 215 220  
Phe Met Ser Ile Tyr Lys Asn Phe Leu Ile Ser Thr Phe Gly  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1148  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569061  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

actatctatt tcttctttca tcatcatcat catcatcatc atcaactctct cttcttcttc 60  
tctctattcc aKggcttttag tacgtgaacg tcgtcagcta aatctccgto ttcctcttcc 120  
tccaatctcc gaccgcccgt tctccacctc ttctctctca gccaccacca ccaccgtcgc 180  
tggtgtgaac ggaatctccg cttgtgatct cgagaaactc aacgtttctcg gatgcggaaa 240  
cgggcgggatt gtttacaaag tccgtcataa aaccacatcg gagatctacg ctttgaaaac 300  
agttaacggc gacatggatc cgattttcac aagacagtgt atgcgagaga tggagattct 360  
ccgacgtaca gattcaccgt acgtcgttaa atgtcacgga atcttcgaga aacctgtcgt 420  
cggtgaagta tcgattctaa tggagtatat ggacggcgga accctagaat cactacgcgg 480  
cggtgtaacg gagcaaaaac tcgccggatt cgctaaacag atcttaaaag gattaagcta 540  
tttacacgct cttaagatcg ttcacgtga tataaaaccc gcgaatcttc ttctcaattc 600  
gaaaaacgaa gttaaaatcg ccgatttcgg agttagtaag atattagtcg gatcattaga 660

(2) INFORMATION FOR SEQ ID NO:1128:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1569062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

|         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |        |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|--------|
| Leu 1   | Ser 5   | Ile 10  | Ser 15  | Phe 20  | Ile 25  | Ile 30  | Ile 35  | Ile 40  | Ile 45  | Ile 50  | Ile 55  | Ile 60  | Ile 65  | Ile 70  | Ile 75  | Ile 80 |
| Ser 1   | Ser 5   | Ser 10  | Ser 15  | Leu 20  | Tyr 25  | Ser 30  | Xaa 35  | Ala 40  | Leu 45  | Val 50  | Arg 55  | Glu 60  | Arg 65  | Arg 70  | Gln 75  |        |
| Leu 1   | Asn 35  | Leu 40  | Arg 45  | Leu 50  | Pro 55  | Leu 60  | Pro 65  | Pro 70  | Ile 75  | Ser 80  | Asp 85  | Arg 90  | Arg 95  | Phe 100 | Ser 105 |        |
| Thr 1   | Ser 50  | Ser 55  | Ser 60  | Ser 65  | Ala 70  | Thr 75  | Thr 80  | Thr 85  | Thr 90  | Val 95  | Ala 100 | Gly 105 | Cys 110 | Asn 115 | Gly 120 |        |
| Ile 65  | Ser 70  | Ala 75  | Cys 80  | Asp 85  | Leu 90  | Glu 95  | Lys 100 | Leu 105 | Asn 110 | Val 115 | Leu 120 | Gly 125 | Cys 130 | Gly 135 | Asn 140 |        |
| Gly 1   | Gly 5   | Ile 10  | Val 15  | Tyr 20  | Lys 25  | Val 30  | Arg 35  | His 40  | Lys 45  | Thr 50  | Thr 55  | Ser 60  | Glu 65  | Ile 70  | Tyr 75  |        |
| Ala 1   | Leu 5   | Lys 10  | Thr 15  | Val 20  | Asn 25  | Gly 30  | Asp 35  | Met 40  | Asp 45  | Pro 50  | Ile 55  | Phe 60  | Thr 65  | Arg 70  | Gln 75  |        |
| Leu 1   | Met 115 | Arg 120 | Glu 125 | Met 130 | Glu 135 | Ile 140 | Leu 145 | Arg 150 | Arg 155 | Thr 160 | Asp 165 | Ser 170 | Pro 175 | Tyr 180 | Val 185 |        |
| Val 1   | Lys 130 | Cys 135 | His 140 | Gly 145 | Ile 150 | Phe 155 | Glu 160 | Lys 165 | Pro 170 | Val 175 | Val 180 | Gly 185 | Glu 190 | Val 195 | Ser 200 |        |
| Ile 145 | Leu 150 | Met 155 | Glu 160 | Tyr 165 | Met 170 | Asp 175 | Gly 180 | Gly 185 | Thr 190 | Leu 195 | Glu 200 | Ser 205 | Leu 210 | Arg 215 | Gly 220 |        |
| Gly 1   | Val 165 | Thr 170 | Glu 175 | Gln 180 | Lys 185 | Leu 190 | Ala 195 | Gly 200 | Phe 205 | Ala 210 | Lys 215 | Gln 220 | Ile 225 | Leu 230 | Lys 235 |        |
| Gly 1   | Leu 180 | Ser 185 | Tyr 190 | Leu 195 | His 200 | Ala 205 | Leu 210 | Lys 215 | Ile 220 | Val 225 | His 230 | Arg 235 | Asp 240 | Ile 245 | Lys 250 |        |
| Pro 1   | Ala 195 | Asn 200 | Leu 205 | Leu 210 | Leu 215 | Asn 220 | Ser 225 | Lys 230 | Asn 235 | Glu 240 | Val 245 | Lys 250 | Ile 255 | Ala 260 | Asp 265 |        |
| Phe 1   | Gly 210 | Val 215 | Ser 220 | Lys 225 | Ile 230 | Leu 235 | Val 240 | Arg 245 | Ser 250 | Leu 255 | Asp 260 | Ser 265 | Cys 270 | Asn 275 | Ser 280 |        |
| Tyr 225 | Val 230 | Gly 235 | Thr 240 | Cys 245 | Ala 250 | Tyr 255 | Met 260 | Ser 265 | Pro 270 | Glu 275 | Arg 280 | Phe 285 | Asp 290 | Ser 295 | Glu 300 |        |
| Ser 1   | Ser 245 | Gly 250 | Gly 255 | Ser 260 | Ser 265 | Asp 270 | Ile 275 | Tyr 280 | Ala 285 | Gly 290 | Asp 295 | Ile 300 | Trp 305 | Ser 310 | Phe 315 |        |
| Gly 1   | Leu 260 | Met 265 | Met 270 | Leu 275 | Glu 280 | Leu 285 | Leu 290 | Val 295 | Gly 300 | His 305 | Phe 310 | Pro 315 | Leu 320 | Leu 325 | Pro 330 |        |
| Pro 1   | Gly 275 | Gln 280 | Arg 285 | Pro 290 | Asp 295 | Trp 300 | Ala 305 | Thr 310 | Leu 315 | Met 320 | Cys 325 | Ala 330 | Val 335 | Cys 340 | Phe 345 |        |
| Gly 1   | Glu 290 | Pro 295 | Pro 300 | Arg 305 | Ala 310 | Pro 315 | Glu 320 | Gly 325 | Cys 330 | Ser 335 | Glu 340 | Phe 345 | Arg 350 | Ser 355 | Glu 360 |        |
| Phe 305 | Val 310 | Glu 315 | Cys 320 | Cys 325 | Leu 330 | Arg 335 | Lys 340 | Asp 345 | Ser 350 | Ser 355 | Lys 360 | Arg 365 | Trp 370 | Thr 375 | Ala 380 |        |

Pro Gln Leu Leu Ala His Pro Phe Leu Arg Glu Asp Leu  
325 330

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

Met Asp Pro Ile Phe Thr Arg Gln Leu Met Arg Glu Met Glu Ile Leu  
1 5 10 15  
Arg Arg Thr Asp Ser Pro Tyr Val Val Lys Cys His Gly Ile Phe Glu  
20 25 30  
Lys Pro Val Val Gly Glu Val Ser Ile Leu Met Glu Tyr Met Asp Gly  
35 40 45  
Gly Thr Leu Glu Ser Leu Arg Gly Gly Val Thr Glu Gln Lys Leu Ala  
50 55 60  
Gly Phe Ala Lys Gln Ile Leu Lys Gly Leu Ser Tyr Leu His Ala Leu  
65 70 75 80  
Lys Ile Val His Arg Asp Ile Lys Pro Ala Asn Leu Leu Leu Asn Ser  
85 90 95  
Lys Asn Glu Val Lys Ile Ala Asp Phe Gly Val Ser Lys Ile Leu Val  
100 105 110  
Arg Ser Leu Asp Ser Cys Asn Ser Tyr Val Gly Thr Cys Ala Tyr Met  
115 120 125  
Ser Pro Glu Arg Phe Asp Ser Glu Ser Ser Gly Gly Ser Ser Asp Ile  
130 135 140  
Tyr Ala Gly Asp Ile Trp Ser Phe Gly Leu Met Met Leu Glu Leu Leu  
145 150 155 160  
Val Gly His Phe Pro Leu Leu Pro Pro Gly Gln Arg Pro Asp Trp Ala  
165 170 175  
Thr Leu Met Cys Ala Val Cys Phe Gly Glu Pro Pro Arg Ala Pro Glu  
180 185 190  
Gly Cys Ser Glu Glu Phe Arg Ser Phe Val Glu Cys Cys Leu Arg Lys  
195 200 205  
Asp Ser Ser Lys Arg Trp Thr Ala Pro Gln Leu Leu Ala His Pro Phe  
210 215 220  
Leu Arg Glu Asp Leu  
225

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..220
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

Met Arg Glu Met Glu Ile Leu Arg Arg Thr Asp Ser Pro Tyr Val Val  
1 5 10 15  
Lys Cys His Gly Ile Phe Glu Lys Pro Val Val Gly Glu Val Ser Ile  
20 25 30  
Leu Met Glu Tyr Met Asp Gly Gly Thr Leu Glu Ser Leu Arg Gly Gly



35 40 45  
Val Thr Glu Gln Lys Leu Ala Gly Phe Ala Lys Gln Ile Leu Lys Gly  
50 55 60  
Leu Ser Tyr Leu His Ala Leu Lys Ile Val His Arg Asp Ile Lys Pro  
65 70 75 80  
Ala Asn Leu Leu Leu Asn Ser Lys Asn Glu Val Lys Ile Ala Asp Phe  
85 90 95  
Gly Val Ser Lys Ile Leu Val Arg Ser Leu Asp Ser Cys Asn Ser Tyr  
100 105 110  
Val Gly Thr Cys Ala Tyr Met Ser Pro Glu Arg Phe Asp Ser Glu Ser  
115 120 125  
Ser Gly Gly Ser Ser Asp Ile Tyr Ala Gly Asp Ile Trp Ser Phe Gly  
130 135 140  
Leu Met Met Leu Glu Leu Leu Val Gly His Phe Pro Leu Leu Pro Pro  
145 150 155 160  
Gly Gln Arg Pro Asp Trp Ala Thr Leu Met Cys Ala Val Cys Phe Gly  
165 170 175  
Glu Pro Pro Arg Ala Pro Glu Gly Cys Ser Glu Glu Phe Arg Ser Phe  
180 185 190  
Val Glu Cys Cys Leu Arg Lys Asp Ser Ser Lys Arg Trp Thr Ala Pro  
195 200 205  
Gln Leu Leu Ala His Pro Phe Leu Arg Glu Asp Leu  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1591  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

atgcacaatc attcccacta atagtttaat aaagtgtata attttttttc aaattaaaac 60  
agctaaacac acacaaccac attcaaaaag gggttaagca ttgaagaata ttctaagaaa 120  
aattgtttct ctctctcaag aagtaaaagc gtctctctct ctcatlaagc atcaaaggag 180  
tttcgttttt cttgctttgc tgttacattc ttcaggaaaa aggcgttacc ttactctct 240  
ctgcatcaac gaggaagcgt gtagaaacta aaggagctta atttgagaga tttttttttt 300  
tgtttctggg tttgttcaaa gatgcaatt tttagtgtct tTctgctgtg gaaaaggatt 360  
tgatcggaac aagaaggtga aaacggagcc atcgtggagg atcttttcac tcaagggaact 420  
tcacgcagca acaaacagtt ttaattacga taacaagctc ggtgaaggca gatttggcag 480  
tgtgtattgg ggtcagctat gggatggatc tcaaattgca gtcaagagat tgaaggcatg 540  
gagtagcaga gaagagatag attttgctgt agaagtcgag attcttgctc gtatccgtca 600  
caagaatcta ttgagtgtac gaggttactg tgcagaagga caagaacgac tcattgtata 660  
tgattacatg ccaaatttga gcttggtctc tcacttctcat ggtcaacatt catctgagtc 720  
gcttcttgat tggactaggc ggatgaatat tgctgtatct tctgctcagg cgattgcta 780  
cttgcatcat tttgcaacac ctagaatagt ccatggagat gtgagagcaa gcaatgtgct 840  
gctagattct gagtttgaag ctcggttac agatttcgga tacgataagc tgatgccaga 900  
tgatggagct aacaaaagca ccaagggtaa taacattggg tatctctcac cagaatgtat 960  
cgaatctgGa aaagaatcag acatgggaga tgtgtatagt ttccgtgttc ttttgctgga 1020  
gottgtaact ggtaagagac ctacagagag ggtaaactta acaacaaaga ggggtattac 1080  
cgaatgggtt ttacctcttg tttacgaaag aaagtttggt gaaattgtgg atcaaaggct 1140  
gaatgggaag tatgtggaag aagagctgaa aaggatagtt ttggttggtc tcatgtgtgc 1200  
tcagaggag tcagagaaga gaccaacaat gtctgaagtt gtggagatgc taatgattga 1260  
atcaaaggag aaaatggctc agcttgaagc taatccactc ttcaatggaa acaatgatgg 1320  
tgaagttata gatgaaagct cagagatcat ttctgaagtg agagatcatc aataacaaga 1380  
acaagaatgt tattcaaatt cacgcattct tgttttcttt tgctagaatc tgggttttgg 1440  
ttgtgcttgt ttttagaaga gtgtttgtgc ttgtttttag aatagcgaag ttggctttta 1500  
aaagtttatt gtgtattttt tttcagctta agattggatt ttgatcattg atatttgagc 1560

ttgtaagaga gtgtagtggt acatatattgg t

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1569066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asn | Leu | Ser | Leu | Val | Ser | His | Leu | His | Gly | Gln | His | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | Leu | Leu | Asp | Trp | Thr | Arg | Arg | Met | Asn | Ile | Ala | Val | Ser | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gln | Ala | Ile | Ala | Tyr | Leu | His | Phe | Ala | Thr | Pro | Arg | Ile | Val |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Gly | Asp | Val | Arg | Ala | Ser | Asn | Val | Leu | Leu | Asp | Ser | Glu | Phe | Glu |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Arg | Val | Thr | Asp | Phe | Gly | Tyr | Asp | Lys | Leu | Met | Pro | Asp | Asp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Asn | Lys | Ser | Thr | Lys | Gly | Asn | Asn | Ile | Gly | Tyr | Leu | Ser | Pro | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Ile | Glu | Ser | Gly | Lys | Glu | Ser | Asp | Met | Gly | Asp | Val | Tyr | Ser | Phe |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Val | Leu | Leu | Leu | Glu | Leu | Val | Thr | Gly | Lys | Arg | Pro | Thr | Glu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Val | Asn | Leu | Thr | Thr | Lys | Arg | Gly | Ile | Thr | Glu | Trp | Val | Leu | Pro | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Tyr | Glu | Arg | Lys | Phe | Gly | Glu | Ile | Val | Asp | Gln | Arg | Leu | Asn | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Tyr | Val | Glu | Glu | Glu | Leu | Lys | Arg | Ile | Val | Leu | Val | Gly | Leu | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Ala | Gln | Arg | Glu | Ser | Glu | Lys | Arg | Pro | Thr | Met | Ser | Glu | Val | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Met | Leu | Met | Ile | Glu | Ser | Lys | Glu | Lys | Met | Ala | Gln | Leu | Glu | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Pro | Leu | Phe | Asn | Gly | Asn | Asn | Asp | Gly | Glu | Val | Ile | Asp | Glu | Ser |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ser | Glu | Ile | Ile | Ser | Glu | Val | Arg | Asp | His | Gln |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1569067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ile | Ala | Val | Ser | Ser | Ala | Gln | Ala | Ile | Ala | Tyr | Leu | His | His |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Phe | Ala | Thr | Pro | Arg | Ile | Val | His | Gly | Asp | Val | Arg | Ala | Ser | Asn | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Asp | Ser | Glu | Phe | Glu | Ala | Arg | Val | Thr | Asp | Phe | Gly | Tyr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1227  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| atatctcaaa  | atatgaataa  | tcaaaaatgg | agtatagggt  | tcatatctct | cgcttttctc | 60   |
| ttcatcactt  | cctcttcagc  | tgagttcatc | attcaacagg  | tcacaaaggg | cagaggaata | 120  |
| gagtacaaca  | gttcttacag  | tctcgaggag | aatcttgagg  | tgacaagaga | gttgagagaa | 180  |
| gagcgaccat  | cgagtaagat  | agtgacaata | acaagcttct  | ctgtgattaa | aggcagagga | 240  |
| gaaccctatg  | aatcctctgt  | ttttgaggCc | tgctgggttac | aaatggagat | tggttttgta | 300  |
| cgtgaatggg  | aataaaaaacg | acggtggaag | tgatcatatt  | tccctttacg | caaggatcga | 360  |
| agagKacaaa  | ctctcttcca  | gtaggatggg | aagtgaatgt  | tgatctcaaa | ctctttgtcc | 420  |
| ataatgggaa  | gctacacaaa  | tatttgactg | ttacagatgg  | cttagtgaag | cgatataaca | 480  |
| atgcgaaaaa  | agaatggggg  | ttcggacaat | tgatttctcg  | atcaacattc | tacaacgcga | 540  |
| acgaagggtta | ccttgaccag  | gacactgggt | cttttggtgc  | tgagatcttt | attgttaaac | 600  |
| cggctcaaca  | acaagagaaa  | gttacattca | tatcaaacc   | tccaaacaat | gttttctact | 660  |
| ggaagatact  | tcgtytctct  | acottggaag | ataaattcta  | ttactccgat | gattttctcg | 720  |
| ttgaagaccg  | atactggaga  | ctaggattta | acccgaaagg  | ggatggagga | ggaagaccac | 780  |
| atgcacttcc  | aatcttcta   | ttgtctcaag | gccataaggc  | aaacgcagtt | gttacaaca  | 840  |
| cttggggagc  | ggttaatctg  | cggttaaaga | atcaacgaag  | tactaaccat | agacaaatat | 900  |
| attctgcagc  | ttggtacccg  | attggaagcg | ggttatggtg  | gggagtgaac | aatatcatac | 960  |
| tgttagctga  | tttaaaccgat | gcataaaaag | gatatttggt  | gaatgatgcc | attatctttg | 1020 |
| aagctgaaat  | ggtaaggtc   | tctataacca | acatogtctc  | cgcttaaata | tctgcacttc | 1080 |
| tttgtctacg  | atcaatcaac  | cttatgaata | aagagatatt  | tgatgagttt | gtaataagaa | 1140 |
| aacgttaatg  | tttgtgaatt  | gtgaaattat | ttctgttctt  | ctgaggtttt | tatttcaatg | 1200 |
| aaaataaaaac | tcttaccggg  | ttaaatt    |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1136:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 253 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..253  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ile | Lys | Thr | Thr | Val | Glu | Met | Ile | Ile | Phe | Pro | Phe | Thr | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Lys | Xaa | Thr | Asn | Ser | Leu | Pro | Val | Gly | Trp | Glu | Val | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Lys | Leu | Phe | Val | His | Asn | Gly | Lys | Leu | His | Lys | Tyr | Leu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Thr | Asp | Gly | Leu | Val | Lys | Arg | Tyr | Asn | Asn | Ala | Lys | Lys | Glu | Trp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Phe | Gly | Gln | Leu | Ile | Ser | Arg | Ser | Thr | Phe | Tyr | Asn | Ala | Asn | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Tyr | Leu | Asp | Gln | Asp | Thr | Gly | Ser | Phe | Gly | Ala | Glu | Ile | Phe | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Lys | Pro | Ala | Gln | Gln | Gln | Glu | Lys | Val | Thr | Phe | Ile | Ser | Asn | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Asn | Asn | Val | Phe | Thr | Trp | Lys | Ile | Leu | Arg | Xaa | Ser | Thr | Leu | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Lys | Phe | Tyr | Tyr | Ser | Asp | Asp | Phe | Leu | Val | Glu | Asp | Arg | Tyr | Trp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Leu | Gly | Phe | Asn | Pro | Lys | Gly | Asp | Gly | Gly | Gly | Arg | Pro | His | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Pro | Ile | Phe | Leu | Phe | Ala | Gln | Gly | His | Lys | Ala | Asn | Ala | Val | Val |

(2) INFORMATION FOR SEQ ID NO:1137:

(A) LENGTH: 245 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1569099

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1481

(D) OTHER INFORMATION: / Ceres Seq. ID 1569112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| cactgtgctc  | tcttcttcaa  | tggaacaaca | attaacotta  | gtattgcttg | atagcccaaa  | 60   |
| aggcgccaaa  | tatgtagaaa  | cctttgaaga | agocgcttct  | tcttcttctt | cttcttcttc  | 120  |
| ttcttctgtt  | ccctcctgca  | ctgatcaccg | ccatogaacc  | ttcgtcaaat | tcttctctta  | 180  |
| cttctctctc  | gtcgtctctt  | cttactatct | catcatctcc  | agtctcgccg | tctctccaat  | 240  |
| tcccccaaca  | tccgcaatct  | tctcccggaa | acgtttctac  | agcaaagtgt | gatcttttca  | 300  |
| ccggagattg  | gataccagat  | ccaacaggtc | ctctgtagac  | aaatgtcact | tgtcgtcaca  | 360  |
| ttcaagattt  | tcagaactgc  | ctattgaatg | gacgaccaga  | tgtgaattat | ctcttctgga  | 420  |
| gatggaagcc  | tcgtgattgt  | gatcttctta | ggtttagtcc  | atcgcagttt | cttgcttcag  | 480  |
| tgaagaacaa  | atgggtgggt  | tttatcggtg | attccattgc  | tcgtaatcat | gtccagtctc  | 540  |
| tcctctgcat  | tctctctcag  | gtggaagaag | tggaggaaat  | ctatcacgat | aaggagttca  | 600  |
| gatccaagat  | atggagattc  | ccttctcaca | acttcacact  | atcagtcatt | tgggtctcctt | 660  |
| tccttctcaa  | atccgaaaaca | tctagcaact | cggatattca  | gctttacctc | gaccagcttg  | 720  |
| accacaaatg  | gactgtccaa  | taccggaaat | tcgactacgt  | tggtatctct | ggaggcaaat  | 780  |
| ggtttcttaa  | aacaacaatt  | ttccatgaaa | acaacgtagt  | cacgggctgt | cattactgcc  | 840  |
| aaggaagaaa  | caacctaaat  | gatctcggtc | atgattactc  | ctaccgcaaa | accctaaacc  | 900  |
| ttctccgtGa  | cttcgtctta  | aactcaaccc | acaaaccgct  | ggttctgttt | cgaacaacaa  | 960  |
| cgctgacca   | tttcgaaaac  | ggagagtggg | acactgggtg  | gtattgcaac | agaacgatgc  | 1020 |
| cgttttaaaga | aggccaagca  | aatatgaaaa | ctgtagatga  | tgtgatgcgt | gatgttgagc  | 1080 |
| ttgaggtgtt  | tcagaaattt  | gggaaagggt | ttggcttagg  | ttccaacatc | aggctattag  | 1140 |
| acacgactgg  | aatgtctctt  | ctccgtccag | acgggcatcc  | gggaccatac | cggcatccaa  | 1200 |
| atccttttgc  | tggagttaag  | aataagagca | atgttcagaa  | tgattgtctg | cattgggtgct | 1260 |
| tacctgggtc  | aattgattca  | tggaatgatg | tgatgggtgga | aaccacgctt | aaccgggaac  | 1320 |
| gggaactata  | cgatttaacc  | ggttaatgta | ccacgatatc  | gctttagtct | agttacagtc  | 1380 |
| aatagccatt  | ccactgtgta  | atgtctcgta | tatgatagtt  | ctatatttta | attttghta   | 1440 |
| ggttctaaac  | aagaataaac  | gatgcaaaat | tttgcaagtgt | g          |             |      |

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1569113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Leu | Ser | Ser | Ala | Phe | Ser | Leu | Arg | Trp | Lys | Lys | Trp | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Ile | Thr | Ile | Arg | Ser | Ser | Asp | Pro | Arg | Tyr | Gly | Asp | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Thr | Ser | His | Tyr | Gln | Ser | Phe | Gly | Leu | Leu | Ser | Phe | Ser | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Lys | His | Leu | Ala | Thr | Arg | Ile | Phe | Ser | Phe | Thr | Ser | Thr | Ser | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Asn | Gly | Leu | Ser | Asn | Thr | Arg | Asn | Ser | Thr | Thr | Leu | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Glu | Ala | Asn | Gly | Phe | Leu | Lys | Gln | Gln | Phe | Ser | Met | Lys | Thr | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569114  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:  
Met Pro Phe Lys Glu Gly Gln Ala Asn Met Lys Thr Val Asp Asp Val  
1 5 10 15  
Met Arg Asp Val Glu Leu Glu Val Phe Gln Lys Phe Gly Lys Gly Phe  
20 25 30  
Gly Leu Gly Ser Asn Ile Arg Leu Leu Asp Thr Thr Gly Met Ser Leu  
35 40 45  
Leu Arg Pro Asp Gly His Pro Gly Pro Tyr Arg His Pro Asn Pro Phe  
50 55 60  
Ala Gly Val Lys Asn Lys Ser Asn Val Gln Asn Asp Cys Leu His Trp  
65 70 75 80  
Cys Leu Pro Gly Pro Ile Asp Ser Trp Asn Asp Val Met Val Glu Thr  
85 90 95  
Thr Leu Asn Arg Glu Arg Glu Leu Tyr Asp Leu Thr Gly  
100 105  
(2) INFORMATION FOR SEQ ID NO:1141:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..100  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569115  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:  
Met Lys Thr Val Asp Asp Val Met Arg Asp Val Glu Leu Glu Val Phe  
1 5 10 15  
Gln Lys Phe Gly Lys Gly Phe Gly Leu Gly Ser Asn Ile Arg Leu Leu  
20 25 30  
Asp Thr Thr Gly Met Ser Leu Leu Arg Pro Asp Gly His Pro Gly Pro  
35 40 45  
Tyr Arg His Pro Asn Pro Phe Ala Gly Val Lys Asn Lys Ser Asn Val  
50 55 60  
Gln Asn Asp Cys Leu His Trp Cys Leu Pro Gly Pro Ile Asp Ser Trp  
65 70 75 80  
Asn Asp Val Met Val Glu Thr Thr Leu Asn Arg Glu Arg Glu Leu Tyr  
85 90 95  
Asp Leu Thr Gly  
100  
(2) INFORMATION FOR SEQ ID NO:1142:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1794 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1794  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569116  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:  
attcttgtct cgacaatact ctcagaatac gatcttgaag agcaaagatt gttcctttat

tgatgaattg agtgcaaaag agtggttatat aatggctact gcagctgtta taggactcaa 120  
cactggcaaa agattgttga gttcatcggtt ttatcactca gatgttacag agaagtttct 180  
atctgtaaaat gatcattgtt catcacagta tcatattgct tcaacgaaaa gcgggataac 240  
tgcgaaaaaag gcgtcgaaact atagtcagag ttttccttcg tccaatcgct acacacaatc 300  
tgctaaagct ttgaaagaga atgtagatgt tgcttctact gagaagccat ggctacctaa 360  
tggaactgat aaggaattgg aagaagaatg ttatgatgat gatgatctaa ttagtcattc 420  
tgttgaggca attttactgt tacagaagtc tatgttagag aaaagttgga atctttcatt 480  
tgaaaaggcg gtgtcgagtg agtatccggg caAggggact atacggaaga agaagattcc 540  
ggttatcacc tgttcaggga tttcagctcg tcaaagaagg attggtgcta agaagaaaac 600  
taatatgact catgttaaag cagtttctga tgtttctagt ggaaagcaag ttagaggtta 660  
tgtgaaagggt gtaataagtg aagatgtgct tagtcatgag gaagttgtgc gcttgtctaa 720  
gaaaatcaaa tctggtcttc gtcttgatga tcataagtca agattacagg atagattagg 780  
ctgtgagcct tctgatgaac agcttgagtg atctttgaag atatctcggg ccgagctaca 840  
ggcgtggttg atggaatgtc atctagctag agagaagttg gctatgagta atgtgcgttt 900  
ggttatgtct attgctcagc gttatgataa tttgggagca gaaatgtctg acctgtttca 960  
gggtggtctt atcggacttt tgcggggaat agagaaattt gattcttcca aaggtttcag 1020  
aatttcaact tatgtatatt ggtggattcg acaggtgtc tcaagagcac tagtggacaa 1080  
ctcaagaacc ttgaggttac ctactcacct acatgaaaga ctcggtttaa tccgaaatgc 1140  
aaagcttaga cttcaagaga aaggaatcac accctccatt gataggattg cagagtctct 1200  
aaacatgtcg cagaagaaag ttagaaatgc aacagaggct gtaagcaaag tattttctct 1260  
agacagagat gcatttcctt ctttgaatgg tctccctgga gaaactcatc acagttacat 1320  
tgcgataact cgtttggaga acaatccgtg gcacgggtat gatgatttgg cactcaagga 1380  
ggaagtaagc aagcttataa gtgcaacact cggagaacgg gaaaaagaga tcattcgatt 1440  
atactatggt ctagacaaag aatgtctcac atgggaagac attagtaaac ggataggatt 1500  
atcgagagag aggtgagac aggtagggct tgtggcactg gagaaactaa aacacgcagc 1560  
gaggaagaga aaaatggagg caatgatcct taagaattga ttttgttttt gtacattttg 1620  
attacatcag agccatagag agcggttgtg aatgtgtata tatacaggac aaaaaagggg 1680  
gaagagtact actctctttt attttatttt accttcttgg cttcttttgt aaactgagtt 1740  
gagaaacaag agacagttat gtaatatggc ttacgtaaa cttcatcatt cctc

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1569117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

Phe Leu Ser Arg Gln Tyr Ser Gln Asn Thr Ile Leu Lys Ser Lys Asp  
1 5 10 15  
Cys Ser Phe Ile Asp Glu Leu Ser Ala Lys Glu Cys Tyr Ile Met Ala  
20 25 30  
Thr Ala Ala Val Ile Gly Leu Asn Thr Gly Lys Arg Leu Leu Ser Ser  
35 40 45  
Ser Phe Tyr His Ser Asp Val Thr Glu Lys Phe Leu Ser Val Asn Asp  
50 55 60  
His Cys Ser Ser Gln Tyr His Ile Ala Ser Thr Lys Ser Gly Ile Thr  
65 70 75 80  
Ala Lys Lys Ala Ser Asn Tyr Ser Pro Ser Phe Pro Ser Ser Asn Arg  
85 90 95  
His Thr Gln Ser Ala Lys Ala Leu Lys Glu Asn Val Asp Val Ala Ser  
100 105 110  
Thr Glu Lys Pro Trp Leu Pro Asn Gly Thr Asp Lys Glu Leu Glu Glu  
115 120 125  
Glu Cys Tyr Asp Asp Asp Asp Leu Ile Ser His Ser Val Glu Ala Ile  
130 135 140  
Leu Leu Leu Gln Lys Ser Met Leu Glu Lys Ser Trp Asn Leu Ser Phe  
145 150 155 160



Glu Lys Ala Val Ser Ser Glu Tyr Pro Gly Lys Gly Thr Ile Arg Lys  
165 170 175  
Lys Lys Ile Pro Val Ile Thr Cys Ser Gly Ile Ser Ala Arg Gln Arg  
180 185 190  
Arg Ile Gly Ala Lys Lys Lys Thr Asn Met Thr His Val Lys Ala Val  
195 200 205  
Ser Asp Val Ser Ser Gly Lys Gln Val Arg Gly Tyr Val Lys Gly Val  
210 215 220  
Ile Ser Glu Asp Val Leu Ser His Ala Glu Val Val Arg Leu Ser Lys  
225 230 235 240  
Lys Ile Lys Ser Gly Leu Arg Leu Asp Asp His Lys Ser Arg Leu Gln  
245 250 255  
Asp Arg Leu Gly Cys Glu Pro Ser Asp Glu Gln Leu Ala Val Ser Leu  
260 265 270  
Lys Ile Ser Arg Ala Glu Leu Gln Ala Trp Leu Met Glu Cys His Leu  
275 280 285  
Ala Arg Glu Lys Leu Ala Met Ser Asn Val Arg Leu Val Met Ser Ile  
290 295 300  
Ala Gln Arg Tyr Asp Asn Leu Gly Ala Glu Met Ser Asp Leu Val Gln  
305 310 315 320  
Gly Gly Leu Ile Gly Leu Leu Arg Gly Ile Glu Lys Phe Asp Ser Ser  
325 330 335  
Lys Gly Phe Arg Ile Ser Thr Tyr Val Tyr Trp Trp Ile Arg Gln Gly  
340 345 350  
Val Ser Arg Ala Leu Val Asp Asn Ser Arg Thr Leu Arg Leu Pro Thr  
355 360 365  
His Leu His Glu Arg Leu Gly Leu Ile Arg Asn Ala Lys Leu Arg Leu  
370 375 380  
Gln Glu Lys Gly Ile Thr Pro Ser Ile Asp Arg Ile Ala Glu Ser Leu  
385 390 395 400  
Asn Met Ser Gln Lys Lys Val Arg Asn Ala Thr Glu Ala Val Ser Lys  
405 410 415  
Val Phe Ser Leu Asp Arg Asp Ala Phe Pro Ser Leu Asn Gly Leu Pro  
420 425 430  
Gly Glu Thr His His Ser Tyr Ile Ala Asp Thr Arg Leu Glu Asn Asn  
435 440 445  
Pro Trp His Gly Tyr Asp Asp Leu Ala Leu Lys Glu Glu Val Ser Lys  
450 455 460  
Leu Ile Ser Ala Thr Leu Gly Glu Arg Glu Lys Glu Ile Ile Arg Leu  
465 470 475 480  
Tyr Tyr Gly Leu Asp Lys Glu Cys Leu Thr Trp Glu Asp Ile Ser Lys  
485 490 495  
Arg Ile Gly Leu Ser Arg Glu Arg Val Arg Gln Val Gly Leu Val Ala  
500 505 510  
Leu Glu Lys Leu Lys His Ala Ala Arg Lys Arg Lys Met Glu Ala Met  
515 520 525  
Ile Leu Lys Asn  
530

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

Met Ala Thr Ala Ala Val Ile Gly Leu Asn Thr Gly Lys Arg Leu Leu



Ala Met Ile Leu Lys Asn  
500

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..382
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Glu | Lys | Ser | Trp | Asn | Leu | Ser | Phe | Glu | Lys | Ala | Val | Ser | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Tyr | Pro | Gly | Lys | Gly | Thr | Ile | Arg | Lys | Lys | Lys | Ile | Pro | Val | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Cys | Ser | Gly | Ile | Ser | Ala | Arg | Gln | Arg | Arg | Ile | Gly | Ala | Lys | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Thr | Asn | Met | Thr | His | Val | Lys | Ala | Val | Ser | Asp | Val | Ser | Ser | Gly |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Gln | Val | Arg | Gly | Tyr | Val | Lys | Gly | Val | Ile | Ser | Glu | Asp | Val | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | His | Ala | Glu | Val | Val | Arg | Leu | Ser | Lys | Lys | Ile | Lys | Ser | Gly | Leu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Arg | Leu | Asp | Asp | His | Lys | Ser | Arg | Leu | Gln | Asp | Arg | Leu | Gly | Cys | Glu |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Ser | Asp | Glu | Gln | Leu | Ala | Val | Ser | Leu | Lys | Ile | Ser | Arg | Ala | Glu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Gln | Ala | Trp | Leu | Met | Glu | Cys | His | Leu | Ala | Arg | Glu | Lys | Leu | Ala |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Ser | Asn | Val | Arg | Leu | Val | Met | Ser | Ile | Ala | Gln | Arg | Tyr | Asp | Asn |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Leu | Gly | Ala | Glu | Met | Ser | Asp | Leu | Val | Gln | Gly | Gly | Leu | Ile | Gly | Leu |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Leu | Arg | Gly | Ile | Glu | Lys | Phe | Asp | Ser | Ser | Lys | Gly | Phe | Arg | Ile | Ser |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Thr | Tyr | Val | Tyr | Trp | Trp | Ile | Arg | Gln | Gly | Val | Ser | Arg | Ala | Leu | Val |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Asp | Asn | Ser | Arg | Thr | Leu | Arg | Leu | Pro | Thr | His | Leu | His | Glu | Arg | Leu |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gly | Leu | Ile | Arg | Asn | Ala | Lys | Leu | Arg | Leu | Gln | Glu | Lys | Gly | Ile | Thr |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Pro | Ser | Ile | Asp | Arg | Ile | Ala | Glu | Ser | Leu | Asn | Met | Ser | Gln | Lys | Lys |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Val | Arg | Asn | Ala | Thr | Glu | Ala | Val | Ser | Lys | Val | Phe | Ser | Leu | Asp | Arg |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asp | Ala | Phe | Pro | Ser | Leu | Asn | Gly | Leu | Pro | Gly | Glu | Thr | His | His | Ser |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Tyr | Ile | Ala | Asp | Thr | Arg | Leu | Glu | Asn | Asn | Pro | Trp | His | Gly | Tyr | Asp |  |
|     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |  |
| Asp | Leu | Ala | Leu | Lys | Glu | Val | Ser | Lys | Leu | Ile | Ser | Ala | Thr | Leu |     |  |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |  |
| Gly | Glu | Arg | Glu | Lys | Glu | Ile | Ile | Arg | Leu | Tyr | Tyr | Gly | Leu | Asp | Lys |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |  |
| Glu | Cys | Leu | Thr | Trp | Glu | Asp | Ile | Ser | Lys | Arg | Ile | Gly | Leu | Ser | Arg |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Glu | Arg | Val | Arg | Gln | Val | Gly | Leu | Val | Ala | Leu | Glu | Lys | Leu | Lys | His |  |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |
| Ala | Ala | Arg | Lys | Arg | Lys | Met | Glu | Ala | Met | Ile | Leu | Lys | Asn |     |     |  |

370 375 380

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| aaaaRcccct | tctctcttca  | gtctctctct | ctctagacga  | tctctatctt  | gaataaaaata | 60   |
| ccgataatga | cctcaaccaa  | tccggtggtc | gccgaagtaa  | taccggcgga  | aacttctaca  | 120  |
| gatgctacag | agacgacgat  | tgcaacgacg | gaagctgggtg | aagcaccgga  | gaagaagggtg | 180  |
| aggaaagctt | atacaatcac  | caagtctaga | gagagttgga  | ctgaaggaga  | acacgacaag  | 240  |
| tttctggaag | ctcttcaatt  | gtttgatcgt | gactggaaaa  | agatagaaga  | ttttgttggt  | 300  |
| tcaaagacag | ttattcagat  | cagtagccat | gccccaaaaat | acttttctaaa | ggtccaaaaa  | 360  |
| aatgggactt | tagcacatgt  | tccaccccct | aggcctaagc  | gcaaagctgc  | tcattccatat | 420  |
| cctcaaaaag | catcgaaaaa  | tgctcaaatg | tcgcttcacg  | tttccatgtc  | ctttcctact  | 480  |
| caaataaata | acctgcctgg  | atatactcca | tgggatgatg  | atacatctgc  | attgttaaacc | 540  |
| attgctgtaa | gtgggggttat | tccaccagaa | gatgaacttg  | atactctttg  | tgagacagaa  | 600  |
| gttgatgttg | gatcaaatga  | catgataagt | gaaactagtc  | cttcagcatc  | tggtatcgga  | 660  |
| agctcaagca | gaacactatc  | agattctaag | ggtttgagac  | tggcgaaaca  | agctccctca  | 720  |
| atgcatggtc | ttcctgattt  | tgctgagggt | tataacttca  | ttgggagtg   | gttcgatcct  | 780  |
| gacagcaaag | gccgcatgaa  | aaagctcaag | gaaatggatc  | ctataaaatt  | cgaaactgtt  | 840  |
| ttgctgttga | tgagaaacct  | cacagtgaac | ttgtcaaacc  | ctgactttga  | acctacttct  | 900  |
| gaatatgttg | atgctgcaga  | ggaaggatc  | gaacacttaa  | gctcttagct  | gtttgtgcac  | 960  |
| tcaacaagtt | atatacttct  | ttgacgactt | cttgctcgca  | acaactctct  | accagctatc  | 1020 |
| aaatgcatcg | tacggttggt  | gtctgaggag | aacataactg  | agtcgtcgtc  | acaaacaaga  | 1080 |
| ggaacatatg | cagtttccgt  | cagaaccagt | cgtgtgaatg  | gtagatatat  | gtatgtgtgt  | 1140 |
| gtagaaaatg | gttaccatt   | gtatcttctt | tttgataatt  | atTTTTTcat  | gccttttgta  | 1200 |
| atatgtaagt | ttctttacct  | cgttctctga | ttgggtattt  | tctcgttatc  | tgtttaacca  | 1260 |
| aaagctatgt | aacacagtag  | caaattgtta | cttaactcgg  | aagtgagata  | cataactctg  | 1320 |
| ttgtattgca | cttgtatcaa  | gcgttaacgt | cc          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Thr | Asn | Pro | Val | Val | Ala | Glu | Val | Ile | Pro | Ala | Glu | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Thr | Asp | Ala | Thr | Glu | Thr | Thr | Ile | Ala | Thr | Thr | Glu | Ala | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Pro | Glu | Lys | Lys | Val | Arg | Lys | Ala | Tyr | Thr | Ile | Thr | Lys | Ser | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ser | Trp | Thr | Glu | Gly | Glu | His | Asp | Lys | Phe | Leu | Glu | Ala | Leu | Gln |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Asp | Arg | Asp | Trp | Lys | Lys | Ile | Glu | Asp | Phe | Val | Gly | Ser | Lys |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Val | Ile | Gln | Ile | Ser | Ser | His | Ala | Gln | Lys | Tyr | Phe | Leu | Lys | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Lys | Asn | Gly | Thr | Leu | Ala | His | Val | Pro | Pro | Pro | Arg | Pro | Lys | Arg |

100 105 110  
Lys Ala Ala His Pro Tyr Pro Gln Lys Ala Ser Lys Asn Ala Gln Met  
115 120 125  
Ser Leu His Val Ser Met Ser Phe Pro Thr Gln Ile Asn Asn Leu Pro  
130 135 140  
Gly Tyr Thr Pro Trp Asp Asp Asp Thr Ser Ala Leu Leu Asn Ile Ala  
145 150 155 160  
Val Ser Gly Val Ile Pro Pro Glu Asp Glu Leu Asp Thr Leu Cys Gly  
165 170 175  
Ala Glu Val Asp Val Gly Ser Asn Asp Met Ile Ser Glu Thr Ser Pro  
180 185 190  
Ser Ala Ser Gly Ile Gly Ser Ser Arg Thr Leu Ser Asp Ser Lys  
195 200 205  
Gly Leu Arg Leu Ala Lys Gln Ala Pro Ser Met His Gly Leu Pro Asp  
210 215 220  
Phe Ala Glu Val Tyr Asn Phe Ile Gly Ser Val Phe Asp Pro Asp Ser  
225 230 235 240  
Lys Gly Arg Met Lys Lys Leu Lys Glu Met Asp Pro Ile Asn Phe Glu  
245 250 255  
Thr Val Leu Leu Met Arg Asn Leu Thr Val Asn Leu Ser Asn Pro  
260 265 270  
Asp Phe Glu Pro Thr Ser Glu Tyr Val Asp Ala Ala Glu Glu Gly His  
275 280 285  
Glu His Leu Ser Ser  
290

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1569146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

Met Ser Leu His Val Ser Met Ser Phe Pro Thr Gln Ile Asn Asn Leu  
1 5 10 15  
Pro Gly Tyr Thr Pro Trp Asp Asp Asp Thr Ser Ala Leu Leu Asn Ile  
20 25 30  
Ala Val Ser Gly Val Ile Pro Pro Glu Asp Glu Leu Asp Thr Leu Cys  
35 40 45  
Gly Ala Glu Val Asp Val Gly Ser Asn Asp Met Ile Ser Glu Thr Ser  
50 55 60  
Pro Ser Ala Ser Gly Ile Gly Ser Ser Ser Arg Thr Leu Ser Asp Ser  
65 70 75 80  
Lys Gly Leu Arg Leu Ala Lys Gln Ala Pro Ser Met His Gly Leu Pro  
85 90 95  
Asp Phe Ala Glu Val Tyr Asn Phe Ile Gly Ser Val Phe Asp Pro Asp  
100 105 110  
Ser Lys Gly Arg Met Lys Lys Leu Lys Glu Met Asp Pro Ile Asn Phe  
115 120 125  
Glu Thr Val Leu Leu Leu Met Arg Asn Leu Thr Val Asn Leu Ser Asn  
130 135 140  
Pro Asp Phe Glu Pro Thr Ser Glu Tyr Val Asp Ala Ala Glu Glu Gly  
145 150 155 160  
His Glu His Leu Ser Ser  
165

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..160
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569147
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

Met Ser Phe Pro Thr Gln Ile Asn Asn Leu Pro Gly Tyr Thr Pro Trp  
1 5 10 15  
Asp Asp Asp Thr Ser Ala Leu Leu Asn Ile Ala Val Ser Gly Val Ile  
20 25 30  
Pro Pro Glu Asp Glu Leu Asp Thr Leu Cys Gly Ala Glu Val Asp Val  
35 40 45  
Gly Ser Asn Asp Met Ile Ser Glu Thr Ser Pro Ser Ala Ser Gly Ile  
50 55 60  
Gly Ser Ser Ser Arg Thr Leu Ser Asp Ser Lys Gly Leu Arg Leu Ala  
65 70 75 80  
Lys Gln Ala Pro Ser Met His Gly Leu Pro Asp Phe Ala Glu Val Tyr  
85 90 95  
Asn Phe Ile Gly Ser Val Phe Asp Pro Asp Ser Lys Gly Arg Met Lys  
100 105 110  
Lys Leu Lys Glu Met Asp Pro Ile Asn Phe Glu Thr Val Leu Leu Leu  
115 120 125  
Met Arg Asn Leu Thr Val Asn Leu Ser Asn Pro Asp Phe Glu Pro Thr  
130 135 140  
Ser Glu Tyr Val Asp Ala Ala Glu Glu Gly His Glu His Leu Ser Ser  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1198 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1198
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569148
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

aaaaaccaac aaatggggat gagtcgtcaa agactgcact ctctctctct cctctggctc 60  
cggcgaaaaa ccccttttcg atttcattga taaaacgcaa atcgatctct cgtgtggaag 120  
aagaagaaga acacgatggg aacaatgggt aaagcattct acagcgtagg attctggatc 180  
cgtgaaactg gtcaagcact tgatcggctc ggttgctgcc tccaagggaa aaatcatttc 240  
cgagaacagc tatcaaggca ccgcacactc atgaatgttt ttgacaaaac ccctaattgtg 300  
gataaggggg cttttgtggc tcctaacgct tctctctctg gtgatgtcca tgtgggaaga 360  
ggttcttcca tttggtatgg atgtgtcttg agaggagatg ctaacagcat tagtggttga 420  
gctgggacca atattcagga caacgctctt gtccacgttg ctaagaccaa cttaagtggg 480  
aaggtcttac ctactgtcat tggagacaat gtcaccattg gtcatagtgc tgttttacat 540  
ggctgcactg tcgaggatga ggcctatatt ggtacaagtg caactgtctt ggatggagct 600  
catgttgaaa aacatgccat ggttgcttca ggagctcttg ttaggcagaa cactagaatt 660  
Ccctctggcg aggtttggg aggcaacca gctaaatttc tgaggaaggt gacagaagaa 720  
gaaagagtct tcttctccag ttcggtgtg gagtactcca acttagctca agctcacgcc 780  
acagagaacg caaagaactt ggacgaggct gagttcaaga agcttctaaa caagaagaac 840  
gctcgcgata cagaatatga ttcagtactc gatgatctca cgctccctga gaatgtacca 900  
aaagcagctt gaggcgttta acctgtgccg ccttgccaat cttgatttgt ttggatttga 960  
aaagtaaaaa caaagAactt gatttctctg ttctccaata aagttttctt gggcgtaaaa 1020

tccattggcc agtgcctcact gggaaagttt tccggcttaaa ggcatttcatt tctctgttaa 1080  
agattgtgag gggttttgtt ctcttgtaac ttgagaaaga aaagttgtaa ccttttcttc 1140  
ctttttatgt cgtctaataa attgttgatc agacagacat ttaggttgac ctttgccc

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258

(D) OTHER INFORMATION: / Ceres Seq. ID 1569149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

Met Gly Thr Met Gly Lys Ala Phe Tyr Ser Val Gly Phe Trp Ile Arg  
1 5 10 15  
Glu Thr Gly Gln Ala Leu Asp Arg Leu Gly Cys Arg Leu Gln Gly Lys  
20 25 30  
Asn His Phe Arg Glu Gln Leu Ser Arg His Arg Thr Leu Met Asn Val  
35 40 45  
Phe Asp Lys Thr Pro Asn Val Asp Lys Gly Ala Phe Val Ala Pro Asn  
50 55 60  
Ala Ser Leu Ser Gly Asp Val His Val Gly Arg Gly Ser Ser Ile Trp  
65 70 75 80  
Tyr Gly Cys Val Leu Arg Gly Asp Ala Asn Ser Ile Ser Val Gly Ala  
85 90 95  
Gly Thr Asn Ile Gln Asp Asn Ala Leu Val His Val Ala Lys Thr Asn  
100 105 110  
Leu Ser Gly Lys Val Leu Pro Thr Val Ile Gly Asp Asn Val Thr Ile  
115 120 125  
Gly His Ser Ala Val Leu His Gly Cys Thr Val Glu Asp Glu Ala Tyr  
130 135 140  
Ile Gly Thr Ser Ala Thr Val Leu Asp Gly Ala His Val Glu Lys His  
145 150 155 160  
Ala Met Val Ala Ser Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro  
165 170 175  
Ser Gly Glu Val Trp Gly Gly Asn Pro Ala Lys Phe Leu Arg Lys Val  
180 185 190  
Thr Glu Glu Glu Arg Val Phe Phe Ser Ser Ser Ala Val Glu Tyr Ser  
195 200 205  
Asn Leu Ala Gln Ala His Ala Thr Glu Asn Ala Lys Asn Leu Asp Glu  
210 215 220  
Ala Glu Phe Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg Asp Thr Glu  
225 230 235 240  
Tyr Asp Ser Val Leu Asp Asp Leu Thr Leu Pro Glu Asn Val Pro Lys  
245 250 255  
Ala Ala

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1569151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Val | Phe | Asp | Lys | Thr | Pro | Asn | Val | Asp | Lys | Gly | Ala | Phe | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Asn | Ala | Ser | Leu | Ser | Gly | Asp | Val | His | Val | Gly | Arg | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Trp | Tyr | Gly | Cys | Val | Leu | Arg | Gly | Asp | Ala | Asn | Ser | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gly | Ala | Gly | Thr | Asn | Ile | Gln | Asp | Asn | Ala | Leu | Val | His | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Thr | Asn | Leu | Ser | Gly | Lys | Val | Leu | Pro | Thr | Val | Ile | Gly | Asp | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Thr | Ile | Gly | His | Ser | Ala | Val | Leu | His | Gly | Cys | Thr | Val | Glu | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ala | Tyr | Ile | Gly | Thr | Ser | Ala | Thr | Val | Leu | Asp | Gly | Ala | His | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | His | Ala | Met | Val | Ala | Ser | Gly | Ala | Leu | Val | Arg | Gln | Asn | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ile | Pro | Ser | Gly | Glu | Val | Trp | Gly | Gly | Asn | Pro | Ala | Lys | Phe | Leu |



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Arg Lys Val Thr Glu Glu Arg Val Phe Phe Ser Ser Ser Ala Val     |     |     |
| 145                                                             | 150 | 155 |
| Glu Tyr Ser Asn Leu Ala Gln Ala His Ala Thr Glu Asn Ala Lys Asn |     |     |
|                                                                 | 165 | 170 |
|                                                                 |     | 175 |
| Leu Asp Glu Ala Glu Phe Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg |     |     |
|                                                                 | 180 | 185 |
|                                                                 |     | 190 |
| Asp Thr Glu Tyr Asp Ser Val Leu Asp Asp Leu Thr Leu Pro Glu Asn |     |     |
|                                                                 | 195 | 200 |
|                                                                 |     | 205 |
| Val Pro Lys Ala Ala                                             |     |     |
| 210                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| atcgaaatta | ttgtggtggt  | ttgtgaacag | aaaccaagca  | ggattaaaga | tggttcaatc | 60   |
| tgtgttaatt | tctcgttaaca | agggtttggc | ggaGcaagat  | ctaactaagc | ttgatgtaac | 120  |
| aaagttacat | cctctgtctc  | ctgaagtcac | ttctcgccaa  | gcaaccataa | atatcggaac | 180  |
| cattggtcat | gtcgtcacg   | gtaaatcgac | tatagtga    | gctatctctg | gtgttcagac | 240  |
| tgtgcgtttt | aagaatgaat  | tagagcgtaa | cattaccatt  | aagcttggtt | atgcaaatgc | 300  |
| aaagatttac | aagtgtgagg  | atgacaagtg | ccctagacca  | atgtgctaca | agtcatatgg | 360  |
| gagtggaaaa | gaagacaacc  | caacttgtga | tgtccccgga  | tttgacaatt | gcaagatgac | 420  |
| actactgaga | catgtctcat  | gtgtcgattg | tccaggacat  | gatattctta | tggcgacaat | 480  |
| gctcaatgga | gcagcaatcg  | tggatggtgc | tttacttcta  | attgctgcta | acgggagttg | 540  |
| tccacaacca | caaaccgctg  | aacatcttgc | ttctgttgat  | atgatgogcc | ttaagcatat | 600  |
| cataatcctt | cagaacaaga  | ttgatctcat | taatgagaaa  | gccgccactg | aacagcacga | 660  |
| ggctattcag | aaatttataa  | cgaacacgaa | tgctgaggat  | gcacctatag | ttcctgtctc | 720  |
| agcacaactg | aaatacaaca  | ttgatgttgt | gagtgaatac  | attgtcaaga | agattccaat | 780  |
| ccctgtgaga | gactttgtgt  | caccaccaaa | gatgattgtg  | attogttctt | tcgatgtcaa | 840  |
| taaacctggc | tcggcgggtc  | atgaaatgaa | agggtggtgt  | gctgggtgaa | gtatcctcca | 900  |
| gtgaaccaac | tgattgaaat  | tagaccttgt | atcaactggca | aagatgagca | tggaaactca | 960  |
| aaatgcactc | caatttactc  | gcgtataact | tcactatacg  | cggaacagaa | cgagcttcag | 1020 |
| tttgctgtac | cgggagggtc  | aatcggagtt | ggaacaacca  | tggaccctac | gcttacgcgt | 1080 |
| gctgataggt | tggttggtca  | agtccttggt | gaaatgggta  | ctctccctga | cgtctttggt | 1140 |
| gagcttgaag | taagttacca  | gcttctgact | cgtctcattg  | gagtgaggac | aaaggaaaaa | 1200 |
| gagaagcaaa | tgaaagtgtc  | aaagctaacc | aaagaagaga  | tattgatggt | gaacatcggg | 1260 |
| tctatgtcta | cgggagctaa  | ggttattgga | gtcaagaaa   | atatggtgaa | actccaactg | 1320 |
| acgtctccgg | tgtgtaccac  | cataggagag | aaggttgctt  | taagccgacg | tgtcgatagg | 1380 |
| cattggcgtc | taattggtaa  | gggtcagatt | atggctggaa  | ccaccatcga | tgttcctcct | 1440 |
| cctcctttct | aatgaagtag  | tgatgagttt | tttatattgt  | ttgcattcaa | aaataattaa | 1500 |
| catgtgcctt | tgtatgttta  | atcactttct | ttcgact     |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

Ser Lys Leu Leu Trp Cys Phe Val Asn Arg Asn Gln Ala Gly Leu Lys  
1 5 10 15  
Met Val Gln Ser Val Leu Ile Ser Arg Asn Lys Gly Leu Ala Glu Gln  
20 25 30  
Asp Leu Thr Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu  
35 40 45  
Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile Gly His Val  
50 55 60  
Ala His Gly Lys Ser Thr Ile Val Lys Ala Ile Ser Gly Val Gln Thr  
65 70 75 80  
Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys Leu Gly  
85 90 95  
Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Lys Cys Pro Arg  
100 105 110  
Pro Met Cys Tyr Lys Ser Tyr Gly Ser Gly Lys Glu Asp Asn Pro Thr  
115 120 125  
Cys Asp Val Pro Gly Phe Asp Asn Cys Lys Met Thr Leu Leu Arg His  
130 135 140  
Val Ser Cys Val Asp Cys Pro Gly His Asp Ile Leu Met Ala Thr Met  
145 150 155 160  
Leu Asn Gly Ala Ala Ile Val Asp Gly Ala Leu Leu Leu Ile Ala Ala  
165 170 175  
Asn Gly Ser Cys Pro Gln Pro Gln Thr Ala Glu His Leu Ala Ser Val  
180 185 190  
Asp Met Met Arg Leu Lys His Ile Ile Ile Leu Gln Asn Lys Ile Asp  
195 200 205  
Leu Ile Asn Glu Lys Ala Ala Thr Glu Gln His Glu Ala Ile Gln Lys  
210 215 220  
Phe Ile Thr Asn Thr Asn Ala Glu Asp Ala Pro Ile Val Pro Val Ser  
225 230 235 240  
Ala Gln Leu Lys Tyr Asn Ile Asp Val Val Ser Glu Tyr Ile Val Lys  
245 250 255  
Lys Ile Pro Ile Pro Val Arg Asp Phe Val Ser Pro Pro Lys Met Ile  
260 265 270  
Val Ile Arg Ser Phe Asp Val Asn Lys Pro Gly Ser Ala Gly His Glu  
275 280 285  
Met Lys Gly Gly Val Ala Gly Gly Ser Ile Leu Gln  
290 295 300

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

Met Val Gln Ser Val Leu Ile Ser Arg Asn Lys Gly Leu Ala Glu Gln  
1 5 10 15  
Asp Leu Thr Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu  
20 25 30  
Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile Gly His Val  
35 40 45  
Ala His Gly Lys Ser Thr Ile Val Lys Ala Ile Ser Gly Val Gln Thr  
50 55 60  
Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys Leu Gly  
65 70 75 80  
Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Lys Cys Pro Arg

SEQUENCE 1156

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Tyr | Lys | Ser | Tyr | Gly | Ser | Gly | Lys | Glu | Asp | Asn | Pro | Thr | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Val | Pro | Gly | Phe | Asp | Asn | Cys | Lys | Met | Thr | Leu | Leu | Arg | His | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Cys | Val | Asp | Cys | Pro | Gly | His | Asp | Ile | Leu | Met | Ala | Thr | Met | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Gly | Ala | Ala | Ile | Val | Asp | Gly | Ala | Leu | Leu | Leu | Ile | Ala | Ala | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Cys | Pro | Gln | Pro | Gln | Thr | Ala | Glu | His | Leu | Ala | Ser | Val | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Met | Arg | Leu | Lys | His | Ile | Ile | Ile | Leu | Gln | Asn | Lys | Ile | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Asn | Glu | Lys | Ala | Ala | Thr | Glu | Gln | His | Glu | Ala | Ile | Gln | Lys | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Asn | Thr | Asn | Ala | Glu | Asp | Ala | Pro | Ile | Val | Pro | Val | Ser | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Leu | Lys | Tyr | Asn | Ile | Asp | Val | Val | Ser | Glu | Tyr | Ile | Val | Lys | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Pro | Ile | Pro | Val | Arg | Asp | Phe | Val | Ser | Pro | Pro | Lys | Met | Ile | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Arg | Ser | Phe | Asp | Val | Asn | Lys | Pro | Gly | Ser | Ala | Gly | His | Glu | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Gly | Gly | Val | Ala | Gly | Gly | Ser | Ile | Leu | Gln |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1311
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| aaggcgtgag  | ataataaaac | cctttggcctt | tctcatagag | atttgtccgg | tctcttgctc | 60   |
| ctctttctcc  | tttcttcact | gtagaatccg  | tgcacaaac  | aactagctcc | aatggcataa | 120  |
| tgagcattgt  | agtttgcaat | ttcttcttcc  | gtgaagaaga | agaagatggc | tttgagagaa | 180  |
| gaggaagaag  | cgtcacaaaa | cgtgctgttt  | tgtgtccttg | atgggctcta | ttgcgaggaa | 240  |
| gaaaccgggt  | ttgtggagga | cgatcttgat  | gacgatggag | atttagattt | tctcgagaaa | 300  |
| tctgatgaga  | gtgttgtaaa | gtttcagttt  | ttacctcttt | tggatatgtt | cttatgggat | 360  |
| gacgatgaga  | ttctgagttt | gatttcaaa   | gaaaacgaaa | cgaatccatg | ttttggggaa | 420  |
| caaactcttag | atggcttttt | ggtttcttgt  | aggaaagagg | ctttagattg | ggttcttagg | 480  |
| gttaaatctc  | attatgggtt | tacttcattg  | acggctatac | ttgctgtgaa | ctacttcgat | 540  |
| aggtttatga  | caagtataaa | gcttcagact  | gataagccat | ggatgtctca | gcttggtgct | 600  |
| gtggcttctt  | tgtctttagc | tgctaaagt   | gaagagattc | aagttccatt | gctcttagac | 660  |
| ctccaagtgg  | aagaagcaag | atatctcttt  | gaagctaaga | cgattcaaag | aatggagctt | 720  |
| ttgattcttt  | ctactcttca | atggagaatg  | caccctgtga | ctccaatctc | tttctttgat | 780  |
| cacattatcc  | ggcgatttgg | ctctaaatgg  | caccagcaat | tagacttctg | taggaagtgt | 840  |
| gagcgtcttc  | tgatctctgt | tattgctgat  | acgagggtta | tgaggtaact | cccttctgtc | 900  |
| ttagctactg  | caataatgat | ccttgtcttc  | gaggaattga | agccatgtga | tgaagttgaa | 960  |
| taccaatctc  | aaataacgac | tctactcaaa  | gtcaatcagg | agaaagtaaa | tgaatgctat | 1020 |
| gaactgttgt  | tggagcaca  | tccaagcaag  | aagaggatga | tgaatttggt | tgatcaggac | 1080 |
| agtccaagtg  | gtgtattaga | ctttgatgac  | agctcaaata | gctcctggaa | tgtctccact | 1140 |
| actgcttcag  | tgtcctcatc | atcttctgtc  | ccagagcctc | tgtcgaagag | aagaagagtt | 1200 |
| caggagcagc  | aaatgagatt | gccctcaata  | aaccgtatgt | ttctcgatgt | gcttagtagt | 1260 |
| cctcgctagt  | acctttcttt | gatcaaatgt  | gtcaaaacat | aaattcaGat | c          |      |

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Glu | Lys | Glu | Glu | Glu | Ala | Ser | Gln | Asn | Gly | Ala | Phe | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Leu | Asp | Gly | Leu | Tyr | Cys | Glu | Glu | Glu | Thr | Gly | Phe | Val | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Asp | Asp | Asp | Gly | Asp | Leu | Asp | Phe | Leu | Glu | Lys | Ser | Asp | Glu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Val | Val | Lys | Phe | Gln | Phe | Leu | Pro | Leu | Leu | Asp | Met | Phe | Leu | Trp |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asp | Asp | Asp | Glu | Ile | Leu | Ser | Leu | Ile | Ser | Lys | Glu | Asn | Glu | Thr | Asn |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Pro | Cys | Phe | Gly | Glu | Gln | Ile | Leu | Asp | Gly | Phe | Leu | Val | Ser | Cys | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Glu | Ala | Leu | Asp | Trp | Val | Leu | Arg | Val | Lys | Ser | His | Tyr | Gly | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Thr | Ser | Leu | Thr | Ala | Ile | Leu | Ala | Val | Asn | Tyr | Phe | Asp | Arg | Phe | Met |

115 120 125  
Thr Ser Ile Lys Leu Gln Thr Asp Lys Pro Trp Met Ser Gln Leu Val  
130 135 140  
Ala Val Ala Ser Leu Ser Leu Ala Ala Lys Val Glu Glu Ile Gln Val  
145 150 155 160  
Pro Leu Leu Leu Asp Leu Gln Val Glu Glu Ala Arg Tyr Leu Phe Glu  
165 170 175  
Ala Lys Thr Ile Gln Arg Met Glu Leu Ile Leu Ser Thr Leu Gln  
180 185 190  
Trp Arg Met His Pro Val Thr Pro Ile Ser Phe Phe Asp His Ile Ile  
195 200 205  
Arg Arg Phe Gly Ser Lys Trp His Gln Gln Leu Asp Phe Cys Arg Lys  
210 215 220  
Cys Glu Arg Leu Leu Ile Ser Val Ile Ala Asp Thr Arg Phe Met Arg  
225 230 235 240  
Tyr Phe Pro Ser Val Leu Ala Thr Ala Ile Met Ile Leu Val Phe Glu  
245 250 255  
Glu Leu Lys Pro Cys Asp Glu Val Glu Tyr Gln Ser Gln Ile Thr Thr  
260 265 270  
Leu Leu Lys Val Asn Gln Glu Lys Val Asn Glu Cys Tyr Glu Leu Leu  
275 280 285  
Leu Glu His Asn Pro Ser Lys Lys Arg Met Met Asn Leu Val Asp Gln  
290 295 300  
Asp Ser Pro Ser Gly Val Leu Asp Phe Asp Asp Ser Ser Asn Ser Ser  
305 310 315 320  
Trp Asn Val Ser Thr Thr Ala Ser Val Ser Ser Ser Ser Ser Pro  
325 330 335  
Glu Pro Leu Leu Lys Arg Arg Arg Val Gln Glu Gln Gln Met Arg Leu  
340 345 350  
Pro Ser Ile Asn Arg Met Phe Leu Asp Val Leu Ser Ser Pro Arg  
355 360 365

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1569166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

Met Phe Leu Trp Asp Asp Asp Glu Ile Leu Ser Leu Ile Ser Lys Glu  
1 5 10 15  
Asn Glu Thr Asn Pro Cys Phe Gly Glu Gln Ile Leu Asp Gly Phe Leu  
20 25 30  
Val Ser Cys Arg Lys Glu Ala Leu Asp Trp Val Leu Arg Val Lys Ser  
35 40 45  
His Tyr Gly Phe Thr Ser Leu Thr Ala Ile Leu Ala Val Asn Tyr Phe  
50 55 60  
Asp Arg Phe Met Thr Ser Ile Lys Leu Gln Thr Asp Lys Pro Trp Met  
65 70 75 80  
Ser Gln Leu Val Ala Val Ala Ser Leu Ser Leu Ala Ala Lys Val Glu  
85 90 95  
Glu Ile Gln Val Pro Leu Leu Leu Asp Leu Gln Val Glu Glu Ala Arg  
100 105 110  
Tyr Leu Phe Glu Ala Lys Thr Ile Gln Arg Met Glu Leu Leu Ile Leu  
115 120 125  
Ser Thr Leu Gln Trp Arg Met His Pro Val Thr Pro Ile Ser Phe Phe  
130 135 140

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | His | Ile | Ile | Arg | Arg | Phe | Gly | Ser | Lys | Trp | His | Gln | Gln | Leu | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Cys | Arg | Lys | Cys | Glu | Arg | Leu | Leu | Ile | Ser | Val | Ile | Ala | Asp | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Phe | Met | Arg | Tyr | Phe | Pro | Ser | Val | Leu | Ala | Thr | Ala | Ile | Met | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Val | Phe | Glu | Glu | Leu | Lys | Pro | Cys | Asp | Glu | Val | Glu | Tyr | Gln | Ser |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gln | Ile | Thr | Thr | Leu | Leu | Lys | Val | Asn | Gln | Glu | Lys | Val | Asn | Glu | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Glu | Leu | Leu | Leu | Glu | His | Asn | Pro | Ser | Lys | Lys | Arg | Met | Met | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Val | Asp | Gln | Asp | Ser | Pro | Ser | Gly | Val | Leu | Asp | Phe | Asp | Asp | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ser | Asn | Ser | Ser | Trp | Asn | Val | Ser | Thr | Thr | Ala | Ser | Val | Ser | Ser | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ser | Ser | Pro | Glu | Pro | Leu | Leu | Lys | Arg | Arg | Arg | Val | Gln | Glu | Gln |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Gln | Met | Arg | Leu | Pro | Ser | Ile | Asn | Arg | Met | Phe | Leu | Asp | Val | Leu | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Pro | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1569167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Ile | Lys | Leu | Gln | Thr | Asp | Lys | Pro | Trp | Met | Ser | Gln | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Val | Ala | Ser | Leu | Ser | Leu | Ala | Lys | Val | Glu | Glu | Ile | Gln |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Pro | Leu | Leu | Leu | Asp | Leu | Gln | Val | Glu | Glu | Ala | Arg | Tyr | Leu | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Ala | Lys | Thr | Ile | Gln | Arg | Met | Glu | Leu | Leu | Ile | Leu | Ser | Thr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Trp | Arg | Met | His | Pro | Val | Thr | Pro | Ile | Ser | Phe | Phe | Asp | His | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Arg | Arg | Phe | Gly | Ser | Lys | Trp | His | Gln | Gln | Leu | Asp | Phe | Cys | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Cys | Glu | Arg | Leu | Leu | Ile | Ser | Val | Ile | Ala | Asp | Thr | Arg | Phe | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Arg | Tyr | Phe | Pro | Ser | Val | Leu | Ala | Thr | Ala | Ile | Met | Ile | Leu | Val | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Glu | Glu | Leu | Lys | Pro | Cys | Asp | Glu | Val | Glu | Tyr | Gln | Ser | Gln | Ile | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Leu | Lys | Val | Asn | Gln | Glu | Lys | Val | Asn | Glu | Cys | Tyr | Glu | Leu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Leu | Glu | His | Asn | Pro | Ser | Lys | Lys | Arg | Met | Met | Asn | Leu | Val | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |
| Gln | Asp | Ser | Pro | Ser | Gly | Val | Leu | Asp | Phe | Asp | Asp | Ser | Ser | Asn | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Ser | Trp | Asn | Val | Ser | Thr | Thr | Ala | Ser | Val | Ser | Ser | Ser | Ser | Ser | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Glu | Pro | Leu | Leu | Lys | Arg | Arg | Arg | Val | Gln | Glu | Gln | Gln | Met | Arg |

210 215 220  
Leu Pro Ser Ile Asn Arg Met Phe Leu Asp Val Leu Ser Ser Pro Arg  
225 230 235 240

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1386

(D) OTHER INFORMATION: / Ceres Seq. ID 1569168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

|              |            |            |            |            |            |      |
|--------------|------------|------------|------------|------------|------------|------|
| attttctctcta | cttgtccact | tttctacagc | cgcctcatcc | ttctcccttg | tgcgatatcg | 60   |
| tttgcgtgag   | atttgtctga | aaagtagcta | accatgggta | aagagaagtt | tcacatcaac | 120  |
| atttgtggtca  | ttggccacgt | cgattctgga | aagtcgacaa | ccactggaca | cttgatctac | 180  |
| aagtgtgggtg  | gtattgacaa | gcgtgtgatc | gagaggttcg | agaaggaggc | tgctgagatg | 240  |
| aacaagaggt   | ccttcaagta | cgcctgggtg | ttggacaaac | ttaaggctga | gcgtgagcgt | 300  |
| ggatcacca    | ttgacattgc | tctctggaag | ttcgagacca | ccaagtacta | ctgcactgtc | 360  |
| attgatgctc   | ctggctatcg | tgatttcac  | aagaactatg | tcactggtag | ctccaggct  | 420  |
| gattgtgctg   | tccttatcat | cgactccacc | actggtGtt  | ttgaggctgg | tatctccaag | 480  |
| gatggtcaga   | cccgtgagca | cgctctcctt | gctttcaccc | ttggtgtcaa | gcagatgatc | 540  |
| tgctgttgta   | acaagatgga | tgccactacc | cccaagtact | ccaaggccag | gtacgatgaa | 600  |
| atcatcaagg   | aggtgtcttc | ctacttgaag | aaggttggtt | acaacccoga | caaaatccca | 660  |
| tttgtgcccc   | tctctggatt | tgagggtgac | aacatgattg | agaggtccac | caacottgac | 720  |
| tggtacaagg   | gaccaactct | ccttgaggct | cttgaccaga | tcaacgagcc | caagaggccg | 780  |
| tcagacaagc   | cccttctgt  | cccacttcag | gatgtctaca | agattggttg | tattggaacg | 840  |
| gtgccattgg   | gacgtgttga | gactggtat  | atcaagcctg | gtatggttgt | gacctttgct | 900  |
| cccacaggat   | tgaccactga | ggtcaagtc  | gttgagatgc | accaagagtc | tcttcttgag | 960  |
| gcacttcag    | gtgacaacgt | tgggttcaat | gttaagaatg | ttgccgtgaa | ggatcttaag | 1020 |
| agagggtacg   | tcgcatccaa | ctccaaggat | gacctgcc   | agggtgctgc | taacttcacc | 1080 |
| tcacaggta    | tcacatgaa  | ccaccttgt  | cagattggta | acggttacgc | cccagtcttg | 1140 |
| gattgccaca   | cctctcacat | tgagtcgaag | ttctctgaga | tcttgaccaa | gattgacagg | 1200 |
| cgttctggta   | aggagattga | gaaggagccc | aaattcttga | agaatggtga | tgctggtatg | 1260 |
| gtgaagatga   | ctccaaccaa | gcccattggt | gtggagacct | tctctgagta | cccaccactt | 1320 |
| ggacggttcg   | ctgttaggga | catgaggcag | actggttcag | tcggtgttat | caagagtgtt | 1380 |
| gacaag       |            |            |            |            |            |      |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..431

(D) OTHER INFORMATION: / Ceres Seq. ID 1569169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Glu | Lys | Phe | His | Ile | Asn | Ile | Val | Val | Ile | Gly | His | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ser | Gly | Lys | Ser | Thr | Thr | Thr | Gly | His | Leu | Ile | Tyr | Lys | Leu | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Asp | Lys | Arg | Val | Ile | Glu | Arg | Phe | Glu | Lys | Glu | Ala | Ala | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Glu | Thr | Thr | Lys | Tyr | Cys | Thr | Val | Ile | Asp | Ala | Pro | Gly | His | Arg |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Asp | Phe | Ile | Lys | Asn | Met | Ile | Thr | Gly | Thr | Ser | Gln | Ala | Asp | Cys | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Leu | Ile | Ile | Asp | Ser | Thr | Thr | Gly | Gly | Phe | Glu | Ala | Gly | Ile | Ser |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Lys | Asp | Gly | Gln | Thr | Arg | Glu | His | Ala | Leu | Leu | Ala | Phe | Thr | Leu | Gly |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |  |
| Val | Lys | Gln | Met | Ile | Cys | Cys | Asn | Lys | Met | Asp | Ala | Thr | Thr | Pro |     |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Lys | Tyr | Ser | Lys | Ala | Arg | Tyr | Asp | Glu | Ile | Ile | Lys | Glu | Val | Ser | Ser |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Tyr | Leu | Lys | Lys | Val | Gly | Tyr | Asn | Pro | Asp | Lys | Ile | Pro | Phe | Val | Pro |  |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ile | Ser | Gly | Phe | Glu | Gly | Asp | Asn | Met | Ile | Glu | Arg | Ser | Thr | Asn | Leu |  |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |  |
| Asp | Trp | Tyr | Lys | Gly | Pro | Thr | Leu | Leu | Glu | Ala | Leu | Asp | Gln | Ile | Asn |  |
|     |     |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |
| Glu | Pro | Lys | Arg | Pro | Ser | Asp | Lys | Pro | Leu | Arg | Leu | Pro | Leu | Gln | Asp |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |  |
| Val | Tyr | Lys | Ile | Gly | Gly | Ile | Gly | Thr | Val | Pro | Leu | Gly | Arg | Val | Glu |  |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Thr | Gly | Met | Ile | Lys | Pro | Gly | Met | Val | Val | Thr | Phe | Ala | Pro | Thr | Gly |  |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Thr | Thr | Glu | Val | Lys | Ser | Val | Glu | Met | His | His | Glu | Ser | Leu | Leu |  |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |  |
| Glu | Ala | Leu | Pro | Gly | Asp | Asn | Val | Gly | Phe | Asn | Val | Lys | Asn | Val | Ala |  |
|     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Val | Lys | Asp | Leu | Lys | Arg | Gly | Tyr | Val | Ala | Ser | Asn | Ser | Lys | Asp | Asp |  |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |  |
| Pro | Ala | Lys | Gly | Ala | Ala | Asn | Phe | Thr | Ser | Gln | Val | Ile | Ile | Met | Asn |  |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |  |
| His | Pro | Gly | Gln | Ile | Gly | Asn | Gly | Tyr | Ala | Pro | Val | Leu | Asp | Cys | His |  |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Thr | Ser | His | Ile | Ala | Val | Lys | Phe | Ser | Glu | Ile | Leu | Thr | Lys | Ile | Asp |  |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |  |
| Arg | Arg | Ser | Gly | Lys | Glu | Ile | Glu | Lys | Glu | Pro | Lys | Phe | Leu | Lys | Asn |  |
|     |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Gly | Asp | Ala | Gly | Met | Val | Lys | Met | Thr | Pro | Thr | Lys | Pro | Met | Val | Val |  |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     | 400 |     |  |
| Glu | Thr | Phe | Ser | Glu | Tyr | Pro | Pro | Leu | Gly | Arg | Phe | Ala | Val | Arg | Asp |  |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |     | 415 |     |  |
| Met | Arg | Gln | Thr | Val | Ala | Val | Gly | Val | Ile | Lys | Ser | Val | Asp | Lys |     |  |
|     |     |     |     | 420 |     |     |     | 425 |     |     |     |     | 430 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |  |



(2) INFORMATION FOR SEQ ID NO:1165:

(A) LENGTH: 330 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp  
1 5 10 15  
Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr  
20 25 30

Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile  
35 40 45  
Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro Lys Tyr Ser Lys Ala  
50 55 60  
Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser Tyr Leu Lys Lys Val  
65 70 75 80  
Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu  
85 90 95  
Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly  
100 105 110  
Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn Glu Pro Lys Arg Pro  
115 120 125  
Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly  
130 135 140  
Gly Ile Gly Thr Val Pro Leu Gly Arg Val Glu Thr Gly Met Ile Lys  
145 150 155 160  
Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly Leu Thr Thr Glu Val  
165 170 175  
Lys Ser Val Glu Met His His Glu Ser Leu Leu Glu Ala Leu Pro Gly  
180 185 190  
Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala Val Lys Asp Leu Lys  
195 200 205  
Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Gly Ala  
210 215 220  
Ala Asn Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile  
225 230 235 240  
Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala  
245 250 255  
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys  
260 265 270  
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met  
275 280 285  
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu  
290 295 300  
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val  
305 310 315 320  
Ala Val Gly Val Ile Lys Ser Val Asp Lys  
325 330

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ctcgaagact attaaaggaa tatccgcaaa gaagaaaaaa aaaacatttt tttggtaaag   | 60  |
| gactaatctt tttgtttgca tcggccatct ctaacottac gatttgtgtg tcttgctttg   | 120 |
| agcgaaaccc tagaatcggg cttaacccat ttgagcagag atgctgcgag tagcaggaag   | 180 |
| gaggcttttt tctgtttcgc agagatcatc gacggtgacc tccttcgtcc tttcccgtag   | 240 |
| ccataccctt tccgatggag gcaactcctc ttccgcttct agatctgtcc octctgcaga   | 300 |
| tctctcatct ttcaattctt accaccggag cgttataaga ggttttgctt ctcaagttat   | 360 |
| tactcagggg aatgagatag gttttggttc ggaagtccca gccacagtcg aagctgtcaa   | 420 |
| aacacctaac tcaaagattg tctatgacga ccataacccat gacggttacc cacctgggtga | 480 |
| ccctagcaag cgggcattcg cctattttgt cttgtcgggt ggaagggttg AtHtWWgcct   | 540 |
| ctgttctccg cctgcttggt ctgaagctta ttgtgagcat gtctgcaagt aaagatgtcc   | 600 |
| ttgcccttgc atccctcgag gttgacctag ggagcataga accaggaact accgtgacag   | 660 |

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| tcaagtggcg | tggaaagccc | gtcttcatca | ggcgaagaac | agaagatgac  | atcaagctgg | 720  |
| ccaatagtgt | ggatgttga  | tcctgaggg  | acccacaaga | agactcgggt  | agagtcaaga | 780  |
| atccagaatg | gttgatcgtg | gttgagtat  | gcactcattt | gggtgcatc   | cccttgcta  | 840  |
| atgctggtga | ttatggtggt | tggttttgtc | cgtgtcacgg | atcacattac  | gatatatctg | 900  |
| gaagaattag | gaaaggtcct | gcaccataca | acctggaagt | accgacctac  | agcttcttgg | 960  |
| aagagaataa | attactcatt | ggttaatgaa | taaagcacia | cagtccgagt  | gtcatggtct | 1020 |
| ggatgatctt | aaatctgttt | ttgtttttat | attttccggc | atttttagcgt | gcaagttcgc | 1080 |
| tttctcaca  | ctttgggctc | agcaaaaatt | ggcttgtttt | gctgaataat  | acaaacttgt | 1140 |
| cattgtatga | cttagtatct | gtctcatctg | gtgaaaatac | attgttcata  | cttcatagtc | 1200 |
| tctgtttatt | atttgaaaag | agttttg    |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1569180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Val | Ala | Gly | Arg | Arg | Leu | Phe | Ser | Val | Ser | Gln | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Val | Thr | Ser | Phe | Val | Leu | Ser | Arg | Asp | His | Thr | Leu | Ser | Asp |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Gly | Gly | Asn | Ser | Ser | Ser | Ala | Ser | Arg | Ser | Val | Pro | Ser | Ala | Asp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Phe | Asn | Ser | Tyr | His | Arg | Ser | Val | Ile | Arg | Gly | Phe | Ala | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Val | Ile | Thr | Gln | Gly | Asn | Glu | Ile | Gly | Phe | Gly | Ser | Glu | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Thr | Val | Glu | Ala | Val | Lys | Thr | Pro | Asn | Ser | Lys | Ile | Val | Tyr | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | His | Asn | His | Glu | Arg | Tyr | Pro | Pro | Gly | Asp | Pro | Ser | Lys | Arg | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ala | Tyr | Phe | Val | Leu | Ser | Gly | Arg | Phe | Asp | Xaa | Xaa | Leu | Cys |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Ser | Pro | Pro | Ala | Cys | Ser | Glu | Ala | Tyr | Cys | Glu | His | Val | Cys | Lys |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1569181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Ile | Thr | Met | Ser | Val | Thr | His | Leu | Val | Thr | Leu | Ala | Ser |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Gly | His | Ser | Pro | Ile | Leu | Ser | Cys | Arg | Val | Glu | Gly | Leu | Xaa | Xaa | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Leu | Arg | Leu | Leu | Val | Leu | Lys | Leu | Ile | Val | Ser | Met | Ser | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Asp | Val | Leu | Ala | Leu | Ala | Ser | Leu | Glu | Val | Asp | Leu | Gly | Ser |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Pro | Gly | Thr | Thr | Val | Thr | Val | Lys | Trp | Arg | Gly | Lys | Pro | Val |

(2) INFORMATION FOR SEQ ID NO:1169:

(A) LENGTH: 175 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1569182

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Thr | His | Leu | Val | Thr | Leu | Ala | Ser | Gly | His | Ser | Pro | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Cys | Arg | Val | Glu | Gly | Leu | Xaa | Xaa | Ala | Ser | Val | Leu | Arg | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Leu | Lys | Leu | Ile | Val | Ser | Met | Ser | Ala | Ser | Lys | Asp | Val | Leu |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Leu | Ala | Ser | Leu | Glu | Val | Asp | Leu | Gly | Ser | Ile | Glu | Pro | Gly | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Val | Thr | Val | Lys | Trp | Arg | Gly | Lys | Pro | Val | Phe | Ile | Arg | Arg | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Glu | Asp | Asp | Ile | Lys | Leu | Ala | Asn | Ser | Val | Asp | Val | Gly | Ser | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Asp | Pro | Gln | Glu | Asp | Ser | Val | Arg | Val | Lys | Asn | Pro | Glu | Trp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Val | Val | Gly | Val | Cys | Thr | His | Leu | Gly | Cys | Ile | Pro | Leu | Pro | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Gly | Asp | Tyr | Gly | Gly | Trp | Phe | Cys | Pro | Cys | His | Gly | Ser | His | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ile | Ser | Gly | Arg | Ile | Arg | Lys | Gly | Pro | Ala | Pro | Tyr | Asn | Leu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Pro | Thr | Tyr | Ser | Phe | Leu | Glu | Glu | Asn | Lys | Leu | Leu | Ile | Gly |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1507

(D) OTHER INFORMATION: / Ceres Seq. ID 1569183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| acctgaatat  | tgactacgca  | ttataagagg | ttttgttttg  | gggtttttcc  | ttcttcacat  | 60   |
| atcatttttc  | tgattctccc  | acgaagatga | accacctcgt  | tcgtaaaagc  | tcgctcggtt  | 120  |
| actccgcctt  | gaggtcogtt  | tcgtacctcc | gtcaatctgc  | cgttacctct  | ccacctccga  | 180  |
| ttttctccgc  | cgcgcgttca  | accgttcgcc | agttcacttc  | cgcgcggtat  | ccttccaaca  | 240  |
| gttttcaatt  | gacgcgcgcg  | acgaattggg | gaatccggat  | agttccggag  | aggaaggcgt  | 300  |
| ttgtgattga  | gcgattccgt  | aaatacgcta | cgacgttgcc  | gtcggggatt  | catttctca   | 360  |
| ttccgttcgt  | ggatcgtatt  | gcttatgttc | attctctcaa  | ggaagaagct  | atcccgatcc  | 420  |
| cgaatcagac  | tgcgattact  | aaagacaacg | ttagtatcca  | catcgatggt  | gttctctacg  | 480  |
| ttaagattgt  | ggatcctaag  | ttagcttctt | atggcggtga  | gagtcctatc  | tatgctgttg  | 540  |
| tacagctggc  | tcagaccaca  | atgcgtagtg | agcttggtta  | gatcactctt  | gataagacct  | 600  |
| ttgaggaacg  | agacactctc  | aacgagaaga | tagtggaagc  | catcaatggt  | gctgcaaaaag | 660  |
| actgggtctt  | tcagtgctct  | cgttatgaga | taagggatat  | tatgccccct  | catggagtg   | 720  |
| gagctgctat  | ggaaatgcaa  | gctgaagctg | agcgtaaaaa  | gagagcccag  | attcttgagt  | 780  |
| ctgaaggaga  | aaggcaatcc  | catatcaaca | ttgctgatgg  | taagaaaagt  | tctgtaatct  | 840  |
| tggcatctga  | agcagcaaag  | atggaccagg | tgaatcgagc  | acaagggtgag | gcagaagcaa  | 900  |
| tactagctag  | agcacaagca  | actgcgaaag | gcctgggtctt | gttatctcag  | tcctccaagg  | 960  |
| aaactggggg  | agtagaggcg  | gcgagtttga | gagttgcaga  | gcaatacatt  | acagCcttcg  | 1020 |
| gtaacattgc  | caaggagggt  | acgataatgt | tgcttccaag  | tggtgcttca  | aatcctgcta  | 1080 |
| gcatgattgc  | tcaagcttta  | acaatgtaca | aaagccttgt  | catcaatggt  | ccaagcaaag  | 1140 |
| atcaccaaga  | aacacaagca  | cttgatgaaa | cagatttgga  | agagttggaa  | gacatgggtg  | 1200 |
| agaaacatat  | atcagaaggc  | tctaataacc | gatcaggctc  | aatatcattt  | gacacagaga  | 1260 |
| aaccagggtca | caccgggtgaa | ccacgatttt | ctcttcagaa  | ccgcaacaag  | gatccgcagt  | 1320 |
| aggcagccga  | accgggggatg | agataaatcc | tttgggcttg  | agaaaactgg  | aaaccatttt  | 1380 |
| tcatctttca  | aatatgaggc  | agtaaccatc | ttttccgttt  | gaatagctag  | aatatcatca  | 1440 |
| ctttgcatat  | agaaacgaat  | ctgaacatct | gttctccgat  | aagaattttc  | ctactggatt  | 1500 |
| tggttatg    |             |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | His | Leu | Val | Arg | Lys | Ser | Ser | Val | Gly | Tyr | Ser | Ala | Leu | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Val | Ser | Tyr | Leu | Arg | Gln | Ser | Ala | Val | Thr | Ser | Pro | Pro | Pro | Ile |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Phe | Ser | Ala | Ala | Ala | Ser | Thr | Val | Arg | Gln | Phe | Thr | Ser | Ala | Gly | Tyr |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Pro | Ser | Asn | Ser | Phe | Gln | Leu | Thr | Pro | Pro | Thr | Asn | Trp | Gly | Ile | Arg |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Ile | Val | Pro | Glu | Arg | Lys | Ala | Phe | Val | Ile | Glu | Arg | Phe | Gly | Lys | Tyr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Thr | Thr | Leu | Pro | Ser | Gly | Ile | His | Phe | Leu | Ile | Pro | Phe | Val | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Ile | Ala | Tyr | Val | His | Ser | Leu | Lys | Glu | Glu | Ala | Ile | Pro | Ile | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Gln | Thr | Ala | Ile | Thr | Lys | Asp | Asn | Val | Ser | Ile | His | Ile | Asp | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Leu | Tyr | Val | Lys | Ile | Val | Asp | Pro | Lys | Leu | Ala | Ser | Tyr | Gly | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu | Ser | Pro | Ile | Tyr | Ala | Val | Val | Gln | Leu | Ala | Gln | Thr | Thr | Met | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Leu | Gly | Lys | Ile | Thr | Leu | Asp | Lys | Thr | Phe | Glu | Glu | Arg | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Leu | Asn | Glu | Lys | Ile | Val | Glu | Ala | Ile | Asn | Val | Ala | Ala | Lys | Asp |

(2) INFORMATION FOR SEQ ID NO:1172:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1569185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Glu | Leu | Gly | Lys | Ile | Thr | Leu | Asp | Lys | Thr | Phe | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Thr | Leu | Asn | Glu | Lys | Ile | Val | Glu | Ala | Ile | Asn | Val | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asp | Trp | Gly | Leu | Gln | Cys | Leu | Arg | Tyr | Glu | Ile | Arg | Asp | Ile | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | His | Gly | Val | Arg | Ala | Ala | Met | Glu | Met | Gln | Ala | Glu | Ala | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Lys | Lys | Arg | Ala | Gln | Ile | Leu | Glu | Ser | Glu | Gly | Glu | Arg | Gln | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Ile | Asn | Ile | Ala | Asp | Gly | Lys | Lys | Ser | Ser | Val | Ile | Leu | Ala | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ala | Ala | Lys | Met | Asp | Gln | Val | Asn | Arg | Ala | Gln | Gly | Glu | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ile | Leu | Ala | Arg | Ala | Gln | Ala | Thr | Ala | Lys | Gly | Leu | Val | Leu | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Gln | Ser | Leu | Lys | Glu | Thr | Gly | Gly | Val | Glu | Ala | Ala | Ser | Leu | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ala | Glu | Gln | Tyr | Ile | Thr | Ala | Phe | Gly | Asn | Ile | Ala | Lys | Glu | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Thr Ile Met Leu Leu Pro Ser Gly Ala Ser Asn Pro Ala Ser Met Ile  
165 170 175  
Ala Gln Ala Leu Thr Met Tyr Lys Ser Leu Val Ile Asn Gly Pro Ser  
180 185 190  
Lys Asp His Gln Glu Thr Gln Ala Leu Asp Glu Thr Asp Leu Glu Glu  
195 200 205  
Leu Glu Asp Met Gly Glu Lys His Ile Ser Glu Gly Ser Asn Asn Arg  
210 215 220  
Ser Gly Ser Ile Ser Phe Asp Thr Glu Lys Pro Gly His Thr Gly Glu  
225 230 235 240  
Pro Arg Phe Ser Leu Gln Asn Arg Asn Lys Asp Pro Gln  
245 250

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

Met Pro Pro His Gly Val Arg Ala Ala Met Glu Met Gln Ala Glu Ala  
1 5 10 15  
Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser Glu Gly Glu Arg Gln  
20 25 30  
Ser His Ile Asn Ile Ala Asp Gly Lys Lys Ser Ser Val Ile Leu Ala  
35 40 45  
Ser Glu Ala Ala Lys Met Asp Gln Val Asn Arg Ala Gln Gly Glu Ala  
50 55 60  
Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala Lys Gly Leu Val Leu  
65 70 75 80  
Leu Ser Gln Ser Leu Lys Glu Thr Gly Gly Val Glu Ala Ala Ser Leu  
85 90 95  
Arg Val Ala Glu Gln Tyr Ile Thr Ala Phe Gly Asn Ile Ala Lys Glu  
100 105 110  
Gly Thr Ile Met Leu Leu Pro Ser Gly Ala Ser Asn Pro Ala Ser Met  
115 120 125  
Ile Ala Gln Ala Leu Thr Met Tyr Lys Ser Leu Val Ile Asn Gly Pro  
130 135 140  
Ser Lys Asp His Gln Glu Thr Gln Ala Leu Asp Glu Thr Asp Leu Glu  
145 150 155 160  
Glu Leu Glu Asp Met Gly Glu Lys His Ile Ser Glu Gly Ser Asn Asn  
165 170 175  
Arg Ser Gly Ser Ile Ser Phe Asp Thr Glu Lys Pro Gly His Thr Gly  
180 185 190  
Glu Pro Arg Phe Ser Leu Gln Asn Arg Asn Lys Asp Pro Gln  
195 200 205

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1646
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569187

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

|            |            |             |             |             |            |      |
|------------|------------|-------------|-------------|-------------|------------|------|
| atcaactcaa | tctgtttgtc | tattttcttct | cccttgtagt  | gttttttgggt | ttttaccaaa | 60   |
| gaccaaccgt | tcacaacaat | gatcgcgcgga | cggatctggc  | gaagccaccg  | gtttctccgc | 120  |
| ccattcagct | cgtcatctgt | ttgctctccg  | ccgttccggg  | taccggagta  | tctttctcag | 180  |
| tcgtcttcct | ctccggcgtc | gcgcccattc  | ttgtttcacc  | ctcccacttt  | gatgaaatgg | 240  |
| ggtggaggaa | gtagaagctg | gttttogaac  | gaagccatgg  | ccactgattc  | aaattcaggg | 300  |
| ttaattgatg | tgccactagc | tcaaactggg  | gaagggtattg | ctgaatgtga  | gcttctcaag | 360  |
| tggtttgtca | aagagggaga | ttctgtggaa  | gagtttcagc  | cactctgtga  | agttcagagc | 420  |
| gataaagcaa | ctatagagat | cacaagtcgt  | tttaaaggga  | aagtggctct  | gatttcacat | 480  |
| tctccaggtg | acattattaa | ggttggagag  | actctgggta  | ggttggcggt  | tgaagactcg | 540  |
| caggattcgc | ttctaaccac | tgatagttca  | gaaattgtaa  | ctctgggagg  | ttcaaagcag | 600  |
| ggaacagaaa | atcttcttgg | agctctctca  | acgcctgogg  | ttcgtaacct  | tgcaaaagac | 660  |
| cttggcatag | atatcaatgt | tataactgga  | actggtaaag  | atggtagagt  | tttgaaagag | 720  |
| gatgttctcc | ggtttagtga | ccagaaagga  | tttgtaacag  | attcagtttc  | ttctgagcat | 780  |
| gctgttatag | gaggagactc | ggtttccact  | aaagctagta  | gtaactttga  | agataaaaca | 840  |
| gttcctctaa | gggattcag  | ccgagcaatg  | gtcaagacaa  | tgactatggc  | tacaagtgtg | 900  |
| ccgcattttc | attttgttga | agagataaac  | tgcgactcac  | ttgtggagct  | caagcagttc | 960  |
| ttcaaagaga | acaatacaga | ttccaccatc  | aaacacactt  | ttcttcttac  | tttaatcaag | 1020 |
| tctctgtcaa | tggtcttaac | caaataatccc | ttcgtgaata  | gttgcttcaa  | cgcggaatct | 1080 |
| ctcgagatca | ttctcaaagg | ttcacataat  | attggagttg  | caatggccac  | tgaacatggc | 1140 |
| cttgtcgttc | ctaataataa | gaatgttcag  | tcattatctc  | tgctagagat  | aaccaaagag | 1200 |
| ctgtcccggt | tacaacattt | ggcagcaaac  | aacaaactta  | accccgagga  | tgtgactggg | 1260 |
| ggaaccataa | ctctgagtaa | cattggagca  | attgggtggt  | aattcggatc  | ccctctttta | 1320 |
| aacttaccgg | aagttgcaat | catcgctctt  | ggaagaatcg  | agaaagttcc  | aaaattctca | 1380 |
| aaagaaggaa | ctgtctatcc | tgcatcgata  | atgatgggta  | acattgctgc  | ggatcataga | 1440 |
| gttctagatg | gggcaacggg | agctcgggtt  | tgctgccagt  | ggaaagagta  | tgtcgagaaa | 1500 |
| ccggagctgc | tgatgcttca | aatgagataa  | gaaggaaagg  | ttcatgttta  | tttgtgaatc | 1560 |
| attatgtatg | aaaccttcat | gttcgaataa  | gatcaagaac  | tgagctagca  | gttgtaaact | 1620 |
| aaacaaSvaa | agtaaaagtc | atatct      |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Asn | Ser | Ile | Cys | Leu | Ser | Ile | Ser | Ser | Pro | Leu | Tyr | Cys | Phe | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Phe | Phe | Thr | Lys | Asp | Gln | Pro | Phe | Thr | Thr | Met | Ile | Ala | Arg | Arg | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Trp | Arg | Ser | His | Arg | Phe | Leu | Arg | Pro | Phe | Ser | Ser | Ser | Ser | Val | Cys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Pro | Pro | Phe | Arg | Val | Pro | Glu | Tyr | Leu | Ser | Gln | Ser | Ser | Ser | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Ala | Ser | Arg | Pro | Phe | Phe | Val | His | Pro | Pro | Thr | Leu | Met | Lys | Trp |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Gly | Gly | Gly | Ser | Arg | Ser | Trp | Phe | Ser | Asn | Glu | Ala | Met | Ala | Thr | Asp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ser | Asn | Ser | Gly | Leu | Ile | Asp | Val | Pro | Leu | Ala | Gln | Thr | Gly | Glu | Gly |  |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Ala | Glu | Cys | Glu | Leu | Leu | Lys | Trp | Phe | Val | Lys | Glu | Gly | Asp | Ser |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Glu | Glu | Phe | Gln | Pro | Leu | Cys | Glu | Val | Gln | Ser | Asp | Lys | Ala | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Glu | Ile | Thr | Ser | Arg | Phe | Lys | Gly | Lys | Val | Ala | Leu | Ile | Ser | His |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |



Ser Pro Gly Asp Ile Ile Lys Val Gly Glu Thr Leu Val Arg Leu Ala  
165 170 175  
Val Glu Asp Ser Gln Asp Ser Leu Leu Thr Thr Asp Ser Ser Glu Ile  
180 185 190  
Val Thr Leu Gly Gly Ser Lys Gln Gly Thr Glu Asn Leu Leu Gly Ala  
195 200 205  
Leu Ser Thr Pro Ala Val Arg Asn Leu Ala Lys Asp Leu Gly Ile Asp  
210 215 220  
Ile Asn Val Ile Thr Gly Thr Gly Lys Asp Gly Arg Val Leu Lys Glu  
225 230 235 240  
Asp Val Leu Arg Phe Ser Asp Gln Lys Gly Phe Val Thr Asp Ser Val  
245 250 255  
Ser Ser Glu His Ala Val Ile Gly Gly Asp Ser Val Ser Thr Lys Ala  
260 265 270  
Ser Ser Asn Phe Glu Asp Lys Thr Val Pro Leu Arg Gly Phe Ser Arg  
275 280 285  
Ala Met Val Lys Thr Met Thr Met Ala Thr Ser Val Pro His Phe His  
290 295 300  
Phe Val Glu Glu Ile Asn Cys Asp Ser Leu Val Glu Leu Lys Gln Phe  
305 310 315 320  
Phe Lys Glu Asn Asn Thr Asp Ser Thr Ile Lys His Thr Phe Leu Pro  
325 330 335  
Thr Leu Ile Lys Ser Leu Ser Met Ala Leu Thr Lys Tyr Pro Phe Val  
340 345 350  
Asn Ser Cys Phe Asn Ala Glu Ser Leu Glu Ile Ile Leu Lys Gly Ser  
355 360 365  
His Asn Ile Gly Val Ala Met Ala Thr Glu His Gly Leu Val Val Pro  
370 375 380  
Asn Ile Lys Asn Val Gln Ser Leu Ser Leu Leu Glu Ile Thr Lys Glu  
385 390 395 400  
Leu Ser Arg Leu Gln His Leu Ala Ala Asn Asn Lys Leu Asn Pro Glu  
405 410 415  
Asp Val Thr Gly Gly Thr Ile Thr Leu Ser Asn Ile Gly Ala Ile Gly  
420 425 430  
Gly Lys Phe Gly Ser Pro Leu Leu Asn Leu Pro Glu Val Ala Ile Ile  
435 440 445  
Ala Leu Gly Arg Ile Glu Lys Val Pro Lys Phe Ser Lys Glu Gly Thr  
450 455 460  
Val Tyr Pro Ala Ser Ile Met Met Val Asn Ile Ala Ala Asp His Arg  
465 470 475 480  
Val Leu Asp Gly Ala Thr Val Ala Arg Phe Cys Cys Gln Trp Lys Glu  
485 490 495  
Tyr Val Glu Lys Pro Glu Leu Leu Met Leu Gln Met Arg  
500 505

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1569189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

Met Ile Ala Arg Arg Ile Trp Arg Ser His Arg Phe Leu Arg Pro Phe  
1 5 10 15  
Ser Ser Ser Ser Val Cys Ser Pro Pro Phe Arg Val Pro Glu Tyr Leu  
20 25 30  
Ser Gln Ser Ser Ser Ser Pro Ala Ser Arg Pro Phe Phe Val His Pro

|                                                                 |     |     |  |  |     |
|-----------------------------------------------------------------|-----|-----|--|--|-----|
| 35                                                              | 40  | 45  |  |  |     |
| Pro Thr Leu Met Lys Trp Gly Gly Ser Arg Ser Trp Phe Ser Asn     |     |     |  |  |     |
| 50                                                              | 55  | 60  |  |  |     |
| Glu Ala Met Ala Thr Asp Ser Asn Ser Gly Leu Ile Asp Val Pro Leu |     |     |  |  |     |
| 65                                                              | 70  | 75  |  |  | 80  |
| Ala Gln Thr Gly Glu Gly Ile Ala Glu Cys Glu Leu Leu Lys Trp Phe |     |     |  |  |     |
|                                                                 | 85  | 90  |  |  | 95  |
| Val Lys Glu Gly Asp Ser Val Glu Glu Phe Gln Pro Leu Cys Glu Val |     |     |  |  |     |
|                                                                 | 100 | 105 |  |  | 110 |
| Gln Ser Asp Lys Ala Thr Ile Glu Ile Thr Ser Arg Phe Lys Gly Lys |     |     |  |  |     |
|                                                                 | 115 | 120 |  |  | 125 |
| Val Ala Leu Ile Ser His Ser Pro Gly Asp Ile Ile Lys Val Gly Glu |     |     |  |  |     |
|                                                                 | 130 | 135 |  |  | 140 |
| Thr Leu Val Arg Leu Ala Val Glu Asp Ser Gln Asp Ser Leu Leu Thr |     |     |  |  |     |
| 145                                                             | 150 | 155 |  |  | 160 |
| Thr Asp Ser Ser Glu Ile Val Thr Leu Gly Gly Ser Lys Gln Gly Thr |     |     |  |  |     |
|                                                                 | 165 | 170 |  |  | 175 |
| Glu Asn Leu Leu Gly Ala Leu Ser Thr Pro Ala Val Arg Asn Leu Ala |     |     |  |  |     |
|                                                                 | 180 | 185 |  |  | 190 |
| Lys Asp Leu Gly Ile Asp Ile Asn Val Ile Thr Gly Thr Gly Lys Asp |     |     |  |  |     |
|                                                                 | 195 | 200 |  |  | 205 |
| Gly Arg Val Leu Lys Glu Asp Val Leu Arg Phe Ser Asp Gln Lys Gly |     |     |  |  |     |
|                                                                 | 210 | 215 |  |  | 220 |
| Phe Val Thr Asp Ser Val Ser Ser Glu His Ala Val Ile Gly Gly Asp |     |     |  |  |     |
| 225                                                             | 230 | 235 |  |  | 240 |
| Ser Val Ser Thr Lys Ala Ser Ser Asn Phe Glu Asp Lys Thr Val Pro |     |     |  |  |     |
|                                                                 | 245 | 250 |  |  | 255 |
| Leu Arg Gly Phe Ser Arg Ala Met Val Lys Thr Met Thr Met Ala Thr |     |     |  |  |     |
|                                                                 | 260 | 265 |  |  | 270 |
| Ser Val Pro His Phe His Phe Val Glu Glu Ile Asn Cys Asp Ser Leu |     |     |  |  |     |
|                                                                 | 275 | 280 |  |  | 285 |
| Val Glu Leu Lys Gln Phe Phe Lys Glu Asn Asn Thr Asp Ser Thr Ile |     |     |  |  |     |
|                                                                 | 290 | 295 |  |  | 300 |
| Lys His Thr Phe Leu Pro Thr Leu Ile Lys Ser Leu Ser Met Ala Leu |     |     |  |  |     |
| 305                                                             | 310 | 315 |  |  | 320 |
| Thr Lys Tyr Pro Phe Val Asn Ser Cys Phe Asn Ala Glu Ser Leu Glu |     |     |  |  |     |
|                                                                 | 325 | 330 |  |  | 335 |
| Ile Ile Leu Lys Gly Ser His Asn Ile Gly Val Ala Met Ala Thr Glu |     |     |  |  |     |
|                                                                 | 340 | 345 |  |  | 350 |
| His Gly Leu Val Val Pro Asn Ile Lys Asn Val Gln Ser Leu Ser Leu |     |     |  |  |     |
|                                                                 | 355 | 360 |  |  | 365 |
| Leu Glu Ile Thr Lys Glu Leu Ser Arg Leu Gln His Leu Ala Ala Asn |     |     |  |  |     |
|                                                                 | 370 | 375 |  |  | 380 |
| Asn Lys Leu Asn Pro Glu Asp Val Thr Gly Gly Thr Ile Thr Leu Ser |     |     |  |  |     |
| 385                                                             | 390 | 395 |  |  | 400 |
| Asn Ile Gly Ala Ile Gly Gly Lys Phe Gly Ser Pro Leu Leu Asn Leu |     |     |  |  |     |
|                                                                 | 405 | 410 |  |  | 415 |
| Pro Glu Val Ala Ile Ile Ala Leu Gly Arg Ile Glu Lys Val Pro Lys |     |     |  |  |     |
|                                                                 | 420 | 425 |  |  | 430 |
| Phe Ser Lys Glu Gly Thr Val Tyr Pro Ala Ser Ile Met Met Val Asn |     |     |  |  |     |
|                                                                 | 435 | 440 |  |  | 445 |
| Ile Ala Ala Asp His Arg Val Leu Asp Gly Ala Thr Val Ala Arg Phe |     |     |  |  |     |
|                                                                 | 450 | 455 |  |  | 460 |
| Cys Cys Gln Trp Lys Glu Tyr Val Glu Lys Pro Glu Leu Leu Met Leu |     |     |  |  |     |
| 465                                                             | 470 | 475 |  |  | 480 |
| Gln Met Arg                                                     |     |     |  |  |     |

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..432  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569190  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Trp | Gly | Gly | Gly | Ser | Arg | Ser | Trp | Phe | Ser | Asn | Glu | Ala | Met |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ala | Thr | Asp | Ser | Asn | Ser | Gly | Leu | Ile | Asp | Val | Pro | Leu | Ala | Gln | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Glu | Gly | Ile | Ala | Glu | Cys | Glu | Leu | Leu | Lys | Trp | Phe | Val | Lys | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Ser | Val | Glu | Glu | Phe | Gln | Pro | Leu | Cys | Glu | Val | Gln | Ser | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Thr | Ile | Glu | Ile | Thr | Ser | Arg | Phe | Lys | Gly | Lys | Val | Ala | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | His | Ser | Pro | Gly | Asp | Ile | Ile | Lys | Val | Gly | Glu | Thr | Leu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Leu | Ala | Val | Glu | Asp | Ser | Gln | Asp | Ser | Leu | Leu | Thr | Thr | Asp | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Glu | Ile | Val | Thr | Leu | Gly | Gly | Ser | Lys | Gln | Gly | Thr | Glu | Asn | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Ala | Leu | Ser | Thr | Pro | Ala | Val | Arg | Asn | Leu | Ala | Lys | Asp | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ile | Asp | Ile | Asn | Val | Ile | Thr | Gly | Thr | Gly | Lys | Asp | Gly | Arg | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Lys | Glu | Asp | Val | Leu | Arg | Phe | Ser | Asp | Gln | Lys | Gly | Phe | Val | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Ser | Val | Ser | Ser | Glu | His | Ala | Val | Ile | Gly | Gly | Asp | Ser | Val | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Lys | Ala | Ser | Ser | Asn | Phe | Glu | Asp | Lys | Thr | Val | Pro | Leu | Arg | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Ser | Arg | Ala | Met | Val | Lys | Thr | Met | Thr | Met | Ala | Thr | Ser | Val | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| His | Phe | His | Phe | Val | Glu | Glu | Ile | Asn | Cys | Asp | Ser | Leu | Val | Glu | Leu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Gln | Phe | Phe | Lys | Glu | Asn | Asn | Thr | Asp | Ser | Thr | Ile | Lys | His | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Leu | Pro | Thr | Leu | Ile | Lys | Ser | Leu | Ser | Met | Ala | Leu | Thr | Lys | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Phe | Val | Asn | Ser | Cys | Phe | Asn | Ala | Glu | Ser | Leu | Glu | Ile | Ile | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Gly | Ser | His | Asn | Ile | Gly | Val | Ala | Met | Ala | Thr | Glu | His | Gly | Leu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Val | Pro | Asn | Ile | Lys | Asn | Val | Gln | Ser | Leu | Ser | Leu | Leu | Glu | Ile |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Lys | Glu | Leu | Ser | Arg | Leu | Gln | His | Leu | Ala | Ala | Asn | Asn | Lys | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Pro | Glu | Asp | Val | Thr | Gly | Gly | Thr | Ile | Thr | Leu | Ser | Asn | Ile | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Ile | Gly | Gly | Lys | Phe | Gly | Ser | Pro | Leu | Leu | Asn | Leu | Pro | Glu | Val |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Ile | Ile | Ala | Leu | Gly | Arg | Ile | Glu | Lys | Val | Pro | Lys | Phe | Ser | Lys |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Gly | Thr | Val | Tyr | Pro | Ala | Ser | Ile | Met | Met | Val | Asn | Ile | Ala | Ala |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |
| Asp | His | Arg | Val | Leu | Asp | Gly | Ala | Thr | Val | Ala | Arg | Phe | Cys | Cys | Gln |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Trp | Lys | Glu | Tyr | Val | Glu | Lys | Pro | Glu | Leu | Leu | Met | Leu | Gln | Met | Arg |

2025 RELEASE UNDER E.O. 14176

420

425

430

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| attcatattt  | gctcacctca | aactctctct | ttctctctct  | ctctggttcc | ctagaatttg | 60   |
| agcaaaattt  | ctaccataat | tgctaattat | taaaaggaaa  | cataagtaat | cgttgcttcg | 120  |
| atcctttgtt  | acatggatgg | atcctgaaca | ggaaatctca  | aacgagactt | tggaactat  | 180  |
| attggttaagt | tcaacaaaag | gaagcaataa | taacAaataa  | gaaaatggaa | gaagaaatga | 240  |
| agaagaaagt  | atcaagagga | gaattaggag | gtgaagctca  | aaattgtcca | agatgtgaat | 300  |
| ctccaaacac  | aaagttttgt | tactacaaca | actatagtct  | ctcacaacct | cgttacttct | 360  |
| gcaaatcttg  | tccgagatat | tggactaaag | gcggtactct  | tcgtaacgtt | cccgtcggtg | 420  |
| gtggttgccg  | tcgaaacaaa | cgatcctctt | cctcagcttt  | ctccaagaac | aacaacaata | 480  |
| agtctattaa  | tttccatact | gatccacttc | agaacccttt  | aattacggga | atgccaccat | 540  |
| catcttttgg  | ttatgatcac | tccattgatc | tcaacctcgc  | tttcgctact | ctccaaaagc | 600  |
| atcattttatc | ctctcaagct | actactcctt | cttttggggt  | tggaggtgat | ctttctattt | 660  |
| atggaaactc  | aacgaatgat | gtagggatct | tccgagggca  | aaacggtact | tataacaata | 720  |
| gtttgtgtta  | tgggtttgtg | tccggaatag | gtaataataa  | tcaaaatgaa | atcaagatgg | 780  |
| cttctacatt  | ggggatgtct | ttggaaggaa | acgagagaaa  | gcaagagaat | gtgaacaata | 840  |
| acaataataa  | ctcagagaat | cctagcaagg | tgttctgggg  | gtttccatgg | cagatgaccg | 900  |
| gagattccgc  | cggagttgta | cgggagattg | atcccgggaag | ggaaagctgg | aatgggatgg | 960  |
| tttcatcttg  | gaataatggg | ttactcaaca | ctcctttggg  | ctagcagatc | attaataaat | 1020 |
| aaatatataa  | tatattacta | tatattaaag | Kttatgtcat  | cacatgtttg | tacaccactt | 1080 |
| tcactaatat  | gggggatgtt | tggtttttat | aattttctagg | gtttctatct | ttttttagtt | 1140 |
| tcccaatttt  | tcttgttgag | acgaagactt | ataagagttc  | ttctatgaaa | actatagaaa | 1200 |
| aaagtttctc  | c          |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Glu | Glu | Met | Lys | Lys | Lys | Val | Ser | Arg | Gly | Glu | Leu | Gly | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Glu | Ala | Gln | Asn | Cys | Pro | Arg | Cys | Glu | Ser | Pro | Asn | Thr | Lys | Phe | Cys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Tyr | Tyr | Asn | Asn | Tyr | Ser | Leu | Ser | Gln | Pro | Arg | Tyr | Phe | Cys | Lys | Ser |  |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Cys | Arg | Arg | Tyr | Trp | Thr | Lys | Gly | Gly | Thr | Leu | Arg | Asn | Val | Pro | Val |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Gly | Gly | Cys | Arg | Arg | Asn | Lys | Arg | Ser | Ser | Ser | Ser | Ala | Phe | Ser |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Asn | Asn | Asn | Asn | Lys | Ser | Ile | Asn | Phe | His | Thr | Asp | Pro | Leu | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asn | Pro | Leu | Ile | Thr | Gly | Met | Pro | Pro | Ser | Ser | Phe | Gly | Tyr | Asp | His |  |

100 105 110  
Ser Ile Asp Leu Asn Leu Ala Phe Ala Thr Leu Gln Lys His His Leu  
115 120 125  
Ser Ser Gln Ala Thr Thr Pro Ser Phe Gly Phe Gly Gly Asp Leu Ser  
130 135 140  
Ile Tyr Gly Asn Ser Thr Asn Asp Val Gly Ile Phe Gly Gly Gln Asn  
145 150 155 160  
Gly Thr Tyr Asn Asn Ser Leu Cys Tyr Gly Phe Val Ser Gly Asn Gly  
165 170 175  
Asn Asn Asn Gln Asn Glu Ile Lys Met Ala Ser Thr Leu Gly Met Ser  
180 185 190  
Leu Glu Gly Asn Glu Arg Lys Gln Glu Asn Val Asn Asn Asn Asn Asn  
195 200 205  
Asn Ser Glu Asn Pro Ser Lys Val Phe Trp Gly Phe Pro Trp Gln Met  
210 215 220  
Thr Gly Asp Ser Ala Gly Val Val Pro Glu Ile Asp Pro Gly Arg Glu  
225 230 235 240  
Ser Trp Asn Gly Met Val Ser Ser Trp Asn Asn Gly Leu Leu Asn Thr  
245 250 255  
Pro Leu Val

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

Met Lys Lys Lys Val Ser Arg Gly Glu Leu Gly Gly Glu Ala Gln Asn  
1 5 10 15  
Cys Pro Arg Cys Glu Ser Pro Asn Thr Lys Phe Cys Tyr Tyr Asn Asn  
20 25 30  
Tyr Ser Leu Ser Gln Pro Arg Tyr Phe Cys Lys Ser Cys Arg Arg Tyr  
35 40 45  
Trp Thr Lys Gly Gly Thr Leu Arg Asn Val Pro Val Gly Gly Gly Cys  
50 55 60  
Arg Arg Asn Lys Arg Ser Ser Ser Ala Phe Ser Lys Asn Asn Asn  
65 70 75 80  
Asn Lys Ser Ile Asn Phe His Thr Asp Pro Leu Gln Asn Pro Leu Ile  
85 90 95  
Thr Gly Met Pro Pro Ser Ser Phe Gly Tyr Asp His Ser Ile Asp Leu  
100 105 110  
Asn Leu Ala Phe Ala Thr Leu Gln Lys His His Leu Ser Ser Gln Ala  
115 120 125  
Thr Thr Pro Ser Phe Gly Phe Gly Gly Asp Leu Ser Ile Tyr Gly Asn  
130 135 140  
Ser Thr Asn Asp Val Gly Ile Phe Gly Gly Gln Asn Gly Thr Tyr Asn  
145 150 155 160  
Asn Ser Leu Cys Tyr Gly Phe Val Ser Gly Asn Gly Asn Asn Gln  
165 170 175  
Asn Glu Ile Lys Met Ala Ser Thr Leu Gly Met Ser Leu Glu Gly Asn  
180 185 190  
Glu Arg Lys Gln Glu Asn Val Asn Asn Asn Asn Asn Asn Ser Glu Asn  
195 200 205  
Pro Ser Lys Val Phe Trp Gly Phe Pro Trp Gln Met Thr Gly Asp Ser  
210 215 220

Ala Gly Val Val Pro Glu Ile Asp Pro Gly Arg Glu Ser Trp Asn Gly  
225 230 235 240  
Met Val Ser Ser Trp Asn Asn Gly Leu Leu Asn Thr Pro Leu Val  
245 250 255

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

Met Pro Pro Ser Ser Phe Gly Tyr Asp His Ser Ile Asp Leu Asn Leu  
1 5 10 15  
Ala Phe Ala Thr Leu Gln Lys His His Leu Ser Ser Gln Ala Thr Thr  
20 30  
Pro Ser Phe Gly Phe Gly Gly Asp Leu Ser Ile Tyr Gly Asn Ser Thr  
35 40 45  
Asn Asp Val Gly Ile Phe Gly Gly Gln Asn Gly Thr Tyr Asn Asn Ser  
50 55 60  
Leu Cys Tyr Gly Phe Val Ser Gly Asn Gly Asn Asn Asn Gln Asn Glu  
65 70 75 80  
Ile Lys Met Ala Ser Thr Leu Gly Met Ser Leu Glu Gly Asn Glu Arg  
85 90 95  
Lys Gln Glu Asn Val Asn Asn Asn Asn Asn Ser Glu Asn Pro Ser  
100 105 110  
Lys Val Phe Trp Gly Phe Pro Trp Gln Met Thr Gly Asp Ser Ala Gly  
115 120 125  
Val Val Pro Glu Ile Asp Pro Gly Arg Glu Ser Trp Asn Gly Met Val  
130 135 140  
Ser Ser Trp Asn Asn Gly Leu Leu Asn Thr Pro Leu Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

gactccatta ttatccctct ctctacaaaa aaaaacagta gagagagata tagagagcat 60  
caatggcgtc gtcgtcaaga ctttgcgatt cgtgcaaadc gacggcagca actctattct 120  
gccgcgcaga cgccgcgttt ctctgcggca actgcgacgg taagatccac acagctaaca 180  
aactcgcatac acgtcacgaa cgagtttggc tatgtgaagt atgcgaacaa gcaccagcac 240  
acgtcacgtg caaagctgac gccgctgcgt tatgcgtcac gtgcgaccgt gatatccact 300  
cagctaatacc actctctcgc cgccacgagc gcgtaccaat cactccttc tacgacgtg 360  
ttggtccagc aaaatccgct tctcctccg tcaatttcgt agatgaagat ggcggtgacg 420  
tcaactgcttc gtggctttta gctaaagaag gaatcgaaat cactaatttg ttttccgac 480  
ttgattatoc gaagattgag gtcacgtcgg aggagaatag ctccggtaac gacggagttg 540  
ttcctgtgca gaataagttg tttctcaatg aagattactt caatttcgat ctctctgctt 600  
ccaaaatttc tcaacaagga ttcaatttca tcaaccaaac tgtttcgacg agaacgatag 660  
atgtaccgtt ggtgcttgaa agtgaggagg tgacggcgga gatgacgaac acggagacgc 720  
cagctgtgca gttatcaccg gcggagaggg aagcaagggt tttgaggtat agagagaaga 780

ggaagaatcg gaaatttgag aagacgatta ggtatgcgtc gcgtaaagCt tacgctgaga 840  
tgaggcccgag aatcaaagga cgttttgcta agagaacaga ttcgagagag aatgatgggtg 900  
gagacgtcgg agtttattgc ggattcgggtg ttgttccgag tttctgatat ttcccggtta 960  
aagaacatg gtagtagtat atcgggttaat agcagattaa ggataattaa aactaaaatg 1020  
tttctgatt taatcagggg ctaagttatt gttagaagat tgttggtttt tgaattaatt 1080  
ctcacaattg tatcctaaat tatatagttt acttaatggt gaact

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1569235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

Met Ala Ser Ser Ser Arg Leu Cys Asp Ser Cys Lys Ser Thr Ala Ala  
1 5 10 15  
Thr Leu Phe Cys Arg Ala Asp Ala Ala Phe Leu Cys Gly Asn Cys Asp  
20 25 30  
Gly Lys Ile His Thr Ala Asn Lys Leu Ala Ser Arg His Glu Arg Val  
35 40 45  
Trp Leu Cys Glu Val Cys Glu Gln Ala Pro Ala His Val Thr Cys Lys  
50 55 60  
Ala Asp Ala Ala Ala Leu Cys Val Thr Cys Asp Arg Asp Ile His Ser  
65 70 75 80  
Ala Asn Pro Leu Ser Arg Arg His Glu Arg Val Pro Ile Thr Pro Phe  
85 90 95  
Tyr Asp Ala Val Gly Pro Ala Lys Ser Ala Ser Ser Ser Val Asn Phe  
100 105 110  
Val Asp Glu Asp Gly Gly Asp Val Thr Ala Ser Trp Leu Leu Ala Lys  
115 120 125  
Glu Gly Ile Glu Ile Thr Asn Leu Phe Ser Asp Leu Asp Tyr Pro Lys  
130 135 140  
Ile Glu Val Thr Ser Glu Glu Asn Ser Ser Gly Asn Asp Gly Val Val  
145 150 155 160  
Pro Val Gln Asn Lys Leu Phe Leu Asn Glu Asp Tyr Phe Asn Phe Asp  
165 170 175  
Leu Ser Ala Ser Lys Ile Ser Gln Gln Gly Phe Asn Phe Ile Asn Gln  
180 185 190  
Thr Val Ser Thr Arg Thr Ile Asp Val Pro Leu Val Pro Glu Ser Gly  
195 200 205  
Gly Val Thr Ala Glu Met Thr Asn Thr Glu Thr Pro Ala Val Gln Leu  
210 215 220  
Ser Pro Ala Glu Arg Glu Ala Arg Val Leu Arg Tyr Arg Glu Lys Arg  
225 230 235 240  
Lys Asn Arg Lys Phe Glu Lys Thr Ile Arg Tyr Ala Ser Arg Lys Ala  
245 250 255  
Tyr Ala Glu Met Arg Pro Arg Ile Lys Gly Arg Phe Ala Lys Arg Thr  
260 265 270  
Asp Ser Arg Glu Asn Asp Gly Gly Asp Val Gly Val Tyr Cys Gly Phe  
275 280 285  
Gly Val Val Pro Ser Phe  
290

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1515 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1515  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569255  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

aagttcagct tcgtacctga gccaaagagt gtttcaggat ggagctaagg tcgagaatgc 60  
tcaaagactg tctcttggaa gattccaact catgttctct aaacgggttc aaatcgattc 120  
ccagacggca tcctctcaac cctttcccaa tgataccaaa gaggaacaaa tccaatgcat 180  
tgcaggctgt gattaacgcc atcaagaacc tccattccaa caccatcaaa tccgctccat 240  
cggggatctt accaaggagc ctttctcggc ggtagcaac caagaacaaa gcagaaaacc 300  
aagcaagcat caccgttatt cgggtcaaag acatcgtgcg atggcactcg tctaaggacc 360  
tgcattgagga catatcacat tttgaacctc atcagtacac aaccaagaac acgacaacaa 420  
ccacaggatc ctccaccaMc agcggcacat cctgcagcag ttggtctgac ttggatttta 480  
catcggagtt tttaccatca tcatggggaa gtaacgttga ggagtgcggt gaaaaacaga 540  
gtgttaaaaa caacttacac tgcgtcggcg aagattcttg cacagcagta atactagccg 600  
acactgaagt gggacctgag gagaacttac agtgtgaaaa ggagcacaac agccctgtct 660  
cagtgtttga gattcaacat gaggaatatg acgaaacatc agactcttct ttcagtcaat 720  
gccttgacaa tgtggaaaga accaaacaaa agctcatgca aacgattcag cggtttgagt 780  
ctttggccaa cattagtcct ttcaatttgg atgaatgggg ctcaatggat gaagcatctt 840  
gcatggaagg aggacaagag acagatacca agtatgatga tgatgagaat tgtgatactg 900  
ttgatagaga aagtgaagat gaatacaatg atgaggttga agagaaggca gcacagctat 960  
ggaaccgagt caaagaaaga caccgccattt ggatccacga agaacatctg ataatggact 1020  
atttcagaga tgaattgatg caaaggacaa actcattcca cgaaactcAa acactttgag 1080  
aaccaattgg tatgagaggc aaaaggatgg ttgcagggaa agagagaatc agagcttgaa 1140  
cgcggaacaa gtgagcagag gagacaagca tgtgctagag aaatcgaaag acgagactgg 1200  
aatgagaaac agatagagga ggagcacgaa gtggtggtta cacagattga ggaagaactc 1260  
ttcagcctgt taatggacga aactttaaca acgctctcta ccaaaactga ttccagtcca 1320  
cctgaacatc acaaaacagt aacatcaatg cttaaagcttt agaaattaga aagcaaaaac 1380  
atTTTTgaat aaggctttga cttaaaagct cagggtttttt tagctctact tttgtaagaa 1440  
tgaagcaaac gaataatata atgtatatg acctctaaaa ccatatatat atatatgcct 1500  
aattcatatt tctgc

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 346 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..346  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569256  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

Met Glu Leu Arg Ser Arg Met Leu Lys Asp Cys Leu Leu Glu Asp Ser  
1 5 10 15  
Asn Ser Cys Ser Ser Asn Gly Phe Lys Ser Ile Pro Arg Arg His Pro  
20 25 30  
Leu Asn Pro Phe Pro Met Ile Pro Lys Arg Lys Gln Ser Asn Ala Leu  
35 40 45  
Gln Ala Val Ile Asn Ala Ile Lys Asn Leu His Ser Asn Thr Ile Lys  
50 55 60  
Ser Ala Pro Ser Gly Ile Leu Pro Arg Ser Leu Ser Arg Arg Leu Ala  
65 70 75 80  
Thr Lys Asn Lys Ala Glu Asn Gln Ala Ser Ile Thr Val Ile Arg Val  
85 90 95  
Lys Asp Ile Val Arg Trp His Ser Ser Lys Asp Leu His Glu Asp Ile  
100 105 110  
Ser His Phe Glu Pro His Gln Tyr Thr Thr Lys Asn Thr Thr Thr Thr  
115 120 125



Thr Gly Ser Ser Thr Xaa Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp  
130 135 140  
Leu Asp Phe Thr Ser Glu Phe Leu Pro Ser Ser Trp Gly Ser Asn Val  
145 150 155 160  
Glu Glu Cys Gly Glu Lys Gln Ser Val Lys Asn Asn Leu His Cys Val  
165 170 175  
Gly Glu Asp Ser Cys Thr Ala Val Ile Leu Ala Asp Thr Glu Val Gly  
180 185 190  
Pro Glu Glu Asn Leu Gln Cys Glu Lys Glu His Asn Ser Pro Val Ser  
195 200 205  
Val Phe Glu Ile Gln His Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser  
210 215 220  
Phe Ser Gln Cys Leu Asp Asn Val Glu Arg Thr Lys Gln Lys Leu Met  
225 230 235 240  
Gln Thr Ile Gln Arg Phe Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn  
245 250 255  
Leu Asp Glu Trp Gly Ser Met Asp Glu Ala Ser Cys Met Glu Gly Gly  
260 265 270  
Gln Glu Thr Asp Thr Lys Tyr Asp Asp Glu Asn Cys Asp Thr Val  
275 280 285  
Asp Arg Glu Ser Glu Asp Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala  
290 295 300  
Ala Gln Leu Trp Asn Arg Val Lys Glu Arg His Ala Ile Trp Ile His  
305 310 315 320  
Glu Glu His Leu Ile Met Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg  
325 330 335  
Thr Asn Ser Phe His Glu Thr Gln Thr Leu  
340 345

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1569257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met Leu Lys Asp Cys Leu Leu Glu Asp Ser Asn Ser Cys Ser Ser Asn  
1 5 10 15  
Gly Phe Lys Ser Ile Pro Arg Arg His Pro Leu Asn Pro Phe Pro Met  
20 25 30  
Ile Pro Lys Arg Lys Gln Ser Asn Ala Leu Gln Ala Val Ile Asn Ala  
35 40 45  
Ile Lys Asn Leu His Ser Asn Thr Ile Lys Ser Ala Pro Ser Gly Ile  
50 55 60  
Leu Pro Arg Ser Leu Ser Arg Arg Leu Ala Thr Lys Asn Lys Ala Glu  
65 70 75 80  
Asn Gln Ala Ser Ile Thr Val Ile Arg Val Lys Asp Ile Val Arg Trp  
85 90 95  
His Ser Ser Lys Asp Leu His Glu Asp Ile Ser His Phe Glu Pro His  
100 105 110  
Gln Tyr Thr Thr Lys Asn Thr Thr Thr Thr Thr Gly Ser Ser Thr Xaa  
115 120 125  
Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp Leu Asp Phe Thr Ser Glu  
130 135 140  
Phe Leu Pro Ser Ser Trp Gly Ser Asn Val Glu Glu Cys Gly Glu Lys  
145 150 155 160  
Gln Ser Val Lys Asn Asn Leu His Cys Val Gly Glu Asp Ser Cys Thr

165 170 175  
Ala Val Ile Leu Ala Asp Thr Glu Val Gly Pro Glu Glu Asn Leu Gln  
180 185 190  
Cys Glu Lys Glu His Asn Ser Pro Val Ser Val Phe Glu Ile Gln His  
195 200 205  
Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser Phe Ser Gln Cys Leu Asp  
210 215 220  
Asn Val Glu Arg Thr Lys Gln Lys Leu Met Gln Thr Ile Gln Arg Phe  
225 230 235 240  
Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn Leu Asp Glu Trp Gly Ser  
245 250 255  
Met Asp Glu Ala Ser Cys Met Glu Gly Gln Glu Thr Asp Thr Lys  
260 265 270  
Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val Asp Arg Glu Ser Glu Asp  
275 280 285  
Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala Ala Gln Leu Trp Asn Arg  
290 295 300  
Val Lys Glu Arg His Ala Ile Trp Ile His Glu Glu His Leu Ile Met  
305 310 315 320  
Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg Thr Asn Ser Phe His Glu  
325 330 335  
Thr Gln Thr Leu  
340

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Ile Pro Lys Arg Lys Gln Ser Asn Ala Leu Gln Ala Val Ile Asn  
1 5 10 15  
Ala Ile Lys Asn Leu His Ser Asn Thr Ile Lys Ser Ala Pro Ser Gly  
20 25 30  
Ile Leu Pro Arg Ser Leu Ser Arg Arg Leu Ala Thr Lys Asn Lys Ala  
35 40 45  
Glu Asn Gln Ala Ser Ile Thr Val Ile Arg Val Lys Asp Ile Val Arg  
50 55 60  
Trp His Ser Ser Lys Asp Leu His Glu Asp Ile Ser His Phe Glu Pro  
65 70 75 80  
His Gln Tyr Thr Thr Lys Asn Thr Thr Thr Thr Gly Ser Ser Thr  
85 90 95  
Xaa Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp Leu Asp Phe Thr Ser  
100 105 110  
Glu Phe Leu Pro Ser Ser Trp Gly Ser Asn Val Glu Glu Cys Gly Glu  
115 120 125  
Lys Gln Ser Val Lys Asn Asn Leu His Cys Val Gly Glu Asp Ser Cys  
130 135 140  
Thr Ala Val Ile Leu Ala Asp Thr Glu Val Gly Pro Glu Glu Asn Leu  
145 150 155 160  
Gln Cys Glu Lys Glu His Asn Ser Pro Val Ser Val Phe Glu Ile Gln  
165 170 175  
His Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser Phe Ser Gln Cys Leu  
180 185 190  
Asp Asn Val Glu Arg Thr Lys Gln Lys Leu Met Gln Thr Ile Gln Arg  
195 200 205

Phe Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn Leu Asp Glu Trp Gly  
210 215 220  
Ser Met Asp Glu Ala Ser Cys Met Glu Gly Gly Gln Glu Thr Asp Thr  
225 230 235 240  
Lys Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val Asp Arg Glu Ser Glu  
245 250 255  
Asp Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala Ala Gln Leu Trp Asn  
260 265 270  
Arg Val Lys Glu Arg His Ala Ile Trp Ile His Glu Glu His Leu Ile  
275 280 285  
Met Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg Thr Asn Ser Phe His  
290 295 300  
Glu Thr Gln Thr Leu  
305

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| actccctatt  | cttcagtaat | gactaatatt  | agaactctct | atactactag  | ctaaaactaa  | 60   |
| aaattgaaga  | aaaaacatga | gtctcaccac  | cgacgaaatc | gaagtgaagag | atttcgtggt  | 120  |
| gaaccaaaag  | aatggagtg  | aaggactcgt  | cgactttcta | accctaacca  | cacttccttc  | 180  |
| tccatacatt  | caacctcctc | aagaacgctt  | cacttccgac | aagatcctcc  | tcggatcacc  | 240  |
| tgtcccggtc  | attgacgtgt | ccaattggaa  | tgaacgcgac | gtggctagag  | agatctgcca  | 300  |
| tgcagcgta   | aagctcggct | tgtttcagat  | agtgaaccac | gggatagctc  | cggctgagtt  | 360  |
| caaggggtgtg | attgctgcgg | cgcgtgggtt  | tttcgagttg | ccggcggagg  | agagaagaag  | 420  |
| gtattggaga  | gggagttcag | tgtcggagac  | ggcgtgggtg | accacaagtt  | tcaatccttg  | 480  |
| catagaaagt  | gttttgaat  | ggagagattt  | cctcaagttt | gagtatcttc  | ctcaacgaca  | 540  |
| tgacttcgct  | gccacgtggc | cttctgtctg  | caaggaacaa | gtgatagacc  | atttcaaaag  | 600  |
| gatcaaacca  | atcacagaga | ggatcttaaa  | catactcatc | aacaatctaa  | acacaatcat  | 660  |
| cgatgagtc   | aataaagaaa | ccctaattggg | aacaatgaga | atgaacttca  | actactatcc  | 720  |
| gaaatgtcct  | gagccaagcc | tggccatagg  | aactggtcgc | cactcagaca  | tcaacactct  | 780  |
| cactctcctc  | ctacaagaag | atgggtgtatt | aagcagtcct | tacgcccagag | ccactgagga  | 840  |
| tggagacaaa  | tggattcatg | tccctccaat  | tccgggagct | attgtcgtta  | atatcggaga  | 900  |
| tgtattacag  | atattgagca | atgataggta  | taggagcgtg | gagcattgtg  | tgggtggtcaa | 960  |
| taagtattgt  | agccgggttt | ccattccggt  | tttctgcgga | ccggttcattg | attcgggttat | 1020 |
| tgagccgtta  | ccggaggtgt | tagataagaa  | caatgagatg | gctcgggtata | gaaagattgt  | 1080 |
| gtattcggac  | tacttgaagt | tttttttttg  | aagacctcat | gatggaaaga  | agactattga  | 1140 |
| gtcgataaaa  | ttaccatgat | atgatttacg  | aagcttaaat | catcattatc  | tacggSc     |      |

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Thr | Thr | Asp | Glu | Ile | Glu | Val | Arg | Asp | Phe | Val | Val | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Lys | Asn | Gly | Val | Lys | Gly | Leu | Val | Asp | Phe | Leu | Thr | Leu | Thr | Thr |

20 25 30  
Leu Pro Ser Pro Tyr Ile Gln Pro Pro Gln Glu Arg Phe Thr Ser Asp  
35 40 45  
Lys Ile Leu Leu Gly Ser Pro Val Pro Val Ile Asp Val Ser Asn Trp  
50 55 60  
Asn Glu Pro His Val Ala Arg Glu Ile Cys His Ala Ala Ser Lys Leu  
65 70 75 80  
Gly Leu Phe Gln Ile Val Asn His Gly Ile Ala Pro Ala Glu Phe Lys  
85 90 95  
Gly Val Ile Ala Ala Ala Arg Gly Phe Phe Glu Leu Pro Ala Glu Glu  
100 105 110  
Arg Arg Arg Tyr Trp Arg Gly Ser Ser Val Ser Glu Thr Ala Trp Leu  
115 120 125  
Thr Thr Ser Phe Asn Pro Cys Ile Glu Ser Val Leu Glu Trp Arg Asp  
130 135 140  
Phe Leu Lys Phe Glu Tyr Leu Pro Gln Arg His Asp Phe Ala Ala Thr  
145 150 155 160  
Trp Pro Ser Val Cys Lys Glu Gln Val Ile Asp His Phe Lys Arg Ile  
165 170 175  
Lys Pro Ile Thr Glu Arg Ile Leu Asn Ile Leu Ile Asn Asn Leu Asn  
180 185 190  
Thr Ile Ile Asp Glu Ser Asn Lys Glu Thr Leu Met Gly Thr Met Arg  
195 200 205  
Met Asn Phe Asn Tyr Tyr Pro Lys Cys Pro Glu Pro Ser Leu Ala Ile  
210 215 220  
Gly Thr Gly Arg His Ser Asp Ile Asn Thr Leu Thr Leu Leu Gln  
225 230 235 240  
Glu Asp Gly Val Leu Ser Ser Leu Tyr Ala Arg Ala Thr Glu Asp Gly  
245 250 255  
Asp Lys Trp Ile His Val Pro Pro Ile Pro Gly Ala Ile Val Val Asn  
260 265 270  
Ile Gly Asp Val Leu Gln Ile Leu Ser Asn Asp Arg Tyr Arg Ser Val  
275 280 285  
Glu His Cys Val Val Val Asn Lys Tyr Cys Ser Arg Val Ser Ile Pro  
290 295 300  
Val Phe Cys Gly Pro Val His Asp Ser Val Ile Glu Pro Leu Pro Glu  
305 310 315 320  
Val Leu Asp Lys Asn Asn Glu Met Ala Arg Tyr Arg Lys Ile Val Tyr  
325 330 335  
Ser Asp Tyr Leu Lys Phe Phe Phe Gly Arg Pro His Asp Gly Lys Lys  
340 345 350  
Thr Ile Glu Ser Ile Lys Leu Pro  
355 360

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

|          |          |          |           |          |          |           |     |
|----------|----------|----------|-----------|----------|----------|-----------|-----|
| attattat | cactctct | ctctagac | tgaattag  | cattcttg | cc       | tccaaacaa | 60  |
| tattcctg | ac       | actcgtaa | gacagacaa | cc       | taaaacta | aagcatcc  | 120 |
| gttctttg | tttgtatt | tggtctga | tc        | atatcc   | at       | aatcaccg  | 180 |
| ccggcag  | ttt      | cacctac  | tg        | ggccgcaa | at       | tcagcgatt | 240 |
| aatgtct  | ca       | ac       | gatgact   | cc       | ct       | ct        | 300 |
| ctgctttc | ag       | cgattgt  | aac       | agcgacag | at       | ccggcgaa  | 360 |
| ttt      | ct       | ct       | ct        | ct       | ct       | ct        |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | His | Arg | Pro | Gly | Ser | Phe | Thr | Tyr | Met | Gly | Arg | Lys | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asp | Leu | Ser | Leu | Asn | Asp | Asp | Ser | Ser | Ala | Phe | Ser | Asp | Cys | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Arg | Ser | Gly | Glu | Phe | Pro | Thr | Ala | Ser | Ser | Glu | Ser | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Leu | Ser | Cys | Ala | Ser | Glu | Asn | Ser | Asp | Asp | Leu | Ile | Asn | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Ser | His | Leu | Asp | Ser | Ser | Tyr | Ser | Ile | Asp | Glu | Gln | Lys | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ala | Met | Glu | Ile | Arg | Leu | Leu | Ser | Lys | Asn | Lys | Pro | Glu | Asn | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Lys | Ile | Ala | Lys | Ala | Gly | Ala | Ile | Lys | Pro | Leu | Ile | Ser | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Ser | Asp | Leu | Gln | Leu | Gln | Glu | Tyr | Gly | Val | Thr | Xaa | Ile | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Ser | Leu | Cys | Asp | Glu | Asn | Lys | Glu | Ser | Ile | Ala | Ser | Ser | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ile | Lys | Pro | Leu | Val | Arg | Ala | Leu | Lys | Met | Gly | Thr | Pro | Thr | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Asp | Asn | Ala | Ala | Cys | Ala | Leu | Leu | Arg | Leu | Ser | Gln | Ile | Glu | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Lys | Val | Ala | Ile | Gly | Arg | Ser | Gly | Ala | Ile | Pro | Leu | Leu | Val | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Glu | Thr | Gly | Gly | Phe | Arg | Ala | Lys | Lys | Asp | Ala | Ser | Thr | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Tyr | Ser | Leu | Cys | Ser | Ala | Lys | Glu | Asn | Lys | Ile | Arg | Ala | Val | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Gly | Ile | Met | Lys | Pro | Leu | Val | Glu | Leu | Met | Ala | Asp | Phe | Gly | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Met | Val | Asp | Lys | Ser | Ala | Phe | Val | Met | Ser | Leu | Leu | Met | Ser | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Glu | Ser | Lys | Pro | Ala | Ile | Val | Glu | Glu | Gly | Gly | Val | Pro | Val | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Glu | Ile | Val | Glu | Val | Gly | Thr | Gln | Arg | Gln | Lys | Glu | Met | Ala | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Lys | Phe | Ser | Asp | Leu | Ser | Leu | Asn | Asp | Asp | Ser | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Asp | Cys | Asn | Ser | Asp | Arg | Ser | Gly | Glu | Phe | Pro | Thr | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Glu | Ser | Arg | Arg | Leu | Leu | Leu | Ser | Cys | Ala | Ser | Glu | Asn | Ser | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Leu | Ile | Asn | His | Leu | Val | Ser | His | Leu | Asp | Ser | Ser | Tyr | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Glu | Gln | Lys | Gln | Ala | Ala | Met | Glu | Ile | Arg | Leu | Leu | Ser | Lys | Asn |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Pro | Glu | Asn | Arg | Ile | Lys | Ile | Ala | Lys | Ala | Gly | Ala | Ile | Lys | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ile | Ser | Leu | Ile | Ser | Ser | Ser | Asp | Leu | Gln | Leu | Gln | Glu | Tyr | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Thr | Xaa | Ile | Leu | Asn | Leu | Ser | Leu | Cys | Asp | Glu | Asn | Lys | Glu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Ser | Ser | Gly | Ala | Ile | Lys | Pro | Leu | Val | Arg | Ala | Leu | Lys | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Thr | Pro | Thr | Ala | Lys | Asp | Asn | Ala | Ala | Cys | Ala | Leu | Leu | Arg | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Gln | Ile | Glu | Glu | Asn | Lys | Val | Ala | Ile | Gly | Arg | Ser | Gly | Ala | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Leu | Leu | Val | Asn | Leu | Leu | Glu | Thr | Gly | Gly | Phe | Arg | Ala | Lys | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Ala | Ser | Thr | Ala | Leu | Tyr | Ser | Leu | Cys | Ser | Ala | Lys | Glu | Asn | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Arg | Ala | Val | Gln | Ser | Gly | Ile | Met | Lys | Pro | Leu | Val | Glu | Leu | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Asp | Phe | Gly | Ser | Asn | Met | Val | Asp | Lys | Ser | Ala | Phe | Val | Met | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Leu | Met | Ser | Val | Pro | Glu | Ser | Lys | Pro | Ala | Ile | Val | Glu | Glu | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Val | Pro | Val | Leu | Val | Glu | Ile | Val | Glu | Val | Gly | Thr | Gln | Arg | Gln |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Glu | Met | Ala | Val | Ser | Ile | Leu | Leu | Gln | Leu | Cys | Glu | Glu | Ser | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Tyr | Arg | Thr | Met | Val | Ala | Arg | Glu | Gly | Ala | Ile | Pro | Pro | Leu | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Leu | Ser | Gln | Ala | Gly | Thr | Ser | Arg | Ala | Lys | Gln | Lys | Ala | Glu | Ala |

(2) INFORMATION FOR SEQ ID NO:1194:

(A) LENGTH: 1204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1204

(D) OTHER INFORMATION: / Ceres Seq. ID 1569294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

| (X1) SEQUENCE DESCRIPTION: SEQ |             |             |             |             |             |      |
|--------------------------------|-------------|-------------|-------------|-------------|-------------|------|
| acacttagct                     | ttctgttatt  | caattcttca  | caaagtttct  | aaaagctttt  | ctcttggtat  | 60   |
| tcaacaacatt                    | ggcaccgagc  | ttcgtaacgc  | cgtgtgtgtg  | ttctacttga  | ttctccCgag  | 120  |
| ctcttgatac                     | tggtgaggat  | gacacaagcg  | taccagtgga  | catcaaagtt  | ccaattctga  | 180  |
| tagctttcca                     | cogtcataata | tacgatgggtg | actggcattt  | ttcatgtggt  | acaaaagagt  | 240  |
| ataaaccttct                    | aatggaccaa  | tttcaccatg  | tttctgcagc  | ttttctgaaa  | cttgaaaaag  | 300  |
| ggtatcaaga                     | ggctattgaa  | gatataacta  | aaagaatggg  | tgcaggaatg  | gccaaagtca  | 360  |
| tttgcaagga                     | ggtagaacaa  | attgatgact  | atgatgaata  | ctgcacattat | gctgcaggac  | 420  |
| ttgttggtgtt                    | gggtttgtca  | aaaattctca  | ttgcttcgga  | attagaaata  | ctgactccag  | 480  |
| attggaagca                     | gatttcaaat  | tctacagggt  | tatttctgca  | gaaaacaaac  | attatcaaag  | 540  |
| attatcttga                     | agacattaat  | gagagaccaa  | agtcgcgcgat | gttttggcct  | cgtgagattt  | 600  |
| ggggaaaata                     | tgttgacaaa  | cttgaggact  | tcaaaaatga  | ggagaaaagct | acaaaagcag  | 660  |
| tgcagtgttt                     | gaatgaaatg  | gtcactaatg  | cattgaatca  | tgttgaagat  | tgtttgaat   | 720  |
| ccttggcNtt                     | CActgcgtga  | tcttgcaata  | tttcagctct  | tggtccatccc | tcagatcgtg  | 780  |
| gcgattggaa                     | cactacatt   | atgctataac  | aatgtacaag  | tgtttagagg  | cgtcgtgaga  | 840  |
| atgagacgag                     | gtctaataagc | taaagtcatt  | gatgcacaa   | agacaatgga  | tgatgtctat  | 900  |
| ggtgcgttct                     | atgatttttc  | ttgcatgcta  | caaacaaagg  | ttgacaataa  | cgatccaaat  | 960  |
| gctatgaaaa                     | cattaaatcg  | actcgaaacc  | atcaagaaaag | tttgagaga   | aaatggagta  | 1020 |
| cttcacaaaa                     | gaaaatctta  | tggttaacgat | gaaacacaat  | ccaaggctat  | ctttgttgtta | 1080 |
| atgtttgtgc                     | ttctactggc  | tatagtcgtt  | gtatatctca  | aagcaaacca  | acgtaaagtga | 1140 |
| ctctgattgt                     | gaagtcacata | tgaacataat  | ttctagcttt  | tttgaaatgt  | ttgatcaaat  | 1200 |
| cttg                           |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1569295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gln | Phe | His | His | Val | Ser | Ala | Ala | Phe | Leu | Lys | Leu | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Tyr | Gln | Glu | Ala | Ile | Glu | Asp | Ile | Thr | Lys | Arg | Met | Gly | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ala | Lys | Phe | Ile | Cys | Lys | Glu | Val | Glu | Thr | Ile | Asp | Asp | Tyr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Tyr | Cys | His | Tyr | Ala | Ala | Gly | Leu | Val | Gly | Leu | Gly | Leu | Ser | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Phe | Ile | Ala | Ser | Glu | Leu | Glu | Ile | Leu | Thr | Pro | Asp | Trp | Lys | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Asn | Ser | Thr | Gly | Leu | Phe | Leu | Gln | Lys | Thr | Asn | Ile | Ile | Lys |



85 90 95  
Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser Arg Met Phe Trp  
100 105 110  
Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu Glu Asp Phe Lys  
115 120 125  
Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu Asn Glu Met Val  
130 135 140  
Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys Ser Leu Xaa Phe  
145 150 155 160  
Thr Ala

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

Met Gly Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Ile  
1 5 10 15  
Asp Asp Tyr Asp Glu Tyr Cys His Tyr Ala Ala Gly Leu Val Gly Leu  
20 25 30  
Gly Leu Ser Lys Ile Phe Ile Ala Ser Glu Leu Glu Ile Leu Thr Pro  
35 40 45  
Asp Trp Lys Gln Ile Ser Asn Ser Thr Gly Leu Phe Leu Gln Lys Thr  
50 55 60  
Asn Ile Ile Lys Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser  
65 70 75 80  
Arg Met Phe Trp Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu  
85 90 95  
Glu Asp Phe Lys Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu  
100 105 110  
Asn Glu Met Val Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys  
115 120 125  
Ser Leu Xaa Phe Thr Ala  
130

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Ile Asp Asp Tyr Asp  
1 5 10 15  
Glu Tyr Cys His Tyr Ala Ala Gly Leu Val Gly Leu Gly Leu Ser Lys  
20 25 30  
Ile Phe Ile Ala Ser Glu Leu Glu Ile Leu Thr Pro Asp Trp Lys Gln  
35 40 45  
Ile Ser Asn Ser Thr Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile Lys  
50 55 60

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Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser Arg Met Phe Trp  
65 70 75 80  
Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu Glu Asp Phe Lys  
85 90 95  
Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu Asn Glu Met Val  
100 105 110  
Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys Ser Leu Xaa Phe  
115 120 125  
Thr Ala  
130

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

atactctctt tttttctcgg acaagaaggc tacagaaaga tatgtcgtcg tcgtcttacc 60  
tcagcccgac ggcgcttcta taaggctacc tccgccgttg tctcagggcg gcaggactga 120  
cgtcgcagAc gctttccata gactctgaaa caaccatcca cttctggggc ccaccacctc 180  
tagaccaccg gagcgacgat gacagaccgg ttatgcttct cctccacggc ttcgggtccgt 240  
cgtoaatgtg gcagtggcgg cgacagatgc aagccttctc tccctccgct ttcaggggtt 300  
attctcccgga tcttgtcttc ttcggcgact ctacctcttc ctccaccaat cgcaccgaag 360  
tcttccaggc ggaatgtatg gcaaagctaa tggcgaaaa aggaataggg aagtataatg 420  
tggctggaac aagctacggg gggtttgttg cgtaccacat ggccaaaatg tggccggaaa 480  
aagtggagaa agtggtgatt gcaagctccg gcatcaacat gcgaaagtgt gacggtgaaa 540  
gtttattgca aagatccaat tgtgagtgc tgcagaagg tatgttacca tccactgcaa 600  
ctgagtttgc cacacttatg gctttggcat cttcatggcg gttagtctgt atgtttcctg 660  
atgctctctg gaacgacgta atcaataatt tgtataaaaa aaatagaaaa gagaagatag 720  
aattgttgaa gggagtgact ttcggccgga gcgaaaattt aaacatcgat tctctttctc 780  
aggaggtcct aattgtatgg ggagacaaag atcagatatt tcctgtgaag atggcttacg 840  
aattaaaaga gattcttggg gacaaaacga aactagaaat cattgacaac acttcacatg 900  
ttcctcagat tgaatgtgct caagagttca acaatattgt tttgagattt ttgaagggtt 960  
cttaagagcc gtaattttat tccatgctac atgattcttc agtttttttt aagtgttaaa 1020  
ctattgggta cgtaattttg cgactttact tgccatgctt tctcattttt catgtaagaa 1080  
ctttatccat tactgtcatt gtagagaact ctatttatag caaaaagtaa tactaatatg 1140  
caacttaatt ttgctc

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

Met Leu Leu Leu His Gly Phe Gly Pro Ser Ser Met Trp Gln Trp Arg  
1 5 10 15  
Arg Gln Met Gln Ala Phe Ser Pro Ser Ala Phe Arg Val Tyr Ser Pro  
20 25 30  
Asp Leu Val Phe Phe Gly Asp Ser Thr Ser Ser Ser Thr Asn Arg Thr  
35 40 45  
Glu Val Phe Gln Ala Glu Cys Met Ala Lys Leu Met Ala Lys Ile Gly

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Ile Gly Lys Tyr Asn Val Ala Gly Thr Ser Tyr Gly Gly Phe Val Ala |     |     |
| 65                                                              | 70  | 75  |
| Tyr His Met Ala Lys Met Trp Pro Glu Lys Val Glu Lys Val Val Ile |     | 80  |
|                                                                 | 85  | 90  |
| Ala Ser Ser Gly Ile Asn Met Arg Lys Cys Asp Gly Glu Ser Leu Leu |     | 95  |
|                                                                 | 100 | 105 |
| Gln Arg Ser Asn Cys Glu Cys Ile Glu Lys Val Met Leu Pro Ser Thr |     | 110 |
|                                                                 | 115 | 120 |
| Ala Thr Glu Phe Arg Thr Leu Met Ala Leu Ala Ser Ser Trp Arg Leu |     | 125 |
|                                                                 | 130 | 135 |
| Val Arg Met Phe Pro Asp Ala Leu Trp Asn Asp Val Ile Asn Asn Leu |     | 140 |
| 145                                                             | 150 | 155 |
| Tyr Lys Lys Asn Arg Lys Glu Lys Ile Glu Leu Leu Lys Gly Val Thr |     | 160 |
|                                                                 | 165 | 170 |
| Phe Gly Arg Ser Glu Asn Leu Asn Ile Asp Ser Leu Ser Gln Glu Val |     | 175 |
|                                                                 | 180 | 185 |
| Leu Ile Val Trp Gly Asp Lys Asp Gln Ile Phe Pro Val Lys Met Ala |     | 190 |
|                                                                 | 195 | 200 |
| Tyr Glu Leu Lys Glu Ile Leu Gly Asp Lys Thr Lys Leu Glu Ile Ile |     | 205 |
|                                                                 | 210 | 215 |
| Asp Asn Thr Ser His Val Pro Gln Ile Glu Cys Ala Gln Glu Phe Asn |     | 220 |
| 225                                                             | 230 | 235 |
| Asn Ile Val Leu Arg Phe Leu Lys Gly Ser                         |     | 240 |
|                                                                 | 245 | 250 |

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1569300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Trp Gln Trp Arg Arg Gln Met Gln Ala Phe Ser Pro Ser Ala Phe |     |     |
| 1                                                               | 5   | 10  |
| Arg Val Tyr Ser Pro Asp Leu Val Phe Phe Gly Asp Ser Thr Ser Ser |     | 15  |
|                                                                 | 20  | 25  |
| Ser Thr Asn Arg Thr Glu Val Phe Gln Ala Glu Cys Met Ala Lys Leu |     | 30  |
|                                                                 | 35  | 40  |
| Met Ala Lys Ile Gly Ile Gly Lys Tyr Asn Val Ala Gly Thr Ser Tyr |     | 45  |
|                                                                 | 50  | 55  |
| Gly Gly Phe Val Ala Tyr His Met Ala Lys Met Trp Pro Glu Lys Val |     | 60  |
| 65                                                              | 70  | 75  |
| Glu Lys Val Val Ile Ala Ser Ser Gly Ile Asn Met Arg Lys Cys Asp |     | 80  |
|                                                                 | 85  | 90  |
| Gly Glu Ser Leu Leu Gln Arg Ser Asn Cys Glu Cys Ile Glu Lys Val |     | 95  |
|                                                                 | 100 | 105 |
| Met Leu Pro Ser Thr Ala Thr Glu Phe Arg Thr Leu Met Ala Leu Ala |     | 110 |
|                                                                 | 115 | 120 |
| Ser Ser Trp Arg Leu Val Arg Met Phe Pro Asp Ala Leu Trp Asn Asp |     | 125 |
|                                                                 | 130 | 135 |
| Val Ile Asn Asn Leu Tyr Lys Lys Asn Arg Lys Glu Lys Ile Glu Leu |     | 140 |
| 145                                                             | 150 | 155 |
| Leu Lys Gly Val Thr Phe Gly Arg Ser Glu Asn Leu Asn Ile Asp Ser |     | 160 |
|                                                                 | 165 | 170 |
| Leu Ser Gln Glu Val Leu Ile Val Trp Gly Asp Lys Asp Gln Ile Phe |     | 175 |
|                                                                 | 180 | 185 |
|                                                                 |     | 190 |

Pro Val Lys Met Ala Tyr Glu Leu Lys Glu Ile Leu Gly Asp Lys Thr  
195 200 205  
Lys Leu Glu Ile Ile Asp Asn Thr Ser His Val Pro Gln Ile Glu Cys  
210 215 220  
Ala Gln Glu Phe Asn Asn Ile Val Leu Arg Phe Leu Lys Gly Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1569301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

Met Gln Ala Phe Ser Pro Ser Ala Phe Arg Val Tyr Ser Pro Asp Leu  
1 5 10 15  
Val Phe Phe Gly Asp Ser Thr Ser Ser Thr Asn Arg Thr Glu Val  
20 25 30  
Phe Gln Ala Glu Cys Met Ala Lys Leu Met Ala Lys Ile Gly Ile Gly  
35 40 45  
Lys Tyr Asn Val Ala Gly Thr Ser Tyr Gly Gly Phe Val Ala Tyr His  
50 55 60  
Met Ala Lys Met Trp Pro Glu Lys Val Glu Lys Val Val Ile Ala Ser  
65 70 75 80  
Ser Gly Ile Asn Met Arg Lys Cys Asp Gly Glu Ser Leu Leu Gln Arg  
85 90 95  
Ser Asn Cys Glu Cys Ile Glu Lys Val Met Leu Pro Ser Thr Ala Thr  
100 105 110  
Glu Phe Arg Thr Leu Met Ala Leu Ala Ser Ser Trp Arg Leu Val Arg  
115 120 125  
Met Phe Pro Asp Ala Leu Trp Asn Asp Val Ile Asn Asn Leu Tyr Lys  
130 135 140  
Lys Asn Arg Lys Glu Lys Ile Glu Leu Leu Lys Gly Val Thr Phe Gly  
145 150 155 160  
Arg Ser Glu Asn Leu Asn Ile Asp Ser Leu Ser Gln Glu Val Leu Ile  
165 170 175  
Val Trp Gly Asp Lys Asp Gln Ile Phe Pro Val Lys Met Ala Tyr Glu  
180 185 190  
Leu Lys Glu Ile Leu Gly Asp Lys Thr Lys Leu Glu Ile Ile Asp Asn  
195 200 205  
Thr Ser His Val Pro Gln Ile Glu Cys Ala Gln Glu Phe Asn Asn Ile  
210 215 220  
Val Leu Arg Phe Leu Lys Gly Ser  
225 230

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1431

(D) OTHER INFORMATION: / Ceres Seq. ID 1569306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

attttatttt ctcgatattt cttcttcttc ctagattcca gcgacttaac aacaacaaca

acaacatatt ctctgctggg tattagattc gaatttctct ttttgtgatc agaaatggat 120  
cgagctccgg tgaccacagg accgttggat atgccgatta tgcacgacag tgatcgatat 180  
gacttcgtta aggatattgg ttctggtaat ttcggtgttg ctcgctttat gagagataaa 240  
ctcactaaag agcttggtgc tgtcaagtac atcgagagag gagacaagat tgatgaaaat 300  
gttcaaaggg agatcattaa ccacaggtca ctaaggcatc ctaatattgt cagattttaa 360  
gaggtcattt tgacgccgac tcatctggct atcataatgg aatatgcttc tggcggtgaa 420  
ctttacgagc ggatttgcaa tgcaggacgg tttagtgaag atgaggctcg gttcttcttt 480  
cagcagcttc tatctggagt cagttattgt catgcgatgc aaatttgcca tcgtgacctg 540  
aagctagaga atacattggt ggatggaagt cctgctcctc gattaaaaat ttgtgatttt 600  
ggatattcaa agtcttctgt tcttcattca caaccaaagt caactgttgg tactcctgca 660  
tacatcgctc cagaggtact gcttcgtcag gaatatgatg gcaagattgc agatgtatgg 720  
tcatgtggtg tgaccttata cgtcatgttg gttggagcgt atccgcttca agatccagaa 780  
gagcaaagag actatcggaa aacaatacag agaatcctta gcgttaaata ctcaatccct 840  
gatgacatac ggatatcacc tgaatgctgt catcttattt caagaatctt cgtggctgat 900  
cccgtacca gaataagcat accagagatc aaaaccata gttggttctt gaagaatctc 960  
cctgctgata taatgaacga gagcaacaca ggaagccagt tccaggagcc tgaacaacca 1020  
atgcaaagcc ttgacacaat catgcaaate atctctgaag ccacaattcc cgtgttctga 1080  
aaccgttgcc tagacgattt catgactgac aatcttgatc ttgacgatga catggatgac 1140  
tttgactctg aatctgaaat cgacattgac agtagcggag agatagttaa cgctctctaa 1200  
taaaaagcct tttttaacaa ccaaaacact tctctatctg ttctaagacc agtagtgctc 1260  
tgatcctctg gtttcaaatt ctaccaattt ttgtattgtc tctgtttgtt tcttgttttc 1320  
ttcatgcaca catatatcat atatgtaatg taaaatatca tctgtgtata tatattccaa 1380  
tgtcacacaa aagcaratta gcaGttaaaa cagttgaagc aagttgaggt c

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1569307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Ala | Pro | Val | Thr | Thr | Gly | Pro | Leu | Asp | Met | Pro | Ile | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| His | Asp | Ser | Asp | Arg | Tyr | Asp | Phe | Val | Lys | Asp | Ile | Gly | Ser | Gly | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Val | Ala | Arg | Leu | Met | Arg | Asp | Lys | Leu | Thr | Lys | Glu | Leu | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Val | Lys | Tyr | Ile | Glu | Arg | Gly | Asp | Lys | Ile | Asp | Glu | Asn | Val | Gln |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Arg | Glu | Ile | Ile | Asn | His | Arg | Ser | Leu | Arg | His | Pro | Asn | Ile | Val | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Lys | Glu | Val | Ile | Leu | Thr | Pro | Thr | His | Leu | Ala | Ile | Ile | Met | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Ala | Ser | Gly | Gly | Glu | Leu | Tyr | Glu | Arg | Ile | Cys | Asn | Ala | Gly | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Glu | Asp | Glu | Ala | Arg | Phe | Phe | Phe | Gln | Gln | Leu | Leu | Ser | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ser | Tyr | Cys | His | Ala | Met | Gln | Ile | Cys | His | Arg | Asp | Leu | Lys | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Asn | Thr | Leu | Leu | Asp | Gly | Ser | Pro | Ala | Pro | Arg | Leu | Lys | Ile | Cys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Phe | Gly | Tyr | Ser | Lys | Ser | Ser | Val | Leu | His | Ser | Gln | Pro | Lys | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Val | Gly | Thr | Pro | Ala | Tyr | Ile | Ala | Pro | Glu | Val | Leu | Leu | Arg | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Tyr | Asp | Gly | Lys | Ile | Ala | Asp | Val | Trp | Ser | Cys | Gly | Val | Thr | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ile | Met | His | Asp | Ser | Asp | Arg | Tyr | Asp | Phe | Val | Lys | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Gly | Asn | Phe | Gly | Val | Ala | Arg | Leu | Met | Arg | Asp | Lys | Leu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Leu | Val | Ala | Val | Lys | Tyr | Ile | Glu | Arg | Gly | Asp | Lys | Ile | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Val | Gln | Arg | Glu | Ile | Ile | Asn | His | Arg | Ser | Leu | Arg | His | Pro |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ile | Val | Arg | Phe | Lys | Glu | Val | Ile | Leu | Thr | Pro | Thr | His | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ile | Met | Glu | Tyr | Ala | Ser | Gly | Gly | Glu | Leu | Tyr | Glu | Arg | Ile | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Ala | Gly | Arg | Phe | Ser | Glu | Asp | Glu | Ala | Arg | Phe | Phe | Phe | Gln | Gln |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Ser | Gly | Val | Ser | Tyr | Cys | His | Ala | Met | Gln | Ile | Cys | His | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Leu | Lys | Leu | Glu | Asn | Thr | Leu | Leu | Asp | Gly | Ser | Pro | Ala | Pro | Arg |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Lys | Ile | Cys | Asp | Phe | Gly | Tyr | Ser | Lys | Ser | Ser | Val | Leu | His | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Pro | Lys | Ser | Thr | Val | Gly | Thr | Pro | Ala | Tyr | Ile | Ala | Pro | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Leu | Arg | Gln | Glu | Tyr | Asp | Gly | Lys | Ile | Ala | Asp | Val | Trp | Ser | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Val | Thr | Leu | Tyr | Val | Met | Leu | Val | Gly | Ala | Tyr | Pro | Phe | Glu | Asp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Glu | Glu | Pro | Arg | Asp | Tyr | Arg | Lys | Thr | Ile | Gln | Arg | Ile | Leu | Ser |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Lys | Tyr | Ser | Ile | Pro | Asp | Asp | Ile | Arg | Ile | Ser | Pro | Glu | Cys | Cys |

225 230 235 240  
His Leu Ile Ser Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser  
245 250 255  
Ile Pro Glu Ile Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala  
260 265 270  
Asp Leu Met Asn Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu  
275 280 285  
Gln Pro Met Gln Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala  
290 295 300  
Thr Ile Pro Ala Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp  
305 310 315 320  
Asn Leu Asp Leu Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu  
325 330 335  
Ile Asp Ile Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu  
340 345

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1569309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

Met His Asp Ser Asp Arg Tyr Asp Phe Val Lys Asp Ile Gly Ser Gly  
1 5 10 15  
Asn Phe Gly Val Ala Arg Leu Met Arg Asp Lys Leu Thr Lys Glu Leu  
20 25 30  
Val Ala Val Lys Tyr Ile Glu Arg Gly Asp Lys Ile Asp Glu Asn Val  
35 40 45  
Gln Arg Glu Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Val  
50 55 60  
Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His Leu Ala Ile Ile Met  
65 70 75 80  
Glu Tyr Ala Ser Gly Gly Glu Leu Tyr Glu Arg Ile Cys Asn Ala Gly  
85 90 95  
Arg Phe Ser Glu Asp Glu Ala Arg Phe Phe Phe Gln Gln Leu Leu Ser  
100 105 110  
Gly Val Ser Tyr Cys His Ala Met Gln Ile Cys His Arg Asp Leu Lys  
115 120 125  
Leu Glu Asn Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg Leu Lys Ile  
130 135 140  
Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser Gln Pro Lys  
145 150 155 160  
Ser Thr Val Gly Thr Pro Ala Tyr Ile Ala Pro Glu Val Leu Leu Arg  
165 170 175  
Gln Glu Tyr Asp Gly Lys Ile Ala Asp Val Trp Ser Cys Gly Val Thr  
180 185 190  
Leu Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Glu  
195 200 205  
Pro Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser Val Lys Tyr  
210 215 220  
Ser Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys His Leu Ile  
225 230 235 240  
Ser Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser Ile Pro Glu  
245 250 255  
Ile Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met  
260 265 270

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Asn Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu Gln Pro Met  
275 280 285  
Gln Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro  
290 295 300  
Ala Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp Asn Leu Asp  
305 310 315 320  
Leu Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu Ile Asp Ile  
325 330 335  
Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu  
340 345

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

ctgattttttt gacgttaaga gatagaaaca gggagagata gagagataga gttatggcctt 60  
tggcgatgat gatccgaaac gcagcttcga agcgaggaat gactccgatc tccgggtgatt 120  
tcgggtggttt gagatctatg tcttcattggt ggaagagcgt tgagcctgct cctaaagatc 180  
cgatcctcgg agttaccgaa gcttttctcg ctgattcctag tcctgaaaaa gttaattgtt 240  
gtgtgggagc atatcgtgat gataatggga agcctgttgt cttggaatgt gtcagagaag 300  
ctgagaaaaa gcttgctggg agcactttca tggagtacct tcctatggga ggaagtgcc 360  
aaatggtgga cctaacatta agcttgccca cggggacaat agtgaattta tcaaagataa 420  
aagaattgct gcagttcaga ctctgtctgg cactggagcc tgccggctct ttgcagactt 480  
ccagaaaagt ttttctcctg gttcacagat ctacattcct gttccaacct ggtccaacca 540  
ccacaacatc tggaaagatg cacaagtccc tcaaaagaca tatcattact atcatccaga 600  
aaccaagggc ttggatttct cagcattgat ggatgatgtg aagaatgctc cggaaggggtc 660  
attcttcctt cttcatgctt gtgctcataa tcctactgga gtagacccta cagaggaaca 720  
atggagagag atatcacagc tattcaaggc taaaaagcat ttgcattctc tcgatatggc 780  
ttaccaaggt tttgctagtg gagatccagc gagagatgcc aagtccatca ggatctttct 840  
tgaagatggt catcatattg gaatttctca gtcctatgca aaaaacatgg gactctacgg 900  
ccagaggggtg ggatgtctca gtgtgctttg tgaagatccg aagcaagccg tggctgtgaa 960  
aagtcaattg cagcagctag ctagaccaat gtacagcaac ccacctttgc atggtgctca 1020  
gctggtctca accattcttg aagaccaga gttaaagagt ctgtggctaa aagaagttaa 1080  
ggatcatggc gataggatca tcggcatgag aactactttg cgagaaagcc ttgagaagtt 1140  
aggatgcct ttgtcatggg agcacgttac caaacagatt ggaatgttct gctacagtgg 1200  
gttaacacca gaacagggtg accgcttaac aagcgaatat cacatctata tgaccgtaa 1260  
cggccgtatc agtatggctg gtgttaCaac aggaaacgtg ggataccttg cgaatgctat 1320  
acatgaagtc accaagtcac cttaaatcat ttacttacat gtttcagcca aacatacaaa 1380  
ttttgtttga agagtcaata agacaggagg ctagatttgt acttctgcaa ttggttttgt 1440  
gagaactgaa agtttaccga taaacagtaa tttattagcg cattttttcg ttagctgggc 1500  
aataaaaagca aagcctaaac gatggatttt tgg

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met Ala Leu Ala Met Met Ile Arg Asn Ala Ala Ser Lys Arg Gly Met

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1 5 10 15  
Thr Pro Ile Ser Gly Asp Phe Gly Gly Leu Arg Ser Met Ser Ser Trp  
20 25 30  
Trp Lys Ser Val Glu Pro Ala Pro Lys Asp Pro Ile Leu Gly Val Thr  
35 40 45  
Glu Ala Phe Leu Ala Asp Pro Ser Pro Glu Lys Val Asn Val Gly Val  
50 55 60  
Gly Ala Tyr Arg Asp Asp Asn Gly Lys Pro Val Val Leu Glu Cys Val  
65 70 75 80  
Arg Glu Ala Glu Lys Arg Leu Ala Gly Ser Thr Phe Met Glu Tyr Leu  
85 90 95  
Pro Met Gly Gly Ser Ala Lys Met Val Asp Leu Thr Leu Ser Leu Pro  
100 105 110  
Thr Gly Thr Ile Val Asn Leu Ser Lys Ile Lys Glu Leu Leu Gln Phe  
115 120 125  
Arg Leu Cys Leu Ala Leu Glu Pro Ala Gly Ser Leu Gln Thr Ser Arg  
130 135 140  
Asn Val Phe Leu Leu Val His Arg Ser Thr Phe Leu Phe Gln Pro Gly  
145 150 155 160  
Pro Thr Thr Thr Thr Ser Gly Lys Met His Lys Ser Leu Lys Arg His  
165 170 175  
Ile Ile Thr Ile Ile Gln Lys Pro Arg Ala Trp Ile Ser Gln His  
180 185 190

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1569312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

Met Asp Asp Val Lys Asn Ala Pro Glu Gly Ser Phe Phe Leu Leu His  
1 5 10 15  
Ala Cys Ala His Asn Pro Thr Gly Val Asp Pro Thr Glu Glu Gln Trp  
20 25 30  
Arg Glu Ile Ser Gln Leu Phe Lys Ala Lys Lys His Phe Ala Phe Phe  
35 40 45  
Asp Met Ala Tyr Gln Gly Phe Ala Ser Gly Asp Pro Ala Arg Asp Ala  
50 55 60  
Lys Ser Ile Arg Ile Phe Leu Glu Asp Gly His Ile Gly Ile Ser  
65 70 75 80  
Gln Ser Tyr Ala Lys Asn Met Gly Leu Tyr Gly Gln Arg Val Gly Cys  
85 90 95  
Leu Ser Val Leu Cys Glu Asp Pro Lys Gln Ala Val Ala Val Lys Ser  
100 105 110  
Gln Leu Gln Gln Leu Ala Arg Pro Met Tyr Ser Asn Pro Pro Leu His  
115 120 125  
Gly Ala Gln Leu Val Ser Thr Ile Leu Glu Asp Pro Glu Leu Lys Ser  
130 135 140  
Leu Trp Leu Lys Glu Val Lys Val Met Ala Asp Arg Ile Ile Gly Met  
145 150 155 160  
Arg Thr Thr Leu Arg Glu Ser Leu Glu Lys Leu Gly Ser Pro Leu Ser  
165 170 175  
Trp Glu His Val Thr Lys Gln Ile Gly Met Phe Cys Tyr Ser Gly Leu  
180 185 190  
Thr Pro Glu Gln Val Asp Arg Leu Thr Ser Glu Tyr His Ile Tyr Met  
195 200 205

Thr Arg Asn Gly Arg Ile Ser Met Ala Gly Val Thr Thr Gly Asn Val  
210 215 220  
Gly Tyr Leu Ala Asn Ala Ile His Glu Val Thr Lys Ser Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met Ala Tyr Gln Gly Phe Ala Ser Gly Asp Pro Ala Arg Asp Ala Lys  
1 5 10 15  
Ser Ile Arg Ile Phe Leu Glu Asp Gly His His Ile Gly Ile Ser Gln  
20 25 30  
Ser Tyr Ala Lys Asn Met Gly Leu Tyr Gly Gln Arg Val Gly Cys Leu  
35 40 45  
Ser Val Leu Cys Glu Asp Pro Lys Gln Ala Val Ala Val Lys Ser Gln  
50 55 60  
Leu Gln Gln Leu Ala Arg Pro Met Tyr Ser Asn Pro Pro Leu His Gly  
65 70 75 80  
Ala Gln Leu Val Ser Thr Ile Leu Glu Asp Pro Glu Leu Lys Ser Leu  
85 90 95  
Trp Leu Lys Glu Val Lys Val Met Ala Asp Arg Ile Ile Gly Met Arg  
100 105 110  
Thr Thr Leu Arg Glu Ser Leu Glu Lys Leu Gly Ser Pro Leu Ser Trp  
115 120 125  
Glu His Val Thr Lys Gln Ile Gly Met Phe Cys Tyr Ser Gly Leu Thr  
130 135 140  
Pro Glu Gln Val Asp Arg Leu Thr Ser Glu Tyr His Ile Tyr Met Thr  
145 150 155 160  
Arg Asn Gly Arg Ile Ser Met Ala Gly Val Thr Thr Gly Asn Val Gly  
165 170 175  
Tyr Leu Ala Asn Ala Ile His Glu Val Thr Lys Ser Ser  
180 185

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cttctcgcac | cttatatgaa | acacattcac | tctccaaaat | aatctatact | tttcctacat | 60  |
| attctcttga | cgatcatgag | actcatttcg | tgaaaatatc | gtcattatat | caaattagaa | 120 |
| gttgatggaa | aacatggggg | attcgagcat | agggccgggc | catccgcac  | tccctcccgg | 180 |
| gtttcggttt | caccgcactg | atgaggaact | agtagttcat | tacctcaaga | agaaagcagc | 240 |
| ttctgttcca | cttccagtct | caatcatcgc | agagattgat | ctttacaagt | ttgatccttg | 300 |
| ggagcttcca | agcaaggcga | gttttgagga | gcacgagtgg | tacttcttta | gtcctcggga | 360 |
| tcggaagtat | ccaaatgggg | ttaggccaaa | ccgggcagca | acttccgggt | attggaaagc | 420 |
| aacgggaacc | gataaaccga | tatttacgtg | caatagtcac | aaggttgggt | tcaagaaagc | 480 |
| gcttggtttt | tacggtggaa | agcctcctaa | agggataaaa | acagattgga | tcatgcatga | 540 |

|            |            |            |             |             |              |      |
|------------|------------|------------|-------------|-------------|--------------|------|
| atategcctc | actgatggta | accttagcac | tgcggctaag  | ccgcctgact  | taaccacgac   | 600  |
| aaggaaaaac | tcactacggc | tagacgattg | ggttctatgt  | aggatctata  | agaagaatag   | 660  |
| ttcacaaagS | accaCacaat | ggagagagta | ttagagagga  | tctaattggaa | ggcatgctct   | 720  |
| caaaatcatc | tgctaattct | tcttctacat | cagtactaga  | caacaacgac  | aacaataatr   | 780  |
| acaataacaa | agaacacttt | ttcgacggta | tggtcgtttc  | ttcagacaaa  | cgttccttgt   | 840  |
| gtggtcaata | ccgaatgggc | gacgaggcct | caggatcatc  | ttcattcgga  | tctttcttat   | 900  |
| cgagcaagag | gtttcatcat | acaggtgatc | tcaacaatga  | taactacaat  | gtctcttttg   | 960  |
| tttcgatgct | tagtgagatt | cctcagagtt | cgggggtttca | tgcaaatggg  | gttatggata   | 1020 |
| cgacgtcgtc | tctagctgat | catgggggtt | taagacaggc  | gtttcagctt  | cctaacatga   | 1080 |
| actggcactc | ataatctata | tagatatata | tgtatgtatc  | atatatgtat  | ctatgcaggc   | 1140 |
| ctaatatagt | ttacacataa | atcatctggg | aatatatata  | tacaagtacg  | cggtctttaca  | 1200 |
| aatgtatacg | tatctgttta | attacgtcaa | gaaaaagtgt  | atacgtttct  | ttttactcaa   | 1260 |
| tggctgcaaa | gatgtgtact | aataacagaa | gctgattaat  | aaaaaatata  | aaagtatatatt | 1320 |
| ttttcc     |            |            |             |             |              |      |

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Met | Gly | Asp | Ser | Ser | Ile | Gly | Pro | Gly | His | Pro | His | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Gly | Phe | Arg | Phe | His | Pro | Thr | Asp | Glu | Glu | Leu | Val | Val | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Lys | Lys | Lys | Ala | Ala | Ser | Val | Pro | Leu | Pro | Val | Ser | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Ile | Asp | Leu | Tyr | Lys | Phe | Asp | Pro | Trp | Glu | Leu | Pro | Ser | Lys |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Ser | Phe | Gly | Glu | His | Glu | Trp | Tyr | Phe | Phe | Ser | Pro | Arg | Asp | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Tyr | Pro | Asn | Gly | Val | Arg | Pro | Asn | Arg | Ala | Ala | Thr | Ser | Gly | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Lys | Ala | Thr | Gly | Thr | Asp | Lys | Pro | Ile | Phe | Thr | Cys | Asn | Ser | His |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Val | Gly | Val | Lys | Lys | Ala | Leu | Val | Phe | Tyr | Gly | Gly | Lys | Pro | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gly | Ile | Lys | Thr | Asp | Trp | Ile | Met | His | Glu | Tyr | Arg | Leu | Thr | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Asn | Leu | Ser | Thr | Ala | Lys | Pro | Pro | Asp | Leu | Thr | Thr | Thr | Thr | Arg |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Lys | Asn | Ser | Leu | Arg | Leu | Asp | Asp | Trp | Val | Leu | Cys | Arg | Ile | Tyr | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Asn | Ser | Ser | Gln | Xaa | Thr | Thr | Gln | Trp | Arg | Glu | Tyr |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

Met Gly Asp Ser Ser Ile Gly Pro Gly His Pro His Leu Pro Pro Gly  
1 5 10 15  
Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Val His Tyr Leu Lys  
20 25 30  
Lys Lys Ala Ala Ser Val Pro Leu Pro Val Ser Ile Ile Ala Glu Ile  
35 40 45  
Asp Leu Tyr Lys Phe Asp Pro Trp Glu Leu Pro Ser Lys Ala Ser Phe  
50 55 60  
Gly Glu His Glu Trp Tyr Phe Phe Ser Pro Arg Asp Arg Lys Tyr Pro  
65 70 75 80  
Asn Gly Val Arg Pro Asn Arg Ala Ala Thr Ser Gly Tyr Trp Lys Ala  
85 90 95  
Thr Gly Thr Asp Lys Pro Ile Phe Thr Cys Asn Ser His Lys Val Gly  
100 105 110  
Val Lys Lys Ala Leu Val Phe Tyr Gly Gly Lys Pro Pro Lys Gly Ile  
115 120 125  
Lys Thr Asp Trp Ile Met His Glu Tyr Arg Leu Thr Asp Gly Asn Leu  
130 135 140  
Ser Thr Ala Ala Lys Pro Pro Asp Leu Thr Thr Thr Arg Lys Asn Ser  
145 150 155 160  
Leu Arg Leu Asp Asp Trp Val Leu Cys Arg Ile Tyr Lys Lys Asn Ser  
165 170 175  
Ser Gln Xaa Thr Thr Gln Trp Arg Glu Tyr  
180 185

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1569329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

Met Glu Gly Met Leu Ser Lys Ser Ser Ala Asn Ser Ser Ser Thr Ser  
1 5 10 15  
Val Leu Asp Asn Asn Asp Asn Asn Asn Xaa Asn Asn Lys Glu His Phe  
20 25 30  
Phe Asp Gly Met Val Val Ser Ser Asp Lys Arg Ser Leu Cys Gly Gln  
35 40 45  
Tyr Arg Met Gly Asp Glu Ala Ser Gly Ser Ser Ser Phe Gly Ser Phe  
50 55 60  
Leu Ser Ser Lys Arg Phe His His Thr Gly Asp Leu Asn Asn Asp Asn  
65 70 75 80  
Tyr Asn Val Ser Phe Val Ser Met Leu Ser Glu Ile Pro Gln Ser Ser  
85 90 95  
Gly Phe His Ala Asn Gly Val Met Asp Thr Thr Ser Ser Leu Ala Asp  
100 105 110  
His Gly Val Leu Arg Gln Ala Phe Gln Leu Pro Asn Met Asn Trp His  
115 120 125  
Ser

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 718 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..718

(D) OTHER INFORMATION: / Ceres Seq. ID 1569338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aattgaaaga  | cgttggggg  | tttctcacta | cccagaaatt | atcatcatcc | acagagaaac | 60  |
| ccaaaagaga  | ttgaagaaga | tgcattacat | gggtttgttt | agtagagctg | gaaacatatt | 120 |
| taggcagcct  | agagcgttgc | aggcctcaaa | cgctatgtta | cagggcaatc | tttcattaac | 180 |
| tccatccaaa  | atctttgttg | gaggtctctc | accatctact | gatgtggagc | tcttgaaaga | 240 |
| agctttttggc | agtttttgaa | aaattgttga | tgcggtagt  | gttttgacc  | gtgaaagtgg | 300 |
| tttatcaagg  | ggcttttggt | tcgtaacata | tgattcgatc | gaagttgcta | ataacgcaat | 360 |
| gcaagctatg  | caaaataagg | agcttgatgg | gcgaataatt | ggagtgcata | cagctgattc | 420 |
| agghgvtggt  | nggSggyvgt | ggtggttttg | caagaagggg | aggttatggt | ggtggtcgtg | 480 |
| ggggatatgc  | tcgtggtgga | tttggtcgcg | gtggatttgg | tgggtgtggc | tatggctttg | 540 |
| ttcgttaact  | ggacatccag | atatgtctac | cgccaagatt | gattagtctg | tggtttaatt | 600 |
| ttctcttcac  | aaagaccact | attttgttat | aacaacgctc | ttatgcttga | acaaacatat | 660 |
| caagcggcta  | aagttggcaa | aaacatttgt | tgattcaatt | ggtatttgat | acaaattc   |     |

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1569339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Glu | Arg | Arg | Trp | Gly | Val | Ser | His | Tyr | Pro | Glu | Ile | Ile | Ile | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| His | Arg | Glu | Thr | Gln | Lys | Arg | Leu | Lys | Lys | Met | His | Tyr | Met | Gly | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Ser | Arg | Ala | Gly | Asn | Ile | Phe | Arg | Gln | Pro | Arg | Ala | Leu | Gln | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Asn | Ala | Met | Leu | Gln | Gly | Asn | Leu | Ser | Leu | Thr | Pro | Ser | Lys | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Val | Gly | Gly | Leu | Ser | Pro | Ser | Thr | Asp | Val | Glu | Leu | Leu | Lys | Glu |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Phe | Gly | Ser | Phe | Gly | Lys | Ile | Val | Asp | Ala | Val | Val | Val | Leu | Asp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Arg | Glu | Ser | Gly | Leu | Ser | Arg | Gly | Phe | Gly | Phe | Val | Thr | Tyr | Asp | Ser |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ile | Glu | Val | Ala | Asn | Asn | Ala | Met | Gln | Ala | Met | Gln | Asn | Lys | Glu | Leu |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Asp | Gly | Arg | Ile | Ile | Gly | Val | His | Pro | Ala | Asp | Ser | Xaa | Xaa | Gly | Xaa |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Xaa | Xaa | Trp | Trp | Phe | Cys | Lys | Lys | Gly | Arg | Leu | Trp | Trp | Trp | Ser | Trp |  |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |  |
| Gly | Ile | Cys | Ser | Trp | Trp | Ile | Trp | Ser | Arg | Trp | Ile | Trp | Trp | Trp | Trp |  |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Leu | Trp | Leu | Cys | Ser | Leu | Thr | Gly | His | Pro | Asp | Met | Ser | Thr | Ala | Lys |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Ile | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Phe |     | Ser | Arg | Ala | Gly | Asn | Ile | Phe | Arg | Gln | Pro | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gln | Ala | Ser | Asn | Ala | Met | Leu | Gln | Gly | Asn | Leu | Ser | Leu | Thr | Pro |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Lys | Ile | Phe | Val | Gly | Gly | Leu | Ser | Pro | Ser | Thr | Asp | Val | Glu | Leu |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Leu | Lys | Glu | Ala | Phe | Gly | Ser | Phe | Gly | Lys | Ile | Val | Asp | Ala | Val | Val |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Val | Leu | Asp | Arg | Glu | Ser | Gly | Leu | Ser | Arg | Gly | Phe | Gly | Phe | Val | Thr |     |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Asp | Ser | Ile | Glu | Val | Ala | Asn | Asn | Ala | Met | Gln | Ala | Met | Gln | Asn |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Glu | Leu | Asp | Gly | Arg | Ile | Ile | Gly | Val | His | Pro | Ala | Asp | Ser | Xaa |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Xaa | Gly | Xaa | Xaa | Xaa | Trp | Trp | Phe | Cys | Lys | Lys | Gly | Arg | Leu | Trp | Trp |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Trp | Ser | Trp | Gly | Ile | Cys | Ser | Trp | Trp | Ile | Trp | Ser | Arg | Trp | Ile | Trp |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Trp | Trp | Trp | Leu | Trp | Leu | Cys | Ser | Leu | Thr | Gly | His | Pro | Asp | Met | Ser |     |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |     |

Thr Ala Lys Ile Asp  
165

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gactacgaaa tagaatcaag ttgtgttctc tgtgatggac attgtgttag tggtaatcaa  | 60   |
| atccggtgaa aatggagcgg aGccgagtga ccagagaagc accgaccgga accaggatcc  | 120  |
| tgtttgcttc actctctgcg atggttgtag agtcagttac gtttccgatt gatctcacia  | 180  |
| agactagaat gcagctccat ggttcgggat ccgcttctgg tgcgcatcgg attggcgctt  | 240  |
| tccgagtcgt atcggagatt gcgagaaaag aaggagtgtg tggctctctac aaaggtctat | 300  |
| ctccggcgat tatcagacac ctgttctaca cgcctatcag aatcattgga tacgagaatt  | 360  |
| tgaaaggact catcgtcaga tctgaaacta acaatagcga gtctcttctt ctccgccaaa  | 420  |
| aggctctcgt cggaggattt tctgggtgta tagctcagaa atgcaggtag tggctagtcc  | 480  |
| agctgatttg gtcaaagtga gaatgcaagc agatggtaga ttggtgagcc aaggcctgaa  | 540  |
| accgaggtac tccgggaccaa tccaggcttt taccaaaatc ctacaatcag aaggagtaaa | 600  |
| agggttatgg aaagggtgtt ttccaaacat ccagagagca tttctagtga atatgggaga  | 660  |
| actagcttgc tatgatcacg ccaaacactt tgtcatcgat aagaagattg ctgaggataa  | 720  |
| cattttttgcg cacactcttg cttctataat gtccggtctt gcttcgacaa gtttgagttg | 780  |
| tccagctgat gtggtgaaga cgaggatgat gaaccagggt gaaaatgctg tgtacagaaa  | 840  |
| ttcttacgac tgtttggtga agacgggttaa gtttgaagga ataagagctt tgtggaaaag | 900  |
| tttcttcccg acatgggcaa ggcttgacc gtggcagttc gtgttttggg tctctatga    | 960  |
| gaagttttaga ctgctggcag gaatctcttc cttctagacc tgagaaactg gaaaagcaaa | 1020 |
| tttgagattt gtgttcttta gttcttactt gttagtgtt acacattttg taagaacctt   | 1080 |
| gagaagtatc atcagtttct gattaacgcg agaagagtta tataaatttg ggcccaaaaag | 1140 |
| tgtaggccca tagatttata attttttttt tgttgattaa attagattgg acatcctaag  | 1200 |
| caaaaaaata ttttaaaaag taagagatta ataaaatatt cc                     |      |

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ser | Arg | Val | Thr | Arg | Glu | Ala | Pro | Thr | Gly | Thr | Arg | Ile |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Ser | Leu | Ser | Ala | Met | Val | Ala | Glu | Ser | Val | Thr | Phe | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ile | Asp | Leu | Thr | Lys | Thr | Arg | Met | Gln | Leu | His | Gly | Ser | Gly | Ser | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Ala | His | Arg | Ile | Gly | Ala | Phe | Gly | Val | Val | Ser | Glu | Ile | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Lys | Glu | Gly | Val | Ile | Gly | Leu | Tyr | Lys | Gly | Leu | Ser | Pro | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Arg | His | Leu | Phe | Tyr | Thr | Pro | Ile | Arg | Ile | Ile | Gly | Tyr | Glu | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Lys | Gly | Leu | Ile | Val | Arg | Ser | Glu | Thr | Asn | Asn | Ser | Glu | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Pro Leu Ala Thr Lys Ala Leu Val Gly Gly Phe Ser Gly Val Ile Ala  
115 120 125  
Gln Lys Cys Arg  
130

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

Met Gln Val Val Ala Ser Pro Ala Asp Leu Val Lys Val Arg Met Gln  
1 5 10 15  
Ala Asp Gly Arg Leu Val Ser Gln Gly Leu Lys Pro Arg Tyr Ser Gly  
20 25 30  
Pro Ile Glu Ala Phe Thr Lys Ile Leu Gln Ser Glu Gly Val Lys Gly  
35 40 45  
Leu Trp Lys Gly Val Leu Pro Asn Ile Gln Arg Ala Phe Leu Val Asn  
50 55 60  
Met Gly Glu Leu Ala Cys Tyr Asp His Ala Lys His Phe Val Ile Asp  
65 70 75 80  
Lys Lys Ile Ala Glu Asp Asn Ile Phe Ala His Thr Leu Ala Ser Ile  
85 90 95  
Met Ser Gly Leu Ala Ser Thr Ser Leu Ser Cys Pro Ala Asp Val Val  
100 105 110  
Lys Thr Arg Met Met Asn Gln Gly Glu Asn Ala Val Tyr Arg Asn Ser  
115 120 125  
Tyr Asp Cys Leu Val Lys Thr Val Lys Phe Glu Gly Ile Arg Ala Leu  
130 135 140  
Trp Lys Gly Phe Phe Pro Thr Trp Ala Arg Leu Gly Pro Trp Gln Phe  
145 150 155 160  
Val Phe Trp Val Ser Tyr Glu Lys Phe Arg Leu Leu Ala Gly Ile Ser  
165 170 175  
Ser Phe

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

Met Gln Ala Asp Gly Arg Leu Val Ser Gln Gly Leu Lys Pro Arg Tyr  
1 5 10 15  
Ser Gly Pro Ile Glu Ala Phe Thr Lys Ile Leu Gln Ser Glu Gly Val  
20 25 30  
Lys Gly Leu Trp Lys Gly Val Leu Pro Asn Ile Gln Arg Ala Phe Leu  
35 40 45  
Val Asn Met Gly Glu Leu Ala Cys Tyr Asp His Ala Lys His Phe Val  
50 55 60  
Ile Asp Lys Lys Ile Ala Glu Asp Asn Ile Phe Ala His Thr Leu Ala



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|----|
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     | 75  |  |  |  |  |  |  |  |  |  |  |  |  |  | 80 |
| Ser | Ile | Met | Ser | Gly | Leu | Ala | Ser | Thr | Ser | Leu | Ser | Cys | Pro | Ala | Asp |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Val | Val | Lys | Thr | Arg | Met | Met | Asn | Gln | Gly | Glu | Asn | Ala | Val | Tyr | Arg |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Asn | Ser | Tyr | Asp | Cys | Leu | Val | Lys | Thr | Val | Lys | Phe | Glu | Gly | Ile | Arg |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Ala | Leu | Trp | Lys | Gly | Phe | Phe | Pro | Thr | Trp | Ala | Arg | Leu | Gly | Pro | Trp |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Gln | Phe | Val | Phe | Trp | Val | Ser | Tyr | Glu | Lys | Phe | Arg | Leu | Leu | Ala | Gly |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Ile | Ser | Ser | Phe |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| acaagagcca | tttgcaatta  | ggcataatat | atgtcctaac  | tcaccaaccc | cctcaaaatt | 60   |
| gccaccaact | tcaaattttct | ctccttttaa | cctttctcaa  | tcacttttct | tctgccttgg | 120  |
| aatcctgac  | atggcgctct  | ctctcacttc | caaatccatt  | ctcgatcca  | caaaccocgg | 180  |
| ttcttcttct | cttccctcgg  | agctccgctg | tctttcttct  | cccgcgcttc | agatctctct | 240  |
| ccgtacccaa | accaggaaga  | acttccagat | acaagctact  | ggaagtcat  | atgggactca | 300  |
| ttttcgagtt | tcaacttttg  | gagaatcaca | tggaggagga  | gttggttgta | tcattgatgg | 360  |
| ttgtcctcct | cgtattccac  | ttactgaatc | tgatttgcaa  | ttcgatctcg | atagaaggag | 420  |
| acctggtcag | agcaggatca  | caactcctag | aaaggagact  | gatacttgcc | ggatatcttc | 480  |
| tggagtctcc | gaaggaatga  | cgacaggaac | acctatccat  | gtgtttgtgc | ctaacacaga | 540  |
| tcagagagga | cttgattaca  | gtgaaatgtc | ggttgccctat | agaccatcgc | atgctgatgc | 600  |
| aacttatgac | atgaagtatg  | gtgtcagatc | agtgcagggt  | ggaggaagat | cttcagctag | 660  |
| agagaccatt | ggaagagttg  | ctcctggagc | tttggccaag  | aaaattttga | agcaatttgc | 720  |
| aggaactgag | attccttgcc  | atgtctcgca | agttcaccat  | gttgacttct | cagaagaatt | 780  |
| ggtagaccac | gagaatttta  | cactcgaaca | gatagaaaat  | aacattgtca | gatgccctaa | 840  |
| tcccagtat  | gcggaaaaaga | tgatagctgc | gattgatgct  | gtcaggacaa | aagggaactc | 900  |
| tggttggtgg | gttggtgacct | gcattgttcg | gaatgctcca  | cgtgggcttg | gtacaccggg | 960  |
| tttcgataaa | cttgaagcag  | aactggcaaa | agcttgatg   | tcgttacctg | caacaaaggg | 1020 |
| atttgagttt | ggaagcggtc  | ttgcaggtag | ctttttgact  | ggtcctgaac | acaatgatga | 1080 |
| gttctatacc | gatgaaaatg  | gaagaatacg | taccagaaca  | aaccgatctg | gtggaattca | 1140 |
| gggaggggac | tcaaattggtg | aaataataaa | catgagagta  | gccttcaagc | caacatcaac | 1200 |
| aattggaagg | aagcagaata  | cggtaccag  | agacaaggta  | gaaaccgaaa | tgattgcgcg | 1260 |
| tggtcgtcat | gatccttggtg | ttgttcctcg | agctgtgcca  | atggtggaat | caatggtggc | 1320 |
| tttagttctt | gtggatcaat  | tgatggcgca | atacgacaaa  | tgccatttgt | ttccaataaa | 1380 |
| tccagagttg | caggaacctc  | tccagataga | gcagccccaa  | aatgctactg | ctttgtaagc | 1440 |
| aaaactcgag | aagataagag  | tcagagacag | taaggYttcg  | cttttggtgt | gtgattatta | 1500 |
| ttatgaataa | aaaaaatgtt  | aattttgtac | ccaccagaga  | aacaaaaaac | atgatttttt | 1560 |
| tgtaagagga | tttgcttcta  | tatcattatt | cagct       |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(D) OTHER INFORMATION: / Ceres Seq. ID 1569359

|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| Gln 1    | Glu 5    | Pro 10   | Phe 15   | Ala 20   | Ile 25   | Arg 30   | His 35   | Asn 40   | Ile 45   | Cys 50   | Pro 55   | Asn 60   | Ser 65   | Pro 70   | Thr 75   |
| Pro 80   | Ser 85   | Lys 90   | Leu 95   | Pro 100  | Pro 105  | Thr 110  | Ser 115  | Asn 120  | Phe 125  | Ser 130  | Pro 135  | Leu 140  | Asn 145  | Leu 150  | Ser 155  |
| Gln 160  | Ser 165  | Ser 170  | Phe 175  | Phe 180  | Cys 185  | Leu 190  | Gly 195  | Ile 200  | Leu 205  | Ile 210  | Met 215  | Ala 220  | Ser 225  | Ser 230  | Leu 235  |
| Thr 240  | Ser 245  | Lys 250  | Ser 255  | Ile 260  | Leu 265  | Gly 270  | Ser 275  | Thr 280  | Lys 285  | Pro 290  | Gly 295  | Ser 300  | Ser 305  | Ser 310  | Leu 315  |
| Pro 320  | Ser 325  | Glu 330  | Leu 335  | Arg 340  | Arg 345  | Leu 350  | Ser 355  | Ser 360  | Pro 365  | Ala 370  | Val 375  | Gln 380  | Ile 385  | Ser 390  | Leu 395  |
| Arg 400  | Thr 405  | Gln 410  | Thr 415  | Arg 420  | Lys 425  | Asn 430  | Phe 435  | Gln 440  | Ile 445  | Gln 450  | Ala 455  | Thr 460  | Gly 465  | Ser 470  | Ser 475  |
| Tyr 480  | Gly 485  | Thr 490  | His 495  | Phe 500  | Arg 505  | Val 510  | Ser 515  | Thr 520  | Phe 525  | Gly 530  | Glu 535  | Ser 540  | His 545  | Gly 550  | Gly 555  |
| Gly 560  | Val 565  | Gly 570  | Cys 575  | Ile 580  | Ile 585  | Asp 590  | Gly 595  | Cys 600  | Pro 605  | Pro 610  | Arg 615  | Ile 620  | Pro 625  | Leu 630  | Thr 635  |
| Glu 640  | Ser 645  | Asp 650  | Leu 655  | Gln 660  | Phe 665  | Asp 670  | Leu 675  | Asp 680  | Arg 685  | Arg 690  | Arg 695  | Pro 700  | Gly 705  | Gln 710  | Ser 715  |
| Arg 720  | Ile 725  | Thr 730  | Thr 735  | Pro 740  | Arg 745  | Lys 750  | Glu 755  | Thr 760  | Asp 765  | Thr 770  | Cys 775  | Arg 780  | Ile 785  | Ser 790  | Ser 795  |
| Gly 800  | Val 805  | Ser 810  | Glu 815  | Gly 820  | Met 825  | Thr 830  | Thr 835  | Gly 840  | Thr 845  | Pro 850  | Ile 855  | His 860  | Val 865  | Phe 870  | Val 875  |
| Pro 880  | Asn 885  | Thr 890  | Asp 895  | Gln 900  | Arg 905  | Gly 910  | Leu 915  | Asp 920  | Tyr 925  | Ser 930  | Glu 935  | Met 940  | Ser 945  | Val 950  | Ala 955  |
| Tyr 960  | Arg 965  | Pro 970  | Ser 975  | His 980  | Ala 985  | Asp 990  | Ala 995  | Thr 1000 | Tyr 1005 | Asp 1010 | Met 1015 | Lys 1020 | Tyr 1025 | Gly 1030 | Val 1035 |
| Arg 1040 | Ser 1045 | Val 1050 | Gln 1055 | Gly 1060 | Gly 1065 | Gly 1070 | Arg 1075 | Ser 1080 | Ser 1085 | Ala 1090 | Arg 1095 | Glu 1100 | Thr 1105 | Ile 1110 | Gly 1115 |
| Arg 1120 | Val 1125 | Ala 1130 | Pro 1135 | Gly 1140 | Ala 1145 | Leu 1150 | Ala 1155 | Lys 1160 | Lys 1165 | Ile 1170 | Leu 1175 | Lys 1180 | Gln 1185 | Phe 1190 | Ala 1195 |
| Gly 1200 | Thr 1205 | Glu 1210 | Ile 1215 | Leu 1220 | Ala 1225 | Tyr 1230 | Val 1235 | Ser 1240 | Gln 1245 | Val 1250 | His 1255 | His 1260 | Val 1265 | Val 1270 | Leu 1275 |
| Pro 1280 | Glu 1285 | Glu 1290 | Leu 1295 | Val 1300 | Asp 1305 | His 1310 | Glu 1315 | Asn 1320 | Leu 1325 | Thr 1330 | Leu 1335 | Glu 1340 | Gln 1345 | Ile 1350 | Glu 1355 |
| Asn 1360 | Asn 1365 | Ile 1370 | Val 1375 | Arg 1380 | Cys 1385 | Pro 1390 | Asn 1395 | Pro 1400 | Glu 1405 | Tyr 1410 | Ala 1415 | Glu 1420 | Lys 1425 | Met 1430 | Ile 1435 |
| Ala 1440 | Ala 1445 | Ile 1450 | Asp 1455 | Ala 1460 | Val 1465 | Arg 1470 | Thr 1475 | Lys 1480 | Gly 1485 | Asn 1490 | Ser 1495 | Val 1500 | Gly 1505 | Gly 1510 | Val 1515 |
| Val 1520 | Thr 1525 | Cys 1530 | Ile 1535 | Val 1540 | Arg 1545 | Asn 1550 | Ala 1555 | Pro 1560 | Arg 1565 | Gly 1570 | Leu 1575 | Gly 1580 | Thr 1585 | Pro 1590 | Val 1595 |
| Phe 1600 | Asp 1605 | Lys 1610 | Leu 1615 | Glu 1620 | Ala 1625 | Glu 1630 | Leu 1635 | Ala 1640 | Lys 1645 | Ala 1650 | Cys 1655 | Met 1660 | Ser 1665 | Leu 1670 | Pro 1675 |
| Ala 1680 | Thr 1685 | Lys 1690 | Gly 1695 | Phe 1700 | Glu 1705 | Phe 1710 | Gly 1715 | Ser 1720 | Gly 1725 | Phe 1730 | Ala 1735 | Gly 1740 | Thr 1745 | Phe 1750 | Leu 1755 |
| Thr 1760 | Gly 1765 | Leu 1770 | Glu 1775 | His 1780 | Asn 1785 | Asp 1790 | Glu 1795 | Phe 1800 | Tyr 1805 | Thr 1810 | Asp 1815 | Glu 1820 | Asn 1825 | Gly 1830 | Arg 1835 |
| Ile 1840 | Arg 1845 | Thr 1850 | Arg 1855 | Thr 1860 | Asn 1865 | Arg 1870 | Ser 1875 | Gly 18   |          |          |          |          |          |          |          |

Glu Pro Leu Gln Ile Glu Gln Pro Gln Asn Ala Thr Ala Leu  
465 470 475

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1569360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Leu | Thr | Ser | Lys | Ser | Ile | Leu | Gly | Ser | Thr | Lys | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ser | Ser | Ser | Leu | Pro | Ser | Glu | Leu | Arg | Arg | Leu | Ser | Ser | Pro | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Val | Gln | Ile | Ser | Leu | Arg | Thr | Gln | Thr | Arg | Lys | Asn | Phe | Gln | Ile | Gln |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Thr | Gly | Ser | Ser | Tyr | Gly | Thr | His | Phe | Arg | Val | Ser | Thr | Phe | Gly |
|     |     |     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Glu | Ser | His | Gly | Gly | Gly | Val | Gly | Cys | Ile | Ile | Asp | Gly | Cys | Pro | Pro |
| 65  |     |     |     |     |     |     |     | 70  |     |     | 75  |     |     | 80  |     |
| Arg | Ile | Pro | Leu | Thr | Glu | Ser | Asp | Leu | Gln | Phe | Asp | Leu | Asp | Arg | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |     |
| Arg | Pro | Gly | Gln | Ser | Arg | Ile | Thr | Thr | Pro | Arg | Lys | Glu | Thr | Asp | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |
| Cys | Arg | Ile | Ser | Ser | Gly | Val | Ser | Glu | Gly | Met | Thr | Thr | Gly | Thr | Pro |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |     |
| Ile | His | Val | Phe | Val | Pro | Asn | Thr | Asp | Gln | Arg | Gly | Leu | Asp | Tyr | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |     |
| Glu | Met | Ser | Val | Ala | Tyr | Arg | Pro | Ser | His | Ala | Asp | Ala | Thr | Tyr | Asp |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |     |
| Met | Lys | Tyr | Gly | Val | Arg | Ser | Val | Gln | Gly | Gly | Gly | Arg | Ser | Ser | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |     |
| Arg | Glu | Thr | Ile | Gly | Arg | Val | Ala | Pro | Gly | Ala | Leu | Ala | Lys | Lys | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 190 |     |
| Leu | Lys | Gln | Phe | Ala | Gly | Thr | Glu | Ile | Leu | Ala | Tyr | Val | Ser | Gln | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 205 |     |
| His | His | Val | Val | Leu | Pro | Glu | Glu | Leu | Val | Asp | His | Glu | Asn | Leu | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 220 |     |
| Leu | Glu | Gln | Ile | Glu | Asn | Asn | Ile | Val | Arg | Cys | Pro | Asn | Pro | Glu | Tyr |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     | 240 |     |
| Ala | Glu | Lys | Met | Ile | Ala | Ala | Ile | Asp | Ala | Val | Arg | Thr | Lys | Gly | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 255 |     |
| Ser | Val | Gly | Gly | Val | Val | Thr | Cys | Ile | Val | Arg | Asn | Ala | Pro | Arg | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 270 |     |
| Leu | Gly | Thr | Pro | Val | Phe | Asp | Lys | Leu | Glu | Ala | Glu | Leu | Ala | Lys | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 285 |     |
| Cys | Met | Ser | Leu | Pro | Ala | Thr | Lys | Gly | Phe | Glu | Phe | Gly | Ser | Gly | Phe |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 300 |     |
| Ala | Gly | Thr | Phe | Leu | Thr | Gly | Leu | Glu | His | Asn | Asp | Glu | Phe | Tyr | Thr |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     | 320 |     |
| Asp | Glu | Asn | Gly | Arg | Ile | Arg | Thr | Arg | Thr | Asn | Arg | Ser | Gly | Gly | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 335 |     |
| Gln | Gly | Gly | Ile | Ser | Asn | Gly | Glu | Ile | Ile | Asn | Met | Arg | Val | Ala | Phe |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 350 |     |
| Lys | Pro | Thr | Ser | Thr | Ile | Gly | Arg | Lys | Gln | Asn | Thr | Val | Thr | Arg | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 365 |     |
| Lys | Val | Glu | Thr | Glu | Met | Ile | Ala | Arg | Gly | Arg | His | Asp | Pro | Cys | Val |

370 375 380  
Val Pro Arg Ala Val Pro Met Val Glu Ser Met Val Ala Leu Val Leu  
385 390 395 400  
Val Asp Gln Leu Met Ala Gln Tyr Ala Gln Cys His Leu Phe Pro Ile  
405 410 415  
Asn Pro Glu Leu Gln Glu Pro Leu Gln Ile Glu Gln Pro Gln Asn Ala  
420 425 430  
Thr Ala Leu  
435

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1569361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

Met Thr Thr Gly Thr Pro Ile His Val Phe Val Pro Asn Thr Asp Gln  
1 5 10 15  
Arg Gly Leu Asp Tyr Ser Glu Met Ser Val Ala Tyr Arg Pro Ser His  
20 25 30  
Ala Asp Ala Thr Tyr Asp Met Lys Tyr Gly Val Arg Ser Val Gln Gly  
35 40 45  
Gly Gly Arg Ser Ser Ala Arg Glu Thr Ile Gly Arg Val Ala Pro Gly  
50 55 60  
Ala Leu Ala Lys Lys Ile Leu Lys Gln Phe Ala Gly Thr Glu Ile Leu  
65 70 75 80  
Ala Tyr Val Ser Gln Val His His Val Val Leu Pro Glu Glu Leu Val  
85 90 95  
Asp His Glu Asn Leu Thr Leu Glu Gln Ile Glu Asn Asn Ile Val Arg  
100 105 110  
Cys Pro Asn Pro Glu Tyr Ala Glu Lys Met Ile Ala Ala Ile Asp Ala  
115 120 125  
Val Arg Thr Lys Gly Asn Ser Val Gly Gly Val Val Thr Cys Ile Val  
130 135 140  
Arg Asn Ala Pro Arg Gly Leu Gly Thr Pro Val Phe Asp Lys Leu Glu  
145 150 155 160  
Ala Glu Leu Ala Lys Ala Cys Met Ser Leu Pro Ala Thr Lys Gly Phe  
165 170 175  
Glu Phe Gly Ser Gly Phe Ala Gly Thr Phe Leu Thr Gly Leu Glu His  
180 185 190  
Asn Asp Glu Phe Tyr Thr Asp Glu Asn Gly Arg Ile Arg Thr Arg Thr  
195 200 205  
Asn Arg Ser Gly Gly Ile Gln Gly Gly Ile Ser Asn Gly Glu Ile Ile  
210 215 220  
Asn Met Arg Val Ala Phe Lys Pro Thr Ser Thr Ile Gly Arg Lys Gln  
225 230 235 240  
Asn Thr Val Thr Arg Asp Lys Val Glu Thr Glu Met Ile Ala Arg Gly  
245 250 255  
Arg His Asp Pro Cys Val Val Pro Arg Ala Val Pro Met Val Glu Ser  
260 265 270  
Met Val Ala Leu Val Leu Val Asp Gln Leu Met Ala Gln Tyr Ala Gln  
275 280 285  
Cys His Leu Phe Pro Ile Asn Pro Glu Leu Gln Glu Pro Leu Gln Ile  
290 295 300  
Glu Gln Pro Gln Asn Ala Thr Ala Leu  
305 310

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(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..925
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| acaacccaaaa | acaagaacaa | cagacacata | gagatgagcc | gctgaggctc | tcttgggctc  | 60  |
| tatgccccaa  | atgctttgcc | atctctctcc | ttgaagccac | gcagtttcaa | atctcctttc  | 120 |
| tgtattacat  | ctcacaccaa | acccaacgac | actcttcttc | ataatgttaa | caagatgaga  | 180 |
| gcaaaggcct  | gtgatatact | tggagcaaag | aagacaatct | tggcagctca | actcggggca  | 240 |
| gttcttgcca  | cgattgacca | tccagcctta | gcaataacag | gagttaacaa | ccagcaggaa  | 300 |
| ttgagcagtg  | ttgtgctcga | tatcgggata | atatccgttt | ggtacttcct | agtaatgccca | 360 |
| ccaatcatca  | tgaactggct | aagagtaaga | tggtacagaa | ggaagattag | aacttgcaaa  | 420 |
| aaatggcttc  | caaggctttg | attctgttag | gtctcttctc | agttcttctc | gtcgtctccg  | 480 |
| aagtgtctgc  | cgcaaggCaa | Wtcgggcatg | gtgaagcCag | agagtGagg  | aaactgtgca  | 540 |
| Acctgaaggt  | tatggcggtr | gScCacggag | gacatggtgg | tcacggaggg | ggaggaggcc  | 600 |
| acggacatgg  | aggacacaac | ggaggagggg | gccacggact | tgacggatac | ggaggagggtg | 660 |
| gaggacacta  | tggaggaggt | ggaggacact | acggaggagg | tggaggacac | tacggaggag  | 720 |
| gtggaggaca  | ctacggagga | ggtggtggag | gacacggagg | tggaggacac | tacggagggtg | 780 |
| gtggaggagg  | atacggaggt | ggaggaggac | accacggagg | aggaggccac | gggctaaacg  | 840 |
| aacctgttca  | gactaagccg | ggtgtttaa  | actatataat | atcttcacta | ccatgcatga  | 900 |
| ttgcatatat  | atatatacgs | ttatg      |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Lys | Asn | Lys | Asn | Asn | Arg | His | Ile | Glu | Met | Ser | Arg | Cys | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Gly | Leu | Tyr | Ala | Pro | Asn | Ala | Leu | Pro | Ser | Leu | Ser | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Pro | Arg | Ser | Phe | Lys | Ser | Pro | Phe | Cys | Ile | Thr | Ser | His | Thr | Lys | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asp | Thr | Leu | Leu | His | Asn | Val | Asn | Lys | Met | Arg | Ala | Lys | Ala | Cys |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ile | Leu | Gly | Ala | Lys | Lys | Thr | Ile | Leu | Ala | Ala | Gln | Leu | Gly | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Leu | Ala | Thr | Ile | Asp | His | Pro | Ala | Leu | Ala | Ile | Thr | Gly | Val | Asn |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Gln | Gln | Glu | Leu | Ser | Ser | Val | Val | Leu | Asp | Ile | Gly | Ile | Ile | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Val | Trp | Tyr | Phe | Leu | Val | Met | Pro | Pro | Ile | Ile | Met | Asn | Trp | Leu | Arg |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Val | Arg | Trp | Tyr | Arg | Arg | Lys | Ile | Arg | Thr | Cys | Lys | Lys | Trp | Leu | Pro |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1228:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 135 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..135  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569372  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

Met Ser Arg Cys Gly Ser Leu Gly Leu Tyr Ala Pro Asn Ala Leu Pro  
1                    5                    10                    15  
Ser Leu Ser Leu Lys Pro Arg Ser Phe Lys Ser Pro Phe Cys Ile Thr  
                    20                    25                    30  
Ser His Thr Lys Pro Asn Asp Thr Leu Leu His Asn Val Asn Lys Met  
                    35                    40                    45  
Arg Ala Lys Ala Cys Asp Ile Leu Gly Ala Lys Lys Thr Ile Leu Ala  
50                    55                    60  
Ala Gln Leu Gly Ala Val Leu Ala Thr Ile Asp His Pro Ala Leu Ala  
65                    70                    75                    80  
Ile Thr Gly Val Asn Asn Gln Gln Glu Leu Ser Ser Val Val Leu Asp  
                    85                    90                    95  
Ile Gly Ile Ile Ser Val Trp Tyr Phe Leu Val Met Pro Pro Ile Ile  
                    100                    105                    110  
Met Asn Trp Leu Arg Val Arg Trp Tyr Arg Arg Lys Ile Arg Thr Cys  
115                    120                    125  
Lys Lys Trp Leu Pro Arg Leu  
130                    135

- (2) INFORMATION FOR SEQ ID NO:1229:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 148 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..148  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1569373  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu  
1                    5                    10                    15  
Val Val Ser Glu Val Ser Ala Ala Arg Gln Xaa Gly His Gly Glu Ala  
                    20                    25                    30  
Arg Glu Trp Arg Lys Leu Cys Asn Leu Lys Val Met Ala Xaa Xaa His  
35                    40                    45  
Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly His Gly Gly  
50                    55                    60  
His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly Gly  
65                    70                    75                    80  
Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His  
                    85                    90                    95  
Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Gly  
100                    105                    110  
Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr Gly Gly Gly Gly  
115                    120                    125  
Gly His His Gly Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr  
130                    135                    140  
Lys Pro Gly Val  
145

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

(2) INFORMATION FOR SEQ ID NO:1231:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

(2) INFORMATION FOR SEQ ID NO:1232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1569380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

Met Ser Pro Thr Thr Thr Ser Leu Arg Ser Leu Ser Phe Ser Leu Tyr  
1 5 10 15  
Ala Ser Ser Asn Ser Thr Pro Ile Ser Thr Pro Ile Glu Ala Arg Gln  
20 25 30  
Leu Leu Ser Ser Cys Ser Arg Phe Tyr Gly Leu Ser Ser Ser Ser  
35 40 45  
Ser Ser Ser Leu Thr Thr Ser Ser Leu Ile Gly Asn Leu Val Phe Ser  
50 55 60  
Ser Arg Asn Gln Ser Leu Ser Val Lys Val Gln Ala Leu Xaa Leu Lys  
65 70 75 80  
Pro Asn Ser Gln Asn Gly Gly Arg Gly Lys Gln Gly Gln Thr  
85 90

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1569381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

Met Ile Asp Ile Thr Ser Ala Glu Gln Phe Leu Asn Ala Leu Lys Asp  
1 5 10 15  
Ala Gly Asp Arg Leu Val Ile Val Asp Phe Tyr Gly Thr Trp Cys Gly  
20 25 30  
Ser Cys Arg Ala Met Phe Pro Lys Leu Cys Lys Thr Ala Lys Glu His  
35 40 45  
Pro Asp Ile Leu Phe Leu Lys Val Asn Phe Asp Glu Asn Lys Ser Leu  
50 55 60  
Cys Lys Ser Leu Asn Val Lys Val Leu Pro Tyr Phe His Phe Tyr Arg  
65 70 75 80  
Gly Ala Asp Gly Gln Val Glu Ser Phe Ser Cys Ser Leu Ala Lys Phe  
85 90 95  
Gln Lys Leu Arg Glu Ala Ile Glu Arg His Asn Val Gly Ser Ile Ser  
100 105 110  
Asn Ile Ser Ser Ser Ala Ser Glu Lys Val Glu Asp Ser Ser Glu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1569385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

atatactttc tctgtttaca ttctcgtttc cgaggagaaa agtctcgatc ttctggatct 60  
ggggtttggg ttggtttggg gttgactcgg ttttgactcg ggacaagtcg tctcgtgaga 120  
tggatgtctc tcgtttatta gtatctcttt gagagtctgt ctttctgggt tcaatagatt 180  
cttatagttt cgcttagaaa cagcacaaa aagatgtcgt tgaagcatca tcacagagga 240  
ttagagctct ctgcttcgaa gagttttgtc tcaaagaaat ggactttatt tctctgtatc 300  
ggtttcttct gcgcaggaat tctcttctcc gacagaatgt ggccagagcc tgaatccaat 360



gttgtatcaa gggacacagt agcatcagat gaacggctgc ggtagagtc tgaggactgt 420  
gattcatcaa aaaagggttt taaagcgtga atcgaaagac atccttggag atgtttacaa 480  
gagtcagat gcaattcaaa cgcttgataa aacgatttca aagctggaaa cagaactggc 540  
cgatgcaaga gctgcgcaag aatctatcat gaatggttca ccagtttctg atgactttaa 600  
gctccctgaa actgtcacta aaagaaagta tctgatgggt gttgggtgta atactgcgtt 660  
tagcagcaga aagcgcaggg attcagtcgg tgctacttgg atgcctcccg gtgaggagag 720  
aaagaagctc gaggaagaga aagggatcgt gatgcggttt gtgataggcc atagttctac 780  
tcccgggtgga attcttgata gagcgattca ggctgaagaa agtaaacadg gagacttctt 840  
gaggctggat catgttgaag gttatctcga gctgtcagca aagactaaaa cttactttac 900  
cacggctttt gcaatgtggg atgcagactt ctacgtcaaa gtcgatgatg atgtgcatgt 960  
aaatatagcc acgcttggag cagaattagc aagataccgg atgaagccc gagtgtacat 1020  
tggttgcatg aaatctggac ctgttcttgc tcagaaagga gtgagatata atgaaccgga 1080  
atactggaaa tttggagaag agggtaacaa atacttccgc catgccacag gtcagctcta 1140  
tgcaatatcc agggagttgg cgtcttcat atcgataaac caaaacgtac ttcacaaata 1200  
tgtgaatgaa gatgtctctt taggatcatg gtttcttggg ttagatgtgg agcatgtaga 1260  
tgaccgtagg ctatgtttgt gtacaacaga ttgtgagtg aaggcgcagg cgggcaacat 1320  
ctgtgttgcc tcgttcgatt ggagctgcag tgggatttgt agatcagcgg ataggatgaa 1380  
ggatgttcat cgtaggtgtg gagaaggtga aaaggccctt ctggctgcat ctttctgaaA 1440  
cacaataact aaagaaacac attgaggaag aagagtacag agacaaatcc gtcgacagt 1500  
ctacacttgg tagtatagac acacagtcaa actctctcta tatatgtatg tatgtatgta 1560  
tgtatgtatc ttgtgaactg agatgagaag ggtgcttttt gccctccttt cttgtttctt 1620  
tatgcttttc tcaattctct gaaggtctgg agttctttgc acacagaaaa tgcagatttt 1680  
agctgcaaag gcgactcca tgagtgcacc ttcagagtca tttcattgag gcgttttctc 1740  
tgccctttga gcttttcttc ttcatttctt tttggatttt gcctattttg ttcatttttt 1800  
cctttgccat gattgtggtg aaacatgggt tgtttatgtg tgtacttgaa acgc

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1569386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Ser | Val | Ser | Asp | Asp | Phe | Lys | Leu | Pro | Glu | Thr | Val |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Lys | Arg | Lys | Tyr | Leu | Met | Val | Val | Gly | Val | Asn | Thr | Ala | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     | Ser |
| Ser | Arg | Lys | Arg | Arg | Asp | Ser | Val | Arg | Ala | Thr | Trp | Met | Pro | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     | Gly |
| Glu | Glu | Arg | Lys | Lys | Leu | Glu | Glu | Lys | Gly | Ile | Val | Met | Arg | Phe |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Val | Ile | Gly | His | Ser | Ser | Thr | Pro | Gly | Gly | Ile | Leu | Asp | Arg | Ala |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Gln | Ala | Glu | Glu | Ser | Lys | His | Gly | Asp | Phe | Leu | Arg | Leu | Asp | His |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |
| Glu | Gly | Tyr | Leu | Glu | Leu | Ser | Ala | Lys | Thr | Lys | Thr | Tyr | Phe | Thr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 | Thr |
| Ala | Phe | Ala | Met | Trp | Asp | Ala | Asp | Phe | Tyr | Val | Lys | Val | Asp | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 | Asp |
| Val | His | Val | Asn | Ile | Ala | Thr | Leu | Gly | Ala | Glu | Leu | Ala | Arg | Tyr |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     | Arg |
| Met | Lys | Pro | Arg | Val | Tyr | Ile | Gly | Cys | Met | Lys | Ser | Gly | Pro | Val |
|     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     | 160 |
| Ala | Gln | Lys | Gly | Val | Arg | Tyr | His | Glu | Pro | Glu | Tyr | Trp | Lys | Phe |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |
| Glu | Glu | Gly | Asn | Lys | Tyr | Phe | Arg | His | Ala | Thr | Gly | Gln | Leu | Tyr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 | Ala |

(2) INFORMATION FOR SEQ ID NO:1236:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1569387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

(2) INFORMATION FOR SEQ ID NO:1237:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 245 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..245  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569388  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

Met Pro Pro Gly Glu Glu Arg Lys Lys Leu Glu Glu Glu Lys Gly Ile  
1                  5                  10                  15  
Val Met Arg Phe Val Ile Gly His Ser Ser Thr Pro Gly Gly Ile Leu  
                  20                  25                  30  
Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys His Gly Asp Phe Leu Arg  
                  35                  40                  45  
Leu Asp His Val Glu Gly Tyr Leu Glu Leu Ser Ala Lys Thr Lys Thr  
                  50                  55                  60  
Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp Ala Asp Phe Tyr Val Lys  
65                  70                  75                  80  
Val Asp Asp Asp Val His Val Asn Ile Ala Thr Leu Gly Ala Glu Leu  
                  85                  90                  95  
Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr Ile Gly Cys Met Lys Ser  
                  100                 105                 110  
Gly Pro Val Leu Ala Gln Lys Gly Val Arg Tyr His Glu Pro Glu Tyr  
                  115                 120                 125  
Trp Lys Phe Gly Glu Glu Gly Asn Lys Tyr Phe Arg His Ala Thr Gly  
130                 135                 140  
Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn  
145                 150                 155                 160  
Gln Asn Val Leu His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser  
                  165                 170                 175  
Trp Phe Leu Gly Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys  
                  180                 185                 190  
Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys  
195                 200                 205  
Val Ala Ser Phe Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp  
210                 215                 220  
Arg Met Lys Asp Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu  
225                 230                 235                 240  
Leu Ala Ala Ser Phe  
                  245

(2) INFORMATION FOR SEQ ID NO:1238:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 889 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..889  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569392  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

aaaggttcct tctgtttcca gacaaagaaa acacaaattc attccctcct cctcttcac 60  
tcttttgcag atatggatgg ttattattct ctgtctccca tctctgtcct ccaccggatt 120  
aaagattcct tccatttcgc cgtctctgcc ctctctgcca acctcttctc cgctctcttc 180  
accttcttct tcgctttagg ggctttgatc ggccaagaaa cagagagcgg ttatcatcaga 240  
ggagccgcgc ttggtgctat ctcaggcgcc gtcttctcca tcgaagtctt tgaatcttcc 300  
ctcctccttt ggcaatccga tgagtctgga attggatgcc ttctctactt gccttttgag 360

cgaggaggctt gttcgtgagc gtatcgggtcc tgcaatgcta agtgccggtcc agagtcagat 420  
gggagctgtg gaggctccagt tccaagatca tacagacatc tttgacactg ccatttcaaa 480  
gggtctcact ggggactctc tcaacaggat ccctaagggtc cgaatcacag acacctctcc 540  
ggagattgtc tcttgctctg tctgccttca ggactttcag gtgggagaga cagttagaag 600  
tttgccgcac tgccatcata tgttccacct accatgcac gacaaatggC ttgcgaggca 660  
tgcttcttgt cccttggtgca gaagacatct ttgaattgat tttgaactct tctttcttct 720  
cttctttgta catgaggtat aggcatacac acacacacat atatacacac tagtagtctt 780  
ccttgatttt ttttagatta caggttacac agattttgat gcaccaatca ttgtaacttc 840  
actcatctct tggagatcct gtttatttat gctacttatt cttgggtcc

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1569393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

Lys Gly Ser Phe Cys Phe Gln Thr Lys Lys Thr Gln Ile His Ser Leu  
1 5 10 15  
Leu Leu Phe Ile Ser Phe Ala Asp Met Asp Gly Tyr Tyr Ser Leu Ser  
20 25 30  
Pro Ile Ser Val Leu His Arg Ile Lys Asp Ser Phe His Phe Ala Val  
35 40 45  
Ser Ala Leu Leu Ala Asn Leu Phe Ser Ala Leu Phe Thr Phe Phe Phe  
50 55 60  
Ala Leu Gly Ala Leu Ile Gly Gln Glu Thr Glu Ser Gly Phe Ile Arg  
65 70 75 80  
Gly Ala Ala Val Gly Ala Ile Ser Gly Ala Val Phe Ser Ile Glu Val  
85 90 95  
Phe Glu Ser Ser Leu Leu Leu Trp Gln Ser Asp Glu Ser Gly Ile Gly  
100 105 110  
Cys Leu Leu Tyr Leu Pro Phe Glu Arg Glu Ala Cys Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1569394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met Asp Gly Tyr Tyr Ser Leu Ser Pro Ile Ser Val Leu His Arg Ile  
1 5 10 15  
Lys Asp Ser Phe His Phe Ala Val Ser Ala Leu Leu Ala Asn Leu Phe  
20 25 30  
Ser Ala Leu Phe Thr Phe Phe Phe Ala Leu Gly Ala Leu Ile Gly Gln  
35 40 45  
Glu Thr Glu Ser Gly Phe Ile Arg Gly Ala Ala Val Gly Ala Ile Ser  
50 55 60  
Gly Ala Val Phe Ser Ile Glu Val Phe Glu Ser Ser Leu Leu Leu Trp  
65 70 75 80  
Gln Ser Asp Glu Ser Gly Ile Gly Cys Leu Leu Tyr Leu Pro Phe Glu  
85 90 95

Arg Glu Ala Cys Ser  
100

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

Met Ser Leu Glu Leu Asp Ala Phe Ser Thr Cys Leu Leu Ser Gly Arg  
1 5 10 15  
Leu Val Arg Glu Arg Ile Gly Pro Ala Met Leu Ser Ala Val Gln Ser  
20 25 30  
Gln Met Gly Ala Val Glu Ser Gln Phe Gln Asp His Thr Asp Ile Phe  
35 40 45  
Asp Thr Ala Ile Ser Lys Gly Leu Thr Gly Asp Ser Leu Asn Arg Ile  
50 55 60  
Pro Lys Val Arg Ile Thr Asp Thr Ser Pro Glu Ile Val Ser Cys Ser  
65 70 75 80  
Val Cys Leu Gln Asp Phe Gln Val Gly Glu Thr Val Arg Ser Leu Pro  
85 90 95  
His Cys His His Met Phe His Leu Pro Cys Ile Asp Lys Trp Leu Arg  
100 105 110  
Arg His Ala Ser Cys Pro Leu Cys Arg Arg His Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1580
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

aataggttca gtgtttctga catattgttc cctctctgaa tgaaactctc ccaaatagag 60  
aatggcctaa ccacctatcc aaccgcacatc aggcacttgg tttcatcccc ttgatttctc 120  
tctttttttc ttttccctatc gcaggatttt gtgttcttgt tttgaatatg aaatgttcgt 180  
cgatgtgttg tttgatcctc ttggcccttt ctctctcac cgccttcact cttgcttctt 240  
cgtcaaatgg tatagatgga cctttctacg actctactgc ctacacagag tgtagagccg 300  
aagcagagaa gccactatac aatggaggaa tgctgaagga ccaaaagcct tccgtcccag 360  
gcaaagactc tctcacaggc attggtgctc gttacacacc aacttacata ttgcacaatc 420  
tcacacagaa caccatctat tgcttctcca tatgggtgaa gatagaggct ggtgctgcat 480  
cagctcatgt aagagcaagg ctgagagcag acaacgccac attaaactgc gtcggttctg 540  
taactgccaa acatggttgc tgggtctttcc tcaaaggagg attccttctt gattctcctt 600  
gtaaacaatc catcctcttc tttgagacat cacaggaaga tggttaagatc caattacaag 660  
tgacgagtgc ctctcttcag ccattcacgc aggagcaatg gaggaacaac caagattact 720  
tcataaatatc cgcgagaaaa cgagcagtga caattcacgt gtcaaaagaa aacggagaga 780  
gcgttgaagg agcagaggtg acagtagagc agatctctaa agacttctcc attggttctg 840  
ccatctccaa aactatcctt ggaacattc cttaccaaga atggttcgtc aagagattcg 900  
acgccacggt attcgagaac gagctgaaat ggtacgcgac ggagcccgat caaggcaaac 960  
tcaactacac attggctgat aagatgatga atttcgtcag agccaacaga atcatcgctc 1020  
gcggtcacaa catattctgg gaggatccca aatacaatcc cgattgggtt cgtaattctaa 1080  
ccggcgaa ga tctccggtcg gcggttaacc ggcgaaatcaa gagtctgatg actcggtaca 1140

gaggagagtt cgtgcattgg gacgtgagca acgagatgct tcactttgac ttctacgaga 1200  
ctcgactggg gaagaacgcg tcgtacggat tcttcgccgc ggctcgtgag attgactcat 1260  
tggcgactct gttcttcaat gatttcaacg tgggtggagac ttgcagcgac gagaagtcaa 1320  
cggttgacga atacatcgcg aggttgaggg aactccaacg gtacgacggc gtaaggatgg 1380  
acggaatagg tctcgagggt cacttcacga cgccaaacgt agcgtgatg agagccatcc 1440  
tcgataaacT cgcKtacgct ccagctccca atctggctca ccgagattga tatcagcagc 1500  
agcctcgacc accgctctca ggcgatttat ttggagcaag tgttacgtga aggattctcg 1560  
cacccatcgg taaacgggtat

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..440

(D) OTHER INFORMATION: / Ceres Seq. ID 1569404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

Met Lys Cys Ser Ser Met Cys Cys Leu Ile Leu Leu Ala Leu Ser Leu  
1 5 10 15  
Leu Thr Ala Phe Thr Leu Ala Ser Ser Ser Asn Gly Ile Asp Gly Pro  
20 25 30  
Phe Tyr Asp Ser Thr Ala Tyr Thr Glu Cys Arg Ala Glu Ala Glu Lys  
35 40 45  
Pro Leu Tyr Asn Gly Gly Met Leu Lys Asp Gln Lys Pro Ser Val Pro  
50 55 60  
Gly Lys Asp Ser Leu Thr Gly Ile Gly Ala Arg Tyr Thr Pro Thr Tyr  
65 70 75 80  
Ile Leu His Asn Leu Thr Gln Asn Thr Ile Tyr Cys Phe Ser Ile Trp  
85 90 95  
Val Lys Ile Glu Ala Gly Ala Ala Ser Ala His Val Arg Ala Arg Leu  
100 105 110  
Arg Ala Asp Asn Ala Thr Leu Asn Cys Val Gly Ser Val Thr Ala Lys  
115 120 125  
His Gly Cys Trp Ser Phe Leu Lys Gly Gly Phe Leu Leu Asp Ser Pro  
130 135 140  
Cys Lys Gln Ser Ile Leu Phe Phe Glu Thr Ser Glu Asp Asp Gly Lys  
145 150 155 160  
Ile Gln Leu Gln Val Thr Ser Ala Ser Leu Gln Pro Phe Thr Gln Glu  
165 170 175  
Gln Trp Arg Asn Asn Gln Asp Tyr Phe Ile Asn Thr Ala Arg Lys Arg  
180 185 190  
Ala Val Thr Ile His Val Ser Lys Glu Asn Gly Glu Ser Val Glu Gly  
195 200 205  
Ala Glu Val Thr Val Glu Gln Ile Ser Lys Asp Phe Ser Ile Gly Ser  
210 215 220  
Ala Ile Ser Lys Thr Ile Leu Gly Asn Ile Pro Tyr Gln Glu Trp Phe  
225 230 235 240  
Val Lys Arg Phe Asp Ala Thr Val Phe Glu Asn Glu Leu Lys Trp Tyr  
245 250 255  
Ala Thr Glu Pro Asp Gln Gly Lys Leu Asn Tyr Thr Leu Ala Asp Lys  
260 265 270  
Met Met Asn Phe Val Arg Ala Asn Arg Ile Ile Ala Arg Gly His Asn  
275 280 285  
Ile Phe Trp Glu Asp Pro Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu  
290 295 300  
Thr Gly Glu Asp Leu Arg Ser Ala Val Asn Arg Arg Ile Lys Ser Leu  
305 310 315 320  
Met Thr Arg Tyr Arg Gly Glu Phe Val His Trp Asp Val Ser Asn Glu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Cys | Leu | Ile | Leu | Leu | Ala | Leu | Ser | Leu | Leu | Thr | Ala | Phe | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Ser | Ser | Ser | Asn | Gly | Ile | Asp | Gly | Pro | Phe | Tyr | Asp | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Tyr | Thr | Glu | Cys | Arg | Ala | Glu | Ala | Glu | Lys | Pro | Leu | Tyr | Asn | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Met | Leu | Lys | Asp | Gln | Lys | Pro | Ser | Val | Pro | Gly | Lys | Asp | Ser | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gly | Ile | Gly | Ala | Arg | Tyr | Thr | Pro | Thr | Tyr | Ile | Leu | His | Asn | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Gln | Asn | Thr | Ile | Tyr | Cys | Phe | Ser | Ile | Trp | Val | Lys | Ile | Glu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ala | Ala | Ser | Ala | His | Val | Arg | Ala | Arg | Leu | Arg | Ala | Asp | Asn | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Leu | Asn | Cys | Val | Gly | Ser | Val | Thr | Ala | Lys | His | Gly | Cys | Trp | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Leu | Lys | Gly | Gly | Phe | Leu | Leu | Asp | Ser | Pro | Cys | Lys | Gln | Ser | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Phe | Phe | Glu | Thr | Ser | Glu | Asp | Asp | Gly | Lys | Ile | Gln | Leu | Gln | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Ser | Ala | Ser | Leu | Gln | Pro | Phe | Thr | Gln | Glu | Gln | Trp | Arg | Asn | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asp | Tyr | Phe | Ile | Asn | Thr | Ala | Arg | Lys | Arg | Ala | Val | Thr | Ile | His |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Val | Ser | Lys | Glu | Asn | Gly | Glu | Ser | Val | Glu | Gly | Ala | Glu | Val | Thr | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Gln | Ile | Ser | Lys | Asp | Phe | Ser | Ile | Gly | Ser | Ala | Ile | Ser | Lys | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Leu | Gly | Asn | Ile | Pro | Tyr | Gln | Glu | Trp | Phe | Val | Lys | Arg | Phe | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Thr | Val | Phe | Glu | Asn | Glu | Leu | Lys | Trp | Tyr | Ala | Thr | Glu | Pro | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Gly | Lys | Leu | Asn | Tyr | Thr | Leu | Ala | Asp | Lys | Met | Met | Asn | Phe | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

Arg Ala Asn Arg Ile Ile Ala Arg Gly His Asn Ile Phe Trp Glu Asp  
275 280 285  
Pro Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu Thr Gly Glu Asp Leu  
290 295 300  
Arg Ser Ala Val Asn Arg Arg Ile Lys Ser Leu Met Thr Arg Tyr Arg  
305 310 315 320  
Gly Glu Phe Val His Trp Asp Val Ser Asn Glu Met Leu His Phe Asp  
325 330 335  
Phe Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser Tyr Gly Phe Phe Ala  
340 345 350  
Ala Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu Phe Phe Asn Asp Phe  
355 360 365  
Asn Val Val Glu Thr Cys Ser Asp Glu Lys Ser Thr Val Asp Glu Tyr  
370 375 380  
Ile Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp Gly Val Arg Met Asp  
385 390 395 400  
Gly Ile Gly Leu Glu Gly His Phe Thr Thr Pro Asn Val Ala Leu Met  
405 410 415  
Arg Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro Ala Pro Asn Leu Ala  
420 425 430  
His Arg Asp  
435

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Leu Lys Asp Gln Lys Pro Ser Val Pro Gly Lys Asp Ser Leu Thr  
1 5 10 15  
Gly Ile Gly Ala Arg Tyr Thr Pro Thr Tyr Ile Leu His Asn Leu Thr  
20 25 30  
Gln Asn Thr Ile Tyr Cys Phe Ser Ile Trp Val Lys Ile Glu Ala Gly  
35 40 45  
Ala Ala Ser Ala His Val Arg Ala Arg Leu Arg Ala Asp Asn Ala Thr  
50 55 60  
Leu Asn Cys Val Gly Ser Val Thr Ala Lys His Gly Cys Trp Ser Phe  
65 70 75 80  
Leu Lys Gly Gly Phe Leu Leu Asp Ser Pro Cys Lys Gln Ser Ile Leu  
85 90 95  
Phe Phe Glu Thr Ser Glu Asp Asp Gly Lys Ile Gln Leu Gln Val Thr  
100 105 110  
Ser Ala Ser Leu Gln Pro Phe Thr Gln Glu Gln Trp Arg Asn Asn Gln  
115 120 125  
Asp Tyr Phe Ile Asn Thr Ala Arg Lys Arg Ala Val Thr Ile His Val  
130 135 140  
Ser Lys Glu Asn Gly Glu Ser Val Glu Gly Ala Glu Val Thr Val Glu  
145 150 155 160  
Gln Ile Ser Lys Asp Phe Ser Ile Gly Ser Ala Ile Ser Lys Thr Ile  
165 170 175  
Leu Gly Asn Ile Pro Tyr Gln Glu Trp Phe Val Lys Arg Phe Asp Ala  
180 185 190  
Thr Val Phe Glu Asn Glu Leu Lys Trp Tyr Ala Thr Glu Pro Asp Gln  
195 200 205  
Gly Lys Leu Asn Tyr Thr Leu Ala Asp Lys Met Met Asn Phe Val Arg

SEQUENCE LISTING



210 215 220  
Ala Asn Arg Ile Ile Ala Arg Gly His Asn Ile Phe Trp Glu Asp Pro  
225 230 235 240  
Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu Thr Gly Glu Asp Leu Arg  
245 250 255  
Ser Ala Val Asn Arg Arg Ile Lys Ser Leu Met Thr Arg Tyr Arg Gly  
260 265 270  
Glu Phe Val His Trp Asp Val Ser Asn Glu Met Leu His Phe Asp Phe  
275 280 285  
Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser Tyr Gly Phe Phe Ala Ala  
290 295 300  
Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu Phe Phe Asn Asp Phe Asn  
305 310 315 320  
Val Val Glu Thr Cys Ser Asp Glu Lys Ser Thr Val Asp Glu Tyr Ile  
325 330 335  
Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp Gly Val Arg Met Asp Gly  
340 345 350  
Ile Gly Leu Glu Gly His Phe Thr Thr Pro Asn Val Ala Leu Met Arg  
355 360 365  
Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro Ala Pro Asn Leu Ala His  
370 375 380  
Arg Asp  
385

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1362
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

|             |              |             |             |            |             |      |
|-------------|--------------|-------------|-------------|------------|-------------|------|
| aattttcattc | gttcttttattc | aacaacactc  | tctctcttct  | ctatcaacac | tttcttttcat | 60   |
| ctctcgccgg  | aaaaacccat   | aaccacaaca  | atggccaccg  | aaacccaaat | ccgaatcgga  | 120  |
| gtaatgggtt  | gcgcccgat    | cgctcgaaaa  | gtctctcgag  | caatccacct | cgctcccaac  | 180  |
| gccacaatct  | ccggcgtaGc   | aagccggtct  | ttagaaaaag  | ccaaagcctt | tgccaccgcc  | 240  |
| aataactacc  | cagaatcaac   | caaaatccac  | ggctcttacg  | aatctcttct | cgaagatcca  | 300  |
| gagatcgatg  | cgctctatgt   | tcctctcccc  | actagtctcc  | acgttgagtg | ggctattaaa  | 360  |
| gcagctgaga  | aagggaaaca   | tatccttttg  | gagaagcctg  | ttgctatgaa | cgtaactgag  | 420  |
| tttgataaga  | ttgttgatgc   | ttgtgaagct  | aatgggtgtc  | agattatgga | tggtagtatg  | 480  |
| tgggttcata  | atcctagaac   | tgcttttgctt | aaagagtttc  | tttctgattc | tgaacgtttt  | 540  |
| ggtcagctta  | aaactgtaca   | gagttgtttc  | tcatttgctg  | gagatgaaga | ttttcttaaa  | 600  |
| aacgatatac  | gtgtgaaacc   | tggtcttgac  | gggcttggtg  | cgctaggaga | tgcgggggtg  | 660  |
| tacgcgatca  | gagcaactct   | tttagcta    | aaactttgagc | ttccgaaaac | tgtgactgct  | 720  |
| ttccccgggtg | ctgtgttgaa   | tgaagcagga  | ttgatacttt  | cctgtggagc | atctttgagt  | 780  |
| tgggaagatg  | gacgaactgc   | aactatatat  | tgttcattct  | tggctaactt | aacaatggag  | 840  |
| ataactgcca  | ttggaacgaa   | aggcacactc  | cgtgtacacg  | acttcattat | cccgtataag  | 900  |
| gagactgagg  | cgctggtttac  | cacgagcact  | aaagcttggt  | tcaatgacct | tgtgactgcg  | 960  |
| tgggttagtc  | ccccagagtga  | gcatacgggt  | aagacagagc  | ttccacaaga | ggcatgtatg  | 1020 |
| gtgagagagt  | ttgctcgatt   | ggttggagaa  | atcaagaaca  | atggtgcaaa | gcctgatggg  | 1080 |
| tactggccta  | gtattagccg   | aaagacgcag  | ctagtgtgtg  | atgctgttaa | agagtctgtt  | 1140 |
| gataaaaact  | atcaacagat   | tagtctctct  | ggtcggtgaa  | ggaaaggact | cagactataa  | 1200 |
| atgttgctgt  | gtgtttctctc  | ctctctcgtc  | ctctatgttc  | aaacttcgat | caaccgttta  | 1260 |
| agtgtttgtt  | accacttacc   | aatatgttct  | gtcttctgct  | gtgtccgcct | gtatgtatgt  | 1320 |
| taattgtttt  | agactccaat   | tactagcctt  | caattactaa  | gc         |             |      |

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..392  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569408  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Ile | Arg | Ser | Leu | Ser | Thr | Thr | Leu | Ser | Leu | Phe | Ser | Ile | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Phe | Phe | His | Leu | Ser | Pro | Glu | Lys | Pro | Ile | Thr | Thr | Thr | Met | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Thr | Gln | Ile | Arg | Ile | Gly | Val | Met | Gly | Cys | Ala | Asp | Ile | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Lys | Val | Ser | Arg | Ala | Ile | His | Leu | Ala | Pro | Asn | Ala | Thr | Ile | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Val | Ala | Ser | Arg | Ser | Leu | Glu | Lys | Ala | Lys | Ala | Phe | Ala | Thr | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Asn | Tyr | Pro | Glu | Ser | Thr | Lys | Ile | His | Gly | Ser | Tyr | Glu | Ser | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Asp | Pro | Glu | Ile | Asp | Ala | Leu | Tyr | Val | Pro | Leu | Pro | Thr | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | His | Val | Glu | Trp | Ala | Ile | Lys | Ala | Ala | Glu | Lys | Gly | Lys | His | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Glu | Lys | Pro | Val | Ala | Met | Asn | Val | Thr | Glu | Phe | Asp | Lys | Ile |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asp | Ala | Cys | Glu | Ala | Asn | Gly | Val | Gln | Ile | Met | Asp | Gly | Thr | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Val | His | Asn | Pro | Arg | Thr | Ala | Leu | Leu | Lys | Glu | Phe | Leu | Ser | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Glu | Arg | Phe | Gly | Gln | Leu | Lys | Thr | Val | Gln | Ser | Cys | Phe | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Gly | Asp | Glu | Asp | Phe | Leu | Lys | Asn | Asp | Ile | Arg | Val | Lys | Pro | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Asp | Gly | Leu | Gly | Ala | Leu | Gly | Asp | Ala | Gly | Trp | Tyr | Ala | Ile | Arg |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Thr | Leu | Leu | Ala | Asn | Phe | Glu | Leu | Pro | Lys | Thr | Val | Thr | Ala |     |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Phe | Pro | Gly | Ala | Val | Leu | Asn | Glu | Ala | Gly | Leu | Ile | Leu | Ser | Cys | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ser | Leu | Ser | Trp | Glu | Asp | Gly | Arg | Thr | Ala | Thr | Ile | Tyr | Cys | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Leu | Ala | Asn | Leu | Thr | Met | Glu | Ile | Thr | Ala | Ile | Gly | Thr | Lys | Gly |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Thr | Leu | Arg | Val | His | Asp | Phe | Ile | Ile | Pro | Tyr | Lys | Glu | Thr | Glu | Ala |
|     |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Ser | Phe | Thr | Thr | Ser | Thr | Lys | Ala | Trp | Phe | Asn | Asp | Leu | Val | Thr | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Trp | Val | Ser | Pro | Pro | Ser | Glu | His | Thr | Val | Lys | Thr | Glu | Leu | Pro | Gln |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Ala | Cys | Met | Val | Arg | Glu | Phe | Ala | Arg | Leu | Val | Gly | Glu | Ile | Lys |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Asn | Asn | Gly | Ala | Lys | Pro | Asp | Gly | Tyr | Trp | Pro | Ser | Ile | Ser | Arg | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Thr | Gln | Leu | Val | Val | Asp | Ala | Val | Lys | Glu | Ser | Val | Asp | Lys | Asn | Tyr |
|     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| Gln | Gln | Ile | Ser | Leu | Ser | Gly | Arg |     |     |     |     |     |     |     |     |
| 385 |     |     |     |     | 390 |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:1248:  
(i) SEQUENCE CHARACTERISTICS:

SEQUENCE INFORMATION

- (A) LENGTH: 362 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..362
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

Met Ala Thr Glu Thr Gln Ile Arg Ile Gly Val Met Gly Cys Ala Asp  
1                   5                   10                   15  
Ile Ala Arg Lys Val Ser Arg Ala Ile His Leu Ala Pro Asn Ala Thr  
          20                   25                   30  
Ile Ser Gly Val Ala Ser Arg Ser Leu Glu Lys Ala Lys Ala Phe Ala  
          35                   40                   45  
Thr Ala Asn Asn Tyr Pro Glu Ser Thr Lys Ile His Gly Ser Tyr Glu  
          50                   55                   60  
Ser Leu Leu Glu Asp Pro Glu Ile Asp Ala Leu Tyr Val Pro Leu Pro  
65                   70                   75                   80  
Thr Ser Leu His Val Glu Trp Ala Ile Lys Ala Ala Glu Lys Gly Lys  
          85                   90                   95  
His Ile Leu Leu Glu Lys Pro Val Ala Met Asn Val Thr Glu Phe Asp  
          100                   105                   110  
Lys Ile Val Asp Ala Cys Glu Ala Asn Gly Val Gln Ile Met Asp Gly  
          115                   120                   125  
Thr Met Trp Val His Asn Pro Arg Thr Ala Leu Leu Lys Glu Phe Leu  
          130                   135                   140  
Ser Asp Ser Glu Arg Phe Gly Gln Leu Lys Thr Val Gln Ser Cys Phe  
145                   150                   155                   160  
Ser Phe Ala Gly Asp Glu Asp Phe Leu Lys Asn Asp Ile Arg Val Lys  
          165                   170                   175  
Pro Gly Leu Asp Gly Leu Gly Ala Leu Gly Asp Ala Gly Trp Tyr Ala  
          180                   185                   190  
Ile Arg Ala Thr Leu Leu Ala Asn Asn Phe Glu Leu Pro Lys Thr Val  
          195                   200                   205  
Thr Ala Phe Pro Gly Ala Val Leu Asn Glu Ala Gly Leu Ile Leu Ser  
          210                   215                   220  
Cys Gly Ala Ser Leu Ser Trp Glu Asp Gly Arg Thr Ala Thr Ile Tyr  
225                   230                   235                   240  
Cys Ser Phe Leu Ala Asn Leu Thr Met Glu Ile Thr Ala Ile Gly Thr  
          245                   250                   255  
Lys Gly Thr Leu Arg Val His Asp Phe Ile Ile Pro Tyr Lys Glu Thr  
          260                   265                   270  
Glu Ala Ser Phe Thr Thr Ser Thr Lys Ala Trp Phe Asn Asp Leu Val  
          275                   280                   285  
Thr Ala Trp Val Ser Pro Pro Ser Glu His Thr Val Lys Thr Glu Leu  
          290                   295                   300  
Pro Gln Glu Ala Cys Met Val Arg Glu Phe Ala Arg Leu Val Gly Glu  
305                   310                   315                   320  
Ile Lys Asn Asn Gly Ala Lys Pro Asp Gly Tyr Trp Pro Ser Ile Ser  
          325                   330                   335  
Arg Lys Thr Gln Leu Val Val Asp Ala Val Lys Glu Ser Val Asp Lys  
          340                   345                   350  
Asn Tyr Gln Gln Ile Ser Leu Ser Gly Arg  
          355                   360

(2) INFORMATION FOR SEQ ID NO:1249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

(2) INFORMATION FOR SEQ ID NO:1250:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1202

(D) OTHER INFORMATION: / Ceres Seq. ID 1569411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| aacgccagtt | gccatccagg  | agaggggaga | agaagaattt | gtattctcaa | gttgtcgata | 60   |
| tgagagagat | gaagtcagaa  | acacgtttgt | gagagaacag | cttttagatg | tgattgtgga | 120  |
| tcagattctc | aaagactttt  | cgcgaagagt | ctctgatact | taaatcgctt | ctctctcgct | 180  |
| tgacctcatt | tcgtcgtcga  | aatcagatcc | gtgtgaaaat | gccgaaacag | gatatggaga | 240  |
| agatggagct | tcgtaagaac  | ttccgtaatg | tttggcatac | cgatcttacc | cacagtatcc | 300  |
| agaacgatac | tccttattgt  | tgttcgcgt  | tgtgggtgtg | cccttgtgca | tcataacttg | 360  |
| ttcgcaagcg | tgcgctttac  | gatgatatgt | caaggtagct | ctgctgtgcc | ggttacatgc | 420  |
| cttgtagtgg | taggtgtgga  | gaagccaaat | gtcctcaact | ttgtcttgcc | actgaggtct | 480  |
| tctgctgctt | tgcaaaactct | gtggcctcaa | ctcgctttct | tctgcaagat | gagttccaaa | 540  |
| ttcagacgac | aaaatgtgac  | aactgcatca | ttggtttcat | ggtttgcctc | agccaagtgg | 600  |
| cttgcatatt | ctccatagtt  | gcatgtattg | tcggtatgga | tgagctttca | gaagcttctc | 660  |
| agatactcac | atgttgctct  | gacatggtgt | actgcacggt | ttgctcatgt | atgcagacac | 720  |
| aacacaagat | ggaaatggac  | aagagggacg | gtaagttcgg | gccacagcca | atggcagtGc | 780  |
| ctccggctca | gcaaagtgtc  | cggtttgatc | aagccacccc | accgcagtc  | ggttatcctc | 840  |
| cacaacaagg | ttatccacct  | tctggttacc | ctcaacaccc | tccacaaggt | tatccacctt | 900  |
| ctggctatcc | tcaaaaccct  | cctccctcag | cttattctca | ataccctcct | ggggcttatc | 960  |
| ctcctcctcc | cgcttaccca  | aagtgatcac | tctttgcctg | ttttctctcc | cgattggaaa | 1020 |
| attttatttc | atcttttttt  | aatgctgtct | tgttacgggt | caagaattga | acgttcgctg | 1080 |
| attgttttga | ggtcgttggt  | tgtatgagat | tttgacctca | catgttggtg | ttttctgaaa | 1140 |
| cgccctcttt | ggactaagag  | atttcatgac | tttttccttt | cctttttaa  | tctctctttt | 1200 |
| tc         |             |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Lys | Gln | Asp | Met | Glu | Lys | Met | Glu | Leu | Arg | Lys | Asn | Phe | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Val | Trp | His | Thr | Asp | Leu | Thr | His | Ser | Ile | Gln | Asn | Asp | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Cys | Cys | Phe | Ala | Leu | Trp | Cys | Ala | Pro | Cys | Ala | Ser | Tyr | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Lys | Arg | Ala | Leu | Tyr | Asp | Asp | Met | Ser | Arg | Tyr | Val | Cys | Cys | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Tyr | Met | Pro | Cys | Ser | Gly | Arg | Cys | Gly | Glu | Ala | Lys | Cys | Pro | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Cys | Leu | Ala | Thr | Glu | Val | Phe | Cys | Cys | Phe | Ala | Asn | Ser | Val | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Thr | Arg | Phe | Leu | Leu | Gln | Asp | Glu | Phe | Gln | Ile | Gln | Thr | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Asp | Asn | Cys | Ile | Ile | Gly | Phe | Met | Val | Cys | Leu | Ser | Gln | Val | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Ile | Phe | Ser | Ile | Val | Ala | Cys | Ile | Val | Gly | Met | Asp | Glu | Leu | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Ser | Gln | Ile | Leu | Thr | Cys | Cys | Ser | Asp | Met | Val | Tyr | Cys | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Cys | Ala | Cys | Met | Gln | Thr | Gln | His | Lys | Met | Glu | Met | Asp | Lys | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Gly | Lys | Phe | Gly | Pro | Gln | Pro | Met | Ala | Val | Pro | Pro | Ala | Gln | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Ser | Arg | Phe | Asp | Gln | Ala | Thr | Pro | Pro | Ala | Val | Gly | Tyr | Pro | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Gln Gln Gly Tyr Pro Pro Ser Gly Tyr Pro Gln His Pro Pro Gln Gly  
210 215 220  
Tyr Pro Pro Ser Gly Tyr Pro Gln Asn Pro Pro Pro Ser Ala Tyr Ser  
225 230 235 240  
Gln Tyr Pro Pro Gly Ala Tyr Pro Pro Pro Pro Ala Tyr Pro Lys  
245 250 255

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1569413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

Met Glu Lys Met Glu Leu Arg Lys Asn Phe Arg Asn Val Trp His Thr  
1 5 10 15  
Asp Leu Thr His Ser Ile Gln Asn Asp Thr Pro Tyr Cys Cys Phe Ala  
20 25 30  
Leu Trp Cys Ala Pro Cys Ala Ser Tyr Leu Leu Arg Lys Arg Ala Leu  
35 40 45  
Tyr Asp Asp Met Ser Arg Tyr Val Cys Cys Ala Gly Tyr Met Pro Cys  
50 55 60  
Ser Gly Arg Cys Gly Glu Ala Lys Cys Pro Gln Leu Cys Leu Ala Thr  
65 70 75 80  
Glu Val Phe Cys Cys Phe Ala Asn Ser Val Ala Ser Thr Arg Phe Leu  
85 90 95  
Leu Gln Asp Glu Phe Gln Ile Gln Thr Thr Lys Cys Asp Asn Cys Ile  
100 105 110  
Ile Gly Phe Met Val Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile  
115 120 125  
Val Ala Cys Ile Val Gly Met Asp Glu Leu Ser Glu Ala Ser Gln Ile  
130 135 140  
Leu Thr Cys Cys Ser Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met  
145 150 155 160  
Gln Thr Gln His Lys Met Glu Met Asp Lys Arg Asp Gly Lys Phe Gly  
165 170 175  
Pro Gln Pro Met Ala Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp  
180 185 190  
Gln Ala Thr Pro Pro Ala Val Gly Tyr Pro Pro Gln Gln Gly Tyr Pro  
195 200 205  
Pro Ser Gly Tyr Pro Gln His Pro Pro Gln Gly Tyr Pro Pro Ser Gly  
210 215 220  
Tyr Pro Gln Asn Pro Pro Pro Ser Ala Tyr Ser Gln Tyr Pro Pro Gly  
225 230 235 240  
Ala Tyr Pro Pro Pro Pro Ala Tyr Pro Lys  
245 250

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1569414

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

Met Glu Leu Arg Lys Asn Phe Arg Asn Val Trp His Thr Asp Leu Thr  
1 5 10 15  
His Ser Ile Gln Asn Asp Thr Pro Tyr Cys Cys Phe Ala Leu Trp Cys  
20 25 30  
Ala Pro Cys Ala Ser Tyr Leu Leu Arg Lys Arg Ala Leu Tyr Asp Asp  
35 40 45  
Met Ser Arg Tyr Val Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg  
50 55 60  
Cys Gly Glu Ala Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val Phe  
65 70 75 80  
Cys Cys Phe Ala Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln Asp  
85 90 95  
Glu Phe Gln Ile Gln Thr Thr Lys Cys Asp Asn Cys Ile Ile Gly Phe  
100 105 110  
Met Val Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala Cys  
115 120 125  
Ile Val Gly Met Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Thr Cys  
130 135 140  
Cys Ser Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr Gln  
145 150 155 160  
His Lys Met Glu Met Asp Lys Arg Asp Gly Lys Phe Gly Pro Gln Pro  
165 170 175  
Met Ala Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Ala Thr  
180 185 190  
Pro Pro Ala Val Gly Tyr Pro Pro Gln Gln Gly Tyr Pro Pro Ser Gly  
195 200 205  
Tyr Pro Gln His Pro Pro Gln Gly Tyr Pro Pro Ser Gly Tyr Pro Gln  
210 215 220  
Asn Pro Pro Pro Ser Ala Tyr Ser Gln Tyr Pro Pro Gly Ala Tyr Pro  
225 230 235 240  
Pro Pro Pro Ala Tyr Pro Lys  
245

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

aaaactcgaa aaaaagatgg cggcggttttt gcaaactaac atccgtctgg agatcatacc 60  
gggaagatac agttctctca ccgatcataa gtttcgtgcg ccgtatcgaa ttaggtgcg 120  
cgccgcttca ccggtgaaaa aacggtataa catcactctg cttcccgcg atggtatcgg 180  
tccagaagtt atatctgttg ctaagaatgt gcttcagaaa gctggatttc tccaaggact 240  
agagtttgat ttccaggaga tgcctttcgg cggaGcagct ttggatttgg tccgagttcc 300  
attgccggag gaaacttcca ctgctgctaa acagttctgat gccattcttc ttggagctat 360  
cggagggtac aaatgggaca agaatgagaa acatctgaga cctgagatgg gtctgcttaa 420  
cattcgaaga gatctcaatg tctttgctaa tttgagacct gctacagttt taccacagct 480  
agttgatgct tccacactga agaaagaagt agcacaaggt gttgatatga tgattgtaag 540  
ggagctcact ggaggtattt actttggaga gccaaagaggc attacgatca acgaaaatgg 600  
cgaagaagtc ggttttaata cagagatcta cgctgctcac gagattgaca gaattgctcg 660  
tggttcattc gagactgcta ggaaaaggcg tggcaagctg tggtctgttg acaaagccaa 720  
tgtcttggat gcatcaatat tgtggaggaa aagagtaaca gctttagcct ctgaatatcc 780  
agatgttgaa ctatcacata tgtatgtcga taatgStgcg atgcagcttg tccgtgaccc 840  
gaaacagttt gacacaatcg tcaccaataa catttttggt gatataattg ctgatgaagc 900  
ttcaatgatc actggttagca ttgggatgct tccatctgca agtcttggtg aatcgggacc 960

(2) INFORMATION FOR SEQ ID NO:1255:

(A) LENGTH: 409 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1569428

|            |            |            |            |            |            |            |            |            |            |            |            |     |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|------------|------------|------------|
| Lys<br>1   | Leu        | Glu        | Lys        | Lys<br>5   | Met        | Ala        | Ala        | Phe        | Leu<br>10  | Gln        | Thr        | Asn | Ile        | Arg<br>15  | Leu        |
| Glu        | Ile        | Ile        | Pro<br>20  | Gly        | Arg        | Tyr        | Ser        | Ser<br>25  | Leu        | Thr        | Asp        | His | Lys<br>30  | Phe        | Arg        |
| Ala        | Pro        | Tyr<br>35  | Arg        | Ile        | Arg        | Cys        | Ala<br>40  | Ala        | Ala        | Ser        | Pro<br>45  | Val | Lys        | Lys        | Arg        |
| Tyr        | Asn<br>50  | Ile        | Thr        | Leu        | Leu<br>55  | Pro        | Gly        | Asp        | Gly        | Ile<br>60  | Gly        | Pro | Glu        | Val        | Ile        |
| Ser<br>65  | Val        | Ala        | Lys        | Asn<br>70  | Val        | Leu        | Gln        | Lys        | Ala<br>75  | Gly        | Phe        | Leu | Gln        | Gly        | Leu<br>80  |
| Glu        | Phe        | Asp        | Phe<br>85  | Gln        | Glu        | Met        | Pro        | Phe        | Gly<br>90  | Gly        | Ala        | Ala | Leu        | Asp<br>95  | Leu        |
| Val        | Gly        | Val<br>100 | Pro        | Leu        | Pro        | Glu        | Glu        | Thr<br>105 | Ser        | Thr        | Ala        | Ala | Lys<br>110 | Gln        | Ser        |
| Asp        | Ala<br>115 | Ile        | Leu        | Leu        | Gly        | Ala        | Ile<br>120 | Gly        | Gly        | Tyr        | Lys<br>125 | Trp | Asp        | Lys        | Asn        |
| Glu        | Lys<br>130 | His        | Leu        | Arg        | Pro        | Glu<br>135 | Met        | Gly        | Leu        | Leu<br>140 | Asn        | Ile | Arg        | Arg        | Asp        |
| Leu<br>145 | Asn        | Val        | Phe        | Ala<br>150 | Asn        | Leu        | Arg        | Pro        | Ala<br>155 | Thr        | Val        | Leu | Pro        | Gln        | Leu<br>160 |
| Val        | Asp        | Ala        | Ser<br>165 | Thr        | Leu        | Lys        | Lys        | Glu<br>170 | Val        | Ala        | Gln        | Gly | Val        | Asp<br>175 | Met        |
| Met        | Ile<br>180 | Val        | Arg        | Glu        | Leu        | Thr        | Gly        | Gly<br>185 | Ile        | Tyr        | Phe        | Gly | Glu<br>190 | Pro        | Arg        |
| Gly        | Ile<br>195 | Thr        | Ile        | Asn        | Glu        | Asn<br>200 | Gly        | Glu        | Glu        | Val        | Gly<br>205 | Phe | Asn        | Thr        | Glu        |
| Ile<br>210 | Tyr        | Ala        | Ala        | His        | Glu<br>215 | Ile        | Asp        | Arg        | Ile        | Ala<br>220 | Arg        | Val | Ala        | Phe        | Glu        |
| Thr<br>225 | Ala        | Arg        | Lys        | Arg        | Arg<br>230 | Gly        | Lys        | Leu        | Cys        | Ser<br>235 | Val        | Asp | Lys        | Ala        | Asn<br>240 |
| Val        | Leu        | Asp        | Ala<br>245 | Ser        | Ile        | Leu        | Trp        | Arg        | Lys<br>250 | Arg        | Val        | Thr | Ala        | Leu        | Ala<br>255 |
| Ser        | Glu        | Tyr<br>260 | Pro        | Asp        | Val        | Glu        | Leu        | Ser<br>265 | His        | Met        | Tyr        | Val | Asp<br>270 | Asn        | Xaa        |
| Ala        | Met<br>275 | Gln        | Leu        | Val        | Arg        | Asp        | Pro<br>280 | Lys        | Gln        | Phe        | Asp<br>285 | Thr | Ile        | Val        | Thr        |
| Asn<br>290 | Asn        | Ile        | Phe        | Gly        | Asp<br>295 | Ile        | Leu        | Ser        | Asp        | Glu<br>300 | Ala        | Ser | Met        | Ile        | Thr        |
| Gly<br>305 | Ser        | Ile        | Gly        | Met<br>310 | Leu        | Pro        | Ser        | Ala        | Ser<br>315 | Leu        | Gly        | Glu | Ser        | Gly        | Pro<br>320 |
| Gly        | Leu        | Phe        | Glu<br>325 | Pro        | Ile        | His        | Gly        | Ser<br>330 | Ala        | Pro        | Asp        | Ile | Ala        | Gly<br>335 | Gln        |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Phe | Leu | Gln | Thr | Asn | Ile | Arg | Leu | Glu | Ile | Ile | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Tyr | Ser | Ser | Leu | Thr | Asp | His | Lys | Phe | Arg | Ala | Pro | Tyr | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Cys | Ala | Ala | Ala | Ser | Pro | Val | Lys | Lys | Arg | Tyr | Asn | Ile | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Gly | Asp | Gly | Ile | Gly | Pro | Glu | Val | Ile | Ser | Val | Ala | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Gln | Lys | Ala | Gly | Phe | Leu | Gln | Gly | Leu | Glu | Phe | Asp | Phe | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Met | Pro | Phe | Gly | Gly | Ala | Ala | Leu | Asp | Leu | Val | Gly | Val | Pro | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Glu | Glu | Thr | Ser | Thr | Ala | Ala | Lys | Gln | Ser | Asp | Ala | Ile | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ala | Ile | Gly | Gly | Tyr | Lys | Trp | Asp | Lys | Asn | Glu | Lys | His | Leu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Glu | Met | Gly | Leu | Leu | Asn | Ile | Arg | Arg | Asp | Leu | Asn | Val | Phe | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Leu | Arg | Pro | Ala | Thr | Val | Leu | Pro | Gln | Leu | Val | Asp | Ala | Ser | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Lys | Lys | Glu | Val | Ala | Gln | Gly | Val | Asp | Met | Met | Ile | Val | Arg | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Thr | Gly | Gly | Ile | Tyr | Phe | Gly | Glu | Pro | Arg | Gly | Ile | Thr | Ile | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Asn | Gly | Glu | Glu | Val | Gly | Phe | Asn | Thr | Glu | Ile | Tyr | Ala | Ala | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Ile | Asp | Arg | Ile | Ala | Arg | Val | Ala | Phe | Glu | Thr | Ala | Arg | Lys | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Gly | Lys | Leu | Cys | Ser | Val | Asp | Lys | Ala | Asn | Val | Leu | Asp | Ala | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Leu | Trp | Arg | Lys | Arg | Val | Thr | Ala | Leu | Ala | Ser | Glu | Tyr | Pro | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Glu | Leu | Ser | His | Met | Tyr | Val | Asp | Asn | Xaa | Ala | Met | Gln | Leu | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Asp | Pro | Lys | Gln | Phe | Asp | Thr | Ile | Val | Thr | Asn | Asn | Ile | Phe | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Ile | Leu | Ser | Asp | Glu | Ala | Ser | Met | Ile | Thr | Gly | Ser | Ile | Gly | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Pro | Ser | Ala | Ser | Leu | Gly | Glu | Ser | Gly | Pro | Gly | Leu | Phe | Glu | Pro |

(2) INFORMATION FOR SEQ ID NO:1257:

(A) LENGTH: 323 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1569430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Phe | Gly | Gly | Ala | Ala | Leu | Asp | Leu | Val | Gly | Val | Pro | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Thr | Ser | Thr | Ala | Ala | Lys | Gln | Ser | Asp | Ala | Ile | Leu | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Gly | Gly | Tyr | Lys | Trp | Asp | Lys | Asn | Glu | Lys | His | Leu | Arg | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Met | Gly | Leu | Leu | Asn | Ile | Arg | Arg | Asp | Leu | Asn | Val | Phe | Ala | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Pro | Ala | Thr | Val | Leu | Pro | Gln | Leu | Val | Asp | Ala | Ser | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Lys | Glu | Val | Ala | Gln | Gly | Val | Asp | Met | Met | Ile | Val | Arg | Glu | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Gly | Gly | Ile | Tyr | Phe | Gly | Glu | Pro | Arg | Gly | Ile | Thr | Ile | Asn | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Gly | Glu | Glu | Val | Gly | Phe | Asn | Thr | Glu | Ile | Tyr | Ala | Ala | His | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Asp | Arg | Ile | Ala | Arg | Val | Ala | Phe | Glu | Thr | Ala | Arg | Lys | Arg | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Lys | Leu | Cys | Ser | Val | Asp | Lys | Ala | Asn | Val | Leu | Asp | Ala | Ser | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Trp | Arg | Lys | Arg | Val | Thr | Ala | Leu | Ala | Ser | Glu | Tyr | Pro | Asp | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Leu | Ser | His | Met | Tyr | Val | Asp | Asn | Xaa | Ala | Met | Gln | Leu | Val | Arg |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Pro | Lys | Gln | Phe | Asp | Thr | Ile | Val | Thr | Asn | Asn | Ile | Phe | Gly | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Leu | Ser | Asp | Glu | Ala | Ser | Met | Ile | Thr | Gly | Ser | Ile | Gly | Met | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Ser | Ala | Ser | Leu | Gly | Glu | Ser | Gly | Pro | Gly | Leu | Phe | Glu | Pro | Ile |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Gly | Ser | Ala | Pro | Asp | Ile | Ala | Gly | Gln | Asp | Lys | Ala | Asn | Pro | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Thr | Ile | Leu | Ser | Ala | Ala | Met | Leu | Leu | Lys | Tyr | Gly | Leu | Gly | Glu |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Glu | Lys | Ala | Ala | Lys | Met | Ile | Glu | Asp | Ala | Val | Val | Asp | Ala | Leu | Asn |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser Pro Gly Asn Lys Leu Val  
290 295 300  
Gly Cys Lys Glu Met Gly Glu Glu Val Leu Lys Ser Val Asp Ser Lys  
305 310 315 320  
Val Pro Val

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

gtgatctatc tttgaatctc aaaagcatac ttgagagaga tctgtttcga taatttgctt 60  
caatcaccgt gttaatggcg gccgtagGag tggaggcgag acctcctgtg acagcgatgg 120  
aggaaacctg caacgttaag ggagcggcgg cgaaacaagg agaagggtt aacaagtact 180  
acctccagca tctcgatgag ctccagcgcc tgcaacgcga aaagtcgtat aaccttaatc 240  
gtcttgaagc tcagaggaat gaactcaatt ctcgagtacg aatgctcaga gaagagttac 300  
agctccttca agaacctggg tcctatgtgg gtgaagtggg aaaagtgatg ggaaaaaaca 360  
aggctcttgg taaggttcat ccagagggga agtatgttgt cgatattgac aaaagtatag 420  
acataacgaa actcactcca tcaacgagag ttgctctccg taatgatagc tatgttctcc 480  
acctggttct gccaaagtaa gtagatccct tggttaacct tatgaaagtt gagaaggttc 540  
cagactccac atatgacatg attggtggtc ttgaccagca aatcaaggaa ataaaggagg 600  
tcattgaact gccaatcaag catcctgaat tgtttgagtc tcttggaatt gcgcagccaa 660  
agggtgtggt gttgtacggt ccacctggaa ctgggaagac actattggct cgggctgtgg 720  
cacatcacac tgactgtact ttcacagag tttctgggtc tgagctggtc cagaaataca 780  
ttggagaagg ttctagaatg gtcagagaac tttttgtgat ggcaaggagg catgcaccat 840  
caatcatctt catggatgaa atcgatagta tcgggtctgc tcgtatggaa tctggtagtg 900  
gaaatggtga cagtgagggt caaaggacta tgcttgagct tctcaatcaa cttgacggat 960  
tcgaggcgtc aaacaaaatc aaggttttga tggctacaaa tcgtattgat attctggatc 1020  
aagctcttct ccggcctgga aggattgata ggaaaattga atttcctaata cctaataaag 1080  
agtcacgttt tgatatcttg aagatacact caaggaaaat gaatttgatg cgtggaatcg 1140  
atctgaaaaa gattgcagag aagatgaatg gtgcttcagg tgctgagctg aaggctgtat 1200  
gcacggaggc gggcatgttt gcacttcgtg agaggagagt acatgtgact caggaagact 1260  
ttgagatggc tgtggcgaag gtaatgaaga aagacacaga gaagaacatg tctctgcgta 1320  
agctctggaa gtaggaattt cagagtcaca gattaatttc gattatttct tctctactgt 1380  
ctgtggttct ttctgaaacc ttttcggcta gcgctttaa cttttctaaa caatgtttgt 1440  
acactagttt ctattcattc aattggttgt tcagc

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Met Ala Ala Val Gly Val Glu Ala Arg Pro Pro Val Thr Ala Met Glu  
1 5 10 15  
Glu Thr Cys Asn Val Lys Gly Ala Ala Ala Lys Gln Gly Glu Gly Leu  
20 25 30  
Asn Lys Tyr Tyr Leu Gln His Leu Asp Glu Leu Gln Arg Leu Gln Arg  
35 40 45

Glu Lys Ser Tyr Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn Glu Leu  
50 55 60  
Asn Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu  
65 70 75 80  
Pro Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys Asn Lys  
85 90 95  
Val Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp  
100 105 110  
Lys Ser Ile Asp Ile Thr Lys Leu Thr Pro Ser Thr Arg Val Ala Leu  
115 120 125  
Arg Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys Val Asp  
130 135 140  
Pro Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr  
145 150 155 160  
Asp Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val  
165 170 175  
Ile Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile  
180 185 190  
Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys  
195 200 205  
Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile  
210 215 220  
Arg Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser  
225 230 235 240  
Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser  
245 250 255  
Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu  
260 265 270  
Ser Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu  
275 280 285  
Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val  
290 295 300  
Leu Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg  
305 310 315 320  
Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Glu  
325 330 335  
Ser Arg Phe Asp Ile Leu Lys Ile His Ser Arg Lys Met Asn Leu Met  
340 345 350  
Arg Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser  
355 360 365  
Gly Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu  
370 375 380  
Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val  
385 390 395 400  
Ala Lys Val Met Lys Lys Asp Thr Glu Lys Asn Met Ser Leu Arg Lys  
405 410 415  
Leu Trp Lys

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

Met Glu Glu Thr Cys Asn Val Lys Gly Ala Ala Ala Lys Gln Gly Glu

SEQUENCE CHARACTERISTICS

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Gly | Leu | Asn | Lys | Tyr | Tyr | Leu |
|     |     | 20  |     |     |     | 25  |
| Gln | Arg | Glu | Lys | Ser | Tyr | Asn |
|     |     | 35  |     |     |     | 40  |
| Glu | Leu | Asn | Ser | Arg | Val | Arg |
|     |     | 50  |     |     |     | 55  |
| Gln | Glu | Pro | Gly | Ser | Tyr | Val |
|     |     | 65  |     |     |     | 70  |
| Asn | Lys | Val | Leu | Val | Lys | Val |
|     |     |     | 85  |     |     | 90  |
| Ile | Asp | Lys | Ser | Ile | Asp | Ile |
|     |     |     | 100 |     |     | 105 |
| Ala | Leu | Arg | Asn | Asp | Ser | Tyr |
|     |     |     | 115 |     |     | 120 |
| Val | Asp | Pro | Leu | Val | Asn | Leu |
|     |     |     | 130 |     |     | 135 |
| Thr | Tyr | Asp | Met | Ile | Gly | Gly |
|     |     |     | 145 |     |     | 150 |
| Glu | Val | Ile | Glu | Leu | Pro | Ile |
|     |     |     |     | 165 |     | 170 |
| Gly | Ile | Ala | Gln | Pro | Lys | Gly |
|     |     |     | 180 |     |     | 185 |
| Gly | Lys | Thr | Leu | Leu | Ala | Arg |
|     |     |     | 195 |     |     | 200 |
| Phe | Ile | Arg | Val | Ser | Gly | Ser |
|     |     |     | 210 |     |     | 215 |
| Gly | Ser | Arg | Met | Val | Arg | Glu |
|     |     |     | 225 |     |     | 230 |
| Pro | Ser | Ile | Ile | Phe | Met | Asp |
|     |     |     |     | 245 |     | 250 |
| Met | Glu | Ser | Gly | Ser | Gly | Asn |
|     |     |     | 260 |     |     | 265 |
| Leu | Glu | Leu | Leu | Asn | Gln | Leu |
|     |     |     | 275 |     |     | 280 |
| Lys | Val | Leu | Met | Ala | Thr | Asn |
|     |     |     | 290 |     |     | 295 |
| Leu | Arg | Pro | Gly | Arg | Ile | Asp |
|     |     |     | 305 |     |     | 310 |
| Glu | Glu | Ser | Arg | Phe | Asp | Ile |
|     |     |     |     | 325 |     | 330 |
| Leu | Met | Arg | Gly | Ile | Asp | Leu |
|     |     |     | 340 |     |     | 345 |
| Ala | Ser | Gly | Ala | Glu | Leu | Lys |
|     |     |     | 355 |     |     | 360 |
| Ala | Leu | Arg | Glu | Arg | Arg | Val |
|     |     |     | 370 |     |     | 375 |
| Ala | Val | Ala | Lys | Val | Met | Lys |
|     |     |     | 385 |     |     | 390 |
| Arg | Lys | Leu | Trp | Lys |     |     |
|     |     |     |     | 405 |     |     |

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1569438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

Met Leu Arg Glu Leu Gln Leu Leu Glu Pro Gly Ser Tyr Val  
1 5 10 15  
Gly Glu Val Val Lys Val Met Gly Lys Asn Lys Val Leu Val Lys Val  
20 25 30  
His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp Ile  
35 40 45  
Thr Lys Leu Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr  
50 55 60  
Val Leu His Leu Val Leu Pro Ser Lys Val Asp Pro Leu Val Asn Leu  
65 70 75 80  
Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly  
85 90 95  
Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile Glu Leu Pro Ile  
100 105 110  
Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala Gln Pro Lys Gly  
115 120 125  
Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Arg  
130 135 140  
Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg Val Ser Gly Ser  
145 150 155 160  
Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg Met Val Arg Glu  
165 170 175  
Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile Ile Phe Met Asp  
180 185 190  
Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser Gly Ser Gly Asn  
195 200 205  
Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu Leu Asn Gln Leu  
210 215 220  
Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu Met Ala Thr Asn  
225 230 235 240  
Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro Gly Arg Ile Asp  
245 250 255  
Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Glu Ser Arg Phe Asp Ile  
260 265 270  
Leu Lys Ile His Ser Arg Lys Met Asn Leu Met Arg Gly Ile Asp Leu  
275 280 285  
Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly Ala Glu Leu Lys  
290 295 300  
Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg Glu Arg Arg Val  
305 310 315 320  
His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala Lys Val Met Lys  
325 330 335  
Lys Asp Thr Glu Lys Asn Met Ser Leu Arg Lys Leu Trp Lys  
340 345 350

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aatctagaac aagaaaccaa aacatacacc acttctgttt ttaaaggtaa aaaagatcaa | 60  |
| gaagaaacca aagaaaatca gacagcaaca agaaaagatc agtttttaag agaaggaaag | 120 |
| taggaaacg gtcagattgt tggatagaga gaggaagcga aaaaagagtc gcaagtgttc  | 180 |

(2) INFORMATION FOR SEQ ID NO:1263:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1569440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

- (A) LENGTH: 228 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..228  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569441  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

Met Val Gly Leu Arg Asp Val Phe Leu Val Ala Pro Ala Tyr His His  
1 5 10 15  
Gln Asn Ala Gly Val Ile Ser Gly Ser Asp His Met Asn Ser Asn Ala  
20 25 30  
Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile Pro Leu Leu Thr Ala  
35 40 45  
Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp Ile Asn Phe Leu Gly  
50 55 60  
Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn His Glu Thr Gln Tyr  
65 70 75 80  
Leu His Phe Lys Ser Thr Asn Gln Thr Thr Val Gly Thr Ser Ser Asn  
85 90 95  
Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr Ala Thr Cys Gln Asp  
100 105 110  
Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln Arg Arg Cys Arg Thr  
115 120 125  
Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr His Val Lys Ser Thr  
130 135 140  
Trp Val Ser Ala Ala Arg Arg Glu Arg Gln Val Met Pro Thr Gly  
145 150 155 160  
Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr Ser Ser Gly Thr Lys  
165 170 175  
Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln Gln Gln Gln Gln  
180 185 190  
Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn Thr Pro Pro Gln Ser  
195 200 205  
Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe Thr Phe Ser Leu Val  
210 215 220  
Tyr Ile Ala Thr  
225

(2) INFORMATION FOR SEQ ID NO:1265:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 201 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1569442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met Asn Ser Asn Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile  
1 5 10 15  
Pro Leu Leu Thr Ala Gly Pro Pro Gln Asn Val Glu Asp Ser Asp  
20 25 30  
Ile Asn Phe Leu Gly Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn Asn  
35 40 45  
His Glu Thr Gln Tyr Leu His Phe Lys Ser Thr Asn Gln Thr Thr Val  
50 55 60  
Gly Thr Ser Ser Asn Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Thr | Cys | Gln | Asp | Cys | Gly | Asn | Gln | Ala | Lys | Lys | Glu | Cys | Lys | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Arg | Cys | Arg | Thr | Cys | Cys | Lys | Ser | Arg | Gly | Phe | Asp | Cys | Ser | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Val | Lys | Ser | Thr | Trp | Val | Ser | Ala | Ala | Arg | Arg | Arg | Glu | Arg | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Met | Pro | Thr | Gly | Ala | Asn | Pro | Thr | Ala | Gly | Ser | Ser | Leu | Ser | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Gly | Thr | Lys | Lys | Pro | Arg | Ile | Val | Gly | Ser | Gln | Gln | Gln | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Gln | Gln | Gln | Gln | Gln | Gln | Ala | Thr | Ser | His | Thr | Ser | Thr | Ser | Asn |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Pro | Pro | Gln | Ser | Phe | Glu | Thr | Ser | Ser | Ser | Arg | Gln | Gly | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Phe | Ser | Leu | Val | Tyr | Ile | Ala | Thr |     |     |     |     |     |     |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| tcaatggtga | tacttttgat | gagaaatcca | ggattcctga | tcctaataagg | atgattcgag | 60   |
| cttacctca  | atctgcagct | actttgaatc | ttcttagagc | ctttgccact  | ggaggttacg | 120  |
| ctgctattca | aagagttact | caatggaacc | ttgattttgt | tgaacaaagt  | gagcaagctg | 180  |
| acaggtacca | ggagttagct | aacagggttg | atgaggcctt | ggggttcatg  | tctgcatgtg | 240  |
| gacttggcac | ggatcatcca | cttatgacta | caactgattt | ctacacatcc  | catgagtgtt | 300  |
| tgcttctgcc | ttatgaacag | tcccttaca  | ggttggattc | aacttctggt  | ctctactatg | 360  |
| attgttctgc | acacatggtc | tggtgcggag | agcgtaccag | acaattggat  | ggcgctcatg | 420  |
| tcgagtttct | cagggggatt | gctaatectc | tgggcattaa | ggtgagcaac  | aaaatggatc | 480  |
| ccaatgagct | ggttaagcta | gtagaatcc  | tgaatcctaa | taacaagcct  | ggaagaatca | 540  |
| ctgtaattgt | gagaatgggt | gctgagaaca | tgagagttaa | gcttccccac  | ctgatcagag | 600  |
| cagtcgcgag | atcaggccag | attgtgacat | gggtctgcga | tccaatgcat  | ggaaacacca | 660  |
| tcaaagcaCc | ttgcggtctt | aaaacacgtg | cctttgactc | aatactggct  | gaagtccgag | 720  |
| cattccttga | tgtgcacgag | caagaaggaa | gtcacgcggg | cggtatccat  | ctcgagatga | 780  |
| caggtcagaa | cgtgacagaa | tgcattggag | ggtccgcac  | tgtgacctac  | gatgacctca | 840  |
| gttctcgcta | ccacacacac | tgtgacccaa | ggctgaacgc | gtcacagtct  | cttgaacttg | 900  |
| ccttcattgt | tgcagaacgg | ctcaggaaga | gaagaacggg | tagccagcgt  | gtgtcttgag | 960  |
| tccggttctt | cccttttata | cactttttga | ttccaaacaa | ctcttttctc  | tttgcctgt  | 1020 |
| gactgtgagt | tggtgtcttt | atgacttaag | ttaaaagccc | aaaagcctct  | ctaggaggag | 1080 |
| taaacctgtt | tctgctgtgg | acagaccatg | tcatgtcatt | gttctttatg  | ttaaacttta | 1140 |
| tgtcaaaccg | tgtgacttac | actagtgtat | atattttttt | acgtatctac  | acaaacatga | 1200 |
| aacttgttct |            |            |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Asn Gly Asp Thr Phe Asp Glu Lys Ser Arg Ile Pro Asp Pro Asn Arg  
1 5 10 15  
Met Ile Arg Ala Tyr Thr Gln Ser Ala Ala Thr Leu Asn Leu Leu Arg  
20 25 30  
Ala Phe Ala Thr Gly Gly Tyr Ala Ala Ile Gln Arg Val Thr Gln Trp  
35 40 45  
Asn Leu Asp Phe Val Glu Gln Ser Glu Gln Ala Asp Arg Tyr Gln Glu  
50 55 60  
Leu Ala Asn Arg Val Asp Glu Ala Leu Gly Phe Met Ser Ala Cys Gly  
65 70 75 80  
Leu Gly Thr Asp His Pro Leu Met Thr Thr Asp Phe Tyr Thr Ser  
85 90 95  
His Glu Cys Leu Leu Leu Pro Tyr Glu Gln Ser Leu Thr Arg Leu Asp  
100 105 110  
Ser Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala His Met Val Trp Cys  
115 120 125  
Gly Glu Arg Thr Arg Gln Leu Asp Gly Ala His Val Glu Phe Leu Arg  
130 135 140  
Gly Ile Ala Asn Pro Leu Gly Ile Lys Val Ser Asn Lys Met Asp Pro  
145 150 155 160  
Asn Glu Leu Val Lys Leu Val Glu Ile Leu Asn Pro Asn Asn Lys Pro  
165 170 175  
Gly Arg Ile Thr Val Ile Val Arg Met Gly Ala Glu Asn Met Arg Val  
180 185 190  
Lys Leu Pro His Leu Ile Arg Ala Val Arg Arg Ser Gly Gln Ile Val  
195 200 205  
Thr Trp Val Cys Asp Pro Met His Gly Asn Thr Ile Lys Ala Pro Cys  
210 215 220  
Gly Leu Lys Thr Arg Ala Phe Asp Ser Ile Leu Ala Glu Val Arg Ala  
225 230 235 240  
Phe Leu Asp Val His Glu Gln Glu Gly Ser His Ala Gly Gly Ile His  
245 250 255  
Leu Glu Met Thr Gly Gln Asn Val Thr Glu Cys Ile Gly Gly Ser Arg  
260 265 270  
Thr Val Thr Tyr Asp Asp Leu Ser Ser Arg Tyr His Thr His Cys Asp  
275 280 285  
Pro Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu Ala Phe Ile Val Ala  
290 295 300  
Glu Arg Leu Arg Lys Arg Arg Thr Gly Ser Gln Arg Val Ser  
305 310 315

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

Met Ile Arg Ala Tyr Thr Gln Ser Ala Ala Thr Leu Asn Leu Leu Arg  
1 5 10 15  
Ala Phe Ala Thr Gly Gly Tyr Ala Ala Ile Gln Arg Val Thr Gln Trp  
20 25 30  
Asn Leu Asp Phe Val Glu Gln Ser Glu Gln Ala Asp Arg Tyr Gln Glu  
35 40 45  
Leu Ala Asn Arg Val Asp Glu Ala Leu Gly Phe Met Ser Ala Cys Gly  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Cys | Gly | Leu | Gly | Thr | Asp | His | Pro | Leu | Met | Thr | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Phe | Tyr | Thr | Ser | His | Glu | Cys | Leu | Leu | Leu | Pro | Tyr | Glu | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Arg | Leu | Asp | Ser | Thr | Ser | Gly | Leu | Tyr | Tyr | Asp | Cys | Ser | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Met | Val | Trp | Cys | Gly | Glu | Arg | Thr | Arg | Gln | Leu | Asp | Gly | Ala | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Glu | Phe | Leu | Arg | Gly | Ile | Ala | Asn | Pro | Leu | Gly | Ile | Lys | Val | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Lys | Met | Asp | Pro | Asn | Glu | Leu | Val | Lys | Leu | Val | Glu | Ile | Leu | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asn | Asn | Lys | Pro | Gly | Arg | Ile | Thr | Val | Ile | Val | Arg | Met | Gly | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asn | Met | Arg | Val | Lys | Leu | Pro | His | Leu | Ile | Arg | Ala | Val | Arg | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Gln | Ile | Val | Thr | Trp | Val | Cys | Asp | Pro | Met | His | Gly | Asn | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Lys | Ala | Pro | Cys | Gly | Leu | Lys | Thr | Arg | Ala | Phe | Asp | Ser | Ile | Leu |

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 145                                                             | 150 | 155 | 160 |
| Ala Glu Val Arg Ala Phe Leu Asp Val His Glu Gln Glu Gly Ser His |     |     |     |
|                                                                 | 165 | 170 | 175 |
| Ala Gly Gly Ile His Leu Glu Met Thr Gly Gln Asn Val Thr Glu Cys |     |     |     |
|                                                                 | 180 | 185 | 190 |
| Ile Gly Gly Ser Arg Thr Val Thr Tyr Asp Asp Leu Ser Ser Arg Tyr |     |     |     |
|                                                                 | 195 | 200 | 205 |
| His Thr His Cys Asp Pro Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu |     |     |     |
|                                                                 | 210 | 215 | 220 |
| Ala Phe Ile Val Ala Glu Arg Leu Arg Lys Arg Arg Thr Gly Ser Gln |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Arg Val Ser                                                     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| aggtccagca  | cacgatccta  | aatcctgtga | gcacgtcttc  | catcgtctggt | cttccattat  | 60   |
| tgacgaatct  | ctttgccttt  | ttttcttctt | tcttaaaca   | acccaattcg  | atttcaacga  | 120  |
| acgcctcttc  | tctctcactc  | tctttcgatt | tgttctttgc  | cggagctcgt  | agtgtaaagcg | 180  |
| tgatccgcgg  | cggagagatg  | gtcctaata  | atcctaata   | agccgttggt  | ggcggcgga   | 240  |
| gtggtttctt  | cgctctctt   | gcttcgtcga | tctccaattt  | gggatctgct  | atgaccaa    | 300  |
| cagttaatgg  | tttggttccc  | tatgagggac | ttgaagttat  | caatcctgaa  | ggaagtacag  | 360  |
| atgatgctga  | ggaggaagca  | agcagaggaa | gatggaagca  | agaggatcga  | gatggctatt  | 420  |
| ggaagatgat  | gcagaagtac  | ataggatctg | atgttacatc  | aatggtgacc  | cttctgtga   | 480  |
| ttatttttga  | accaatgaca  | atgcttcaga | aaatggcgga  | gttgatggaA  | tactcgcatc  | 540  |
| tgctagacat  | ggcagacaaa  | accgaggacc | cttatttgcg  | catggtgtat  | gcacatcgt   | 600  |
| gggctatata  | cgtgtattat  | gctttccaac | gtacctggaa  | accattcaat  | ccaatccttg  | 660  |
| gtgagactta  | tgagatggct  | aattacaatg | gtgttaactt  | catatctgaa  | caggtcagcc  | 720  |
| atcaccacc   | aatgagtgtc  | ggcatgtctg | aaaatgagca  | ttttacgtat  | gattgtactt  | 780  |
| caaaactgaa  | aacaaaattt  | ttgggcaatt | ccattgacgt  | ttaccagta   | ggaaggacac  | 840  |
| gggtgacact  | taaaagagat  | ggagttgttc | ttgacttggt  | acctcctctg  | accaaagttc  | 900  |
| acaacctaat  | ctttggacga  | acttgggtcg | attcgctcgt  | ggaaatgatc  | atgacaaatc  | 960  |
| agaccaccgg  | tgacaaagtc  | gtgctttact | ttcaacctatg | tggtctggttc | ggatctggtc  | 1020 |
| gatatgaagt  | ggatggatat  | gtctataacg | cctctgagga  | gcctaagata  | ctcatgactg  | 1080 |
| gcaaattgaa  | cgagtcctatg | agttatcagc | cgtgtgatgg  | tgaagggtgaa | cctctcccag  | 1140 |
| gcaccgaact  | gaaagaggta  | tggaaactcg | ctgatgtgcc  | aaaggatgac  | aaatatcaat  | 1200 |
| acactcactt  | tgctcacaag  | attaatagct | tcgacactgc  | cccgaataag  | ctgttgccct  | 1260 |
| ctgatttcacg | gttacgacct  | gatagatacg | cacttgagat  | gggcgacatg  | tccaaatcag  | 1320 |
| gctatgagaa  | gagcagcatg  | gaagagagac | agagagctga  | aaagagaacc  | cgcgaagaga  | 1380 |
| aaggccaagc  | ctttactcca  | aaatggttcg | atgtaacgga  | agaagtcact  | gctacaccat  | 1440 |
| ggggtgatct  | ggaagtttac  | caattcaatg | gaaagtactc  | ggaacatcgt  | gcagctgcgg  | 1500 |
| ataactctga  | agataacacc  | gaccctaagt | cgatccaatt  | caacccatgg  | caattccaag  | 1560 |
| atctgtctac  | ttaaattgtat | cgctccaaaa | gacagaaaag  | atcaaattctt | tttggaacaa  | 1620 |
| aatgtattct  | tattctctcg  | tagttacaaa | aaactttgtt  | ctacatctgc  | tagctttccc  | 1680 |
| attgctttct  | ctagtattag  | tgtacaactt | ctactgtttt  | gtcttaaatt  | cattcaaate  | 1740 |
| tttcttttg   |             |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

000001-130000

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | His | Thr | Ile | Leu | Asn | Pro | Val | Ser | Ile | Val | Ser | Ile | Ala | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Pro | Leu | Leu | Thr | Asn | Leu | Phe | Ala | Phe | Phe | Ser | Ser | Phe | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Pro | Asn | Ser | Ile | Ser | Thr | Asn | Ala | Ser | Ser | Leu | Ser | Leu | Ser | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | Leu | Phe | Phe | Ala | Gly | Ala | Arg | Ser | Val | Ser | Val | Ile | Arg | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Met | Ala | Pro | Asn | Asp | Pro | Lys | Lys | Ala | Val | Gly | Gly | Gly | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Phe | Phe | Ala | Ser | Leu | Ala | Ser | Ser | Ile | Ser | Asn | Leu | Gly | Ser | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Thr | Lys | Ser | Val | Asn | Gly | Leu | Val | Pro | Tyr | Glu | Gly | Leu | Glu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asn | Pro | Glu | Gly | Ser | Thr | Asp | Asp | Ala | Glu | Glu | Glu | Ala | Ser | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Trp | Lys | Gln | Glu | Asp | Arg | Asp | Gly | Tyr | Trp | Lys | Met | Met | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Tyr | Ile | Gly | Ser | Asp | Val | Thr | Ser | Met | Val | Thr | Leu | Pro | Val | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Phe | Glu | Pro | Met | Thr | Met | Leu | Gln | Lys | Met | Ala | Glu | Leu | Met | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Ser | His | Leu | Leu | Asp | Met | Ala | Asp | Lys | Thr | Glu | Asp | Pro | Tyr | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Met | Val | Tyr | Ala | Ser | Ser | Trp | Ala | Ile | Ser | Val | Tyr | Tyr | Ala | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Arg | Thr | Trp | Lys | Pro | Phe | Asn | Pro | Ile | Leu | Gly | Glu | Thr | Tyr | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Ala | Asn | Tyr | Asn | Gly | Val | Asn | Phe | Ile | Ser | Glu | Gln | Val | Ser | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Pro | Pro | Met | Ser | Ala | Gly | His | Ala | Glu | Asn | Glu | His | Phe | Thr | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Cys | Thr | Ser | Lys | Leu | Lys | Thr | Lys | Phe | Leu | Gly | Asn | Ser | Ile | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Tyr | Pro | Val | Gly | Arg | Thr | Arg | Val | Thr | Leu | Lys | Arg | Asp | Gly | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Leu | Asp | Leu | Val | Pro | Pro | Leu | Thr | Lys | Val | His | Asn | Leu | Ile | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Arg | Thr | Trp | Val | Asp | Ser | Pro | Gly | Glu | Met | Ile | Met | Thr | Asn | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Thr | Gly | Asp | Lys | Val | Val | Leu | Tyr | Phe | Gln | Pro | Cys | Gly | Trp | Phe |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Ser | Gly | Arg | Tyr | Glu | Val | Asp | Gly | Tyr | Val | Tyr | Asn | Ala | Ser | Glu |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Pro | Lys | Ile | Leu | Met | Thr |     |     |     |     |     |     |     |     |     |

435 440 445  
Arg Gln Arg Ala Glu Lys Arg Thr Arg Glu Glu Lys Gly Gln Ala Phe  
450 455 460  
Thr Pro Lys Trp Phe Asp Val Thr Glu Glu Val Thr Ala Thr Pro Trp  
465 470 475 480  
Gly Asp Leu Glu Val Tyr Gln Phe Asn Gly Lys Tyr Ser Glu His Arg  
485 490 495  
Ala Ala Ala Asp Asn Ser Glu Asp Asn Thr Asp Pro Lys Ser Ile Gln  
500 505 510  
Phe Asn Pro Trp Gln Phe Gln Asp Leu Ser Thr  
515 520

(2) INFORMATION FOR SEQ ID NO:1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

Met Ala Pro Asn Asp Pro Lys Lys Ala Val Gly Gly Gly Gly Ser Gly  
1 5 10 15  
Phe Phe Ala Ser Leu Ala Ser Ser Ile Ser Asn Leu Gly Ser Ala Met  
20 25 30  
Thr Lys Ser Val Asn Gly Leu Val Pro Tyr Glu Gly Leu Glu Val Ile  
35 40 45  
Asn Pro Glu Gly Ser Thr Asp Asp Ala Glu Glu Glu Ala Ser Arg Gly  
50 55 60  
Arg Trp Lys Gln Glu Asp Arg Asp Gly Tyr Trp Lys Met Met Gln Lys  
65 70 75 80  
Tyr Ile Gly Ser Asp Val Thr Ser Met Val Thr Leu Pro Val Ile Ile  
85 90 95  
Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Leu Met Glu Tyr  
100 105 110  
Ser His Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Leu Arg  
115 120 125  
Met Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr Ala Phe Gln  
130 135 140  
Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met  
145 150 155 160  
Ala Asn Tyr Asn Gly Val Asn Phe Ile Ser Glu Gln Val Ser His His  
165 170 175  
Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe Thr Tyr Asp  
180 185 190  
Cys Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Ile Asp Val  
195 200 205  
Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val  
210 215 220  
Leu Asp Leu Val Pro Pro Leu Thr Lys Val His Asn Leu Ile Phe Gly  
225 230 235 240  
Arg Thr Trp Val Asp Ser Pro Gly Glu Met Ile Met Thr Asn Gln Thr  
245 250 255  
Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly  
260 265 270  
Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ala Ser Glu Glu  
275 280 285  
Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ser Met Ser Tyr Gln  
290 295 300

Pro Cys Asp Gly Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu  
305 310 315 320  
Val Trp Lys Leu Ala Asp Val Pro Lys Asp Lys Tyr Gln Tyr Thr  
325 330 335  
His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu  
340 345 350  
Leu Pro Ser Asp Ser Arg Leu Arg Pro Asp Arg Tyr Ala Leu Glu Met  
355 360 365  
Gly Asp Met Ser Lys Ser Gly Tyr Glu Lys Ser Ser Met Glu Glu Arg  
370 375 380  
Gln Arg Ala Glu Lys Arg Thr Arg Glu Glu Lys Gly Gln Ala Phe Thr  
385 390 395 400  
Pro Lys Trp Phe Asp Val Thr Glu Glu Val Thr Ala Thr Pro Trp Gly  
405 410 415  
Asp Leu Glu Val Tyr Gln Phe Asn Gly Lys Tyr Ser Glu His Arg Ala  
420 425 430  
Ala Ala Asp Asn Ser Glu Asp Asn Thr Asp Pro Lys Ser Ile Gln Phe  
435 440 445  
Asn Pro Trp Gln Phe Gln Asp Leu Ser Thr  
450 455

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

Met Thr Lys Ser Val Asn Gly Leu Val Pro Tyr Glu Gly Leu Glu Val  
1 5 10 15  
Ile Asn Pro Glu Gly Ser Thr Asp Asp Ala Glu Glu Glu Ala Ser Arg  
20 25 30  
Gly Arg Trp Lys Gln Glu Asp Arg Asp Gly Tyr Trp Lys Met Met Gln  
35 40 45  
Lys Tyr Ile Gly Ser Asp Val Thr Ser Met Val Thr Leu Pro Val Ile  
50 55 60  
Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Leu Met Glu  
65 70 75 80  
Tyr Ser His Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Leu  
85 90 95  
Arg Met Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr Ala Phe  
100 105 110  
Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu  
115 120 125  
Met Ala Asn Tyr Asn Gly Val Asn Phe Ile Ser Glu Gln Val Ser His  
130 135 140  
His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe Thr Tyr  
145 150 155 160  
Asp Cys Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Ile Asp  
165 170 175  
Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val  
180 185 190  
Val Leu Asp Leu Val Pro Pro Leu Thr Lys Val His Asn Leu Ile Phe  
195 200 205  
Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Ile Met Thr Asn Gln  
210 215 220  
Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe

SEQUENCE = 1569473

(2) INFORMATION FOR SEQ ID NO:1274:

(A) LENGTH: 606 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..606  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569509

| (A1) Sequence | Sequence    | Sequence   | Sequence   | Sequence    | Sequence    | Position |
|---------------|-------------|------------|------------|-------------|-------------|----------|
| atcacaaactc   | tcaattttctt | ctctctcgat | tTcttgatat | atcagtaacc  | aaaaaAcaca  | 60       |
| gagaattaaaa   | acatggctta  | cttctccaca | gcgacatctc | ttctcctcct  | cgctcctctct | 120      |
| gtttcctctc    | cttatgttca  | tggagcctcc | gactgcgaca | cccttgatgat | taccctgttc  | 180      |
| ccatgtttac    | cttttatatc  | gatcgggggt | acggccgata | caccacagc   | ttcatgctgc  | 240      |
| tccagtctca    | aaaatattct  | cgatacga   | ccgatatgtc | tatgcgaagg  | gttgaagaag  | 300      |
| gcaccttag     | gaatcaagga  | gaggacacta | cggacgagga | ggaggccacg  | gtggtggtgg  | 360      |
| acactatgga    | ggtggaggac  | accatggagg | aggaggtcac | gggctgaacg  | aacctgttca  | 420      |
| gacgaagccg    | ggtgtttaaa  | agttataact | atcaaataaa | ttccaccatgc | ataattgc    | 480      |
| ctctatatac    | acttatgtct  | tatatgtatc | catcaaaaa  | aaccatggtg  | agtttgaat   | 540      |
| gcagttcctt    | cagaaatgtg  | tggaataatg | tttcacaata | ataatagaat  | atctctgttg  | 600      |
| attctg        |             |            |            |             |             |          |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569510

His Asn Ser His Phe Leu Leu Ser Arg Phe Leu Asp Ile Ser Val Thr



1 5 10 15  
Lys Lys His Arg Glu Leu Lys His Gly Leu Leu Leu His Ser Asp Ile  
20 25 30  
Ser Ser Pro Pro Arg Pro Leu Cys Phe Leu Ser Leu Cys Ser Trp Ser  
35 40 45  
Leu Arg Leu Arg His Pro Cys Asp Tyr Pro Val Pro Met Phe Thr Phe  
50 55 60  
Tyr Ile Asp Arg Gly Tyr Gly Arg Tyr Thr His Ser Phe Met Leu Leu  
65 70 75 80  
Gln Ser Gln Lys Tyr Ser Arg Tyr Glu Thr Asp Met Ser Met Arg Arg  
85 90 95  
Val Glu Glu Gly Thr Phe Arg Asn Gln Gly Glu Asp Thr Thr Asp Glu  
100 105 110  
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met  
115 120 125  
Glu Glu Glu Val Thr Gly  
130

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

Met Ala Tyr Phe Thr Ala Thr Ser Leu Leu Leu Val Leu Ser  
1 5 10 15  
Val Ser Ser Pro Tyr Val His Gly Ala Ser Asp Cys Asp Thr Leu Val  
20 25 30  
Ile Thr Leu Phe Pro Cys Leu Pro Phe Ile Ser Ile Gly Gly Thr Ala  
35 40 45  
Asp Thr Pro Thr Ala Ser Cys Cys Ser Ser Leu Lys Asn Ile Leu Asp  
50 55 60  
Thr Lys Pro Ile Cys Leu Cys Glu Gly Leu Lys Lys Ala Pro Leu Gly  
65 70 75 80  
Ile Lys Glu Arg Thr Leu Arg Thr Arg Arg Arg Pro Arg Trp Trp Trp  
85 90 95  
Thr Leu Trp Arg Trp Arg Thr Pro Trp Arg Arg Arg Ser Arg Ala Glu  
100 105 110  
Arg Thr Cys Ser Asp Glu Ala Gly Cys Leu Lys Val Ile Thr Ile Lys  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

Met Phe Thr Phe Tyr Ile Asp Arg Gly Tyr Gly Arg Tyr Thr His Ser  
1 5 10 15

000001-11666666

Phe Met Leu Leu Gln Ser Gln Lys Tyr Ser Arg Tyr Glu Thr Asp Met  
20 25 30  
Ser Met Arg Arg Val Glu Glu Gly Thr Phe Arg Asn Gln Gly Glu Asp  
35 40 45  
Thr Thr Asp Glu Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val  
50 55 60  
Glu Asp Thr Met Glu Glu Glu Val Thr Gly  
65 70

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..985
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| actttttctca | gctccgacaa  | aaatggctgc | aatcaccatt | tcttcctcct | tgcacgcctc  | 60  |
| agcctctccg  | cgtgttggtc  | gtccacatgt | ttctcgaaat | acccctgtga | tcaccctcta  | 120 |
| ttcacgcttc  | acaccatcct  | tctccttccc | atctctctcc | ttcacactcc | gtgacacagc  | 180 |
| tccgtctcgt  | cgtcgttcc   | tctttatcgc | ctccgcgcgc | aaatctctaa | cggagacgga  | 240 |
| gctgcttcca  | atcacagagg  | ctgattcaat | cccgtccgct | tccggtgtat | acgctgtata  | 300 |
| cgataagagc  | gacgagcttc  | agttogtcgg | aatatctcgg | aacatcgctg | cgagtgtctc  | 360 |
| tgctcatctc  | aaatctgtgc  | cggagctttg | tggtccggtt | aagggttgaa | tagtagaaga  | 420 |
| accagataaa  | gcagttttta  | cacaagcatg | gaaattatgg | atagaagaac | atataaaaagt | 480 |
| aactggaaaa  | gttccgcgcg  | ggaataagtc | agggaacaac | acatttgtca | aacaaactcc  | 540 |
| gaggaagAaa  | atccgatatc  | cgtctcactc | caggtcgcca | tgTttgagct | cacggttcyt  | 600 |
| ttggaGgAac  | tgattgaCcg  | TttagtGaaa | gagagcAaag | tggtagcttt | cataaaaagga | 660 |
| tcaaggagtg  | ctcctcaatg  | tggattctca | cagagagttg | ttgggattct | tgaaagccaa  | 720 |
| ggagttgatt  | atgaaaactgt | tgatgttctt | gacgatgagt | ataatcatgg | gctaagggag  | 780 |
| acgcttaaga  | actacagcaa  | ttggccaacg | tttccacaga | tatttgtgaa | aggagaactt  | 840 |
| gtaggaggat  | gtgatatttt  | gacctcaatg | tatgaaaatg | gtgaacttgc | caatatcttg  | 900 |
| aactagtttc  | atccgatttt  | cttctctatt | tctagttgta | actccaaaca | ttcattatag  | 960 |
| agaaaacatg  | cttggattct  | cttcc      |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Leu Phe Ser Ala Pro Thr Lys Met Ala Ala Ile Thr Ile Ser Ser Ser |  |
| 1 5 10 15                                                       |  |
| Leu His Ala Ser Ala Ser Pro Arg Val Val Arg Pro His Val Ser Arg |  |
| 20 25 30                                                        |  |
| Asn Thr Pro Val Ile Thr Leu Tyr Ser Arg Phe Thr Pro Ser Phe Ser |  |
| 35 40 45                                                        |  |
| Phe Pro Ser Leu Ser Phe Thr Leu Arg Asp Thr Ala Pro Ser Arg Arg |  |
| 50 55 60                                                        |  |
| Arg Ser Phe Phe Ile Ala Ser Ala Val Lys Ser Leu Thr Glu Thr Glu |  |
| 65 70 75 80                                                     |  |
| Leu Leu Pro Ile Thr Glu Ala Asp Ser Ile Pro Ser Ala Ser Gly Val |  |
| 85 90 95                                                        |  |

Tyr Ala Val Tyr Asp Lys Ser Asp Glu Leu Gln Phe Val Gly Ile Ser  
100 105 110  
Arg Asn Ile Ala Ala Ser Val Ser Ala His Leu Lys Ser Val Pro Glu  
115 120 125  
Leu Cys Gly Ser Val Lys Val Gly Ile Val Glu Glu Pro Asp Lys Ala  
130 135 140  
Val Leu Thr Gln Ala Trp Lys Leu Trp Ile Glu Glu His Ile Lys Val  
145 150 155 160  
Thr Gly Lys Val Pro Pro Gly Asn Lys Ser Gly Asn Asn Thr Phe Val  
165 170 175  
Lys Gln Thr Pro Arg Lys Lys Ile Arg Tyr Pro Ser His Ser Arg Ser  
180 185 190  
Pro Cys Leu Ser Ser Arg Phe Xaa Trp Arg Asn  
195 200

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1569524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

Met Ala Ala Ile Thr Ile Ser Ser Ser Leu His Ala Ser Ala Ser Pro  
1 5 10 15  
Arg Val Val Arg Pro His Val Ser Arg Asn Thr Pro Val Ile Thr Leu  
20 25 30  
Tyr Ser Arg Phe Thr Pro Ser Phe Ser Phe Pro Ser Leu Ser Phe Thr  
35 40 45  
Leu Arg Asp Thr Ala Pro Ser Arg Arg Arg Ser Phe Phe Ile Ala Ser  
50 55 60  
Ala Val Lys Ser Leu Thr Glu Thr Glu Leu Leu Pro Ile Thr Glu Ala  
65 70 75 80  
Asp Ser Ile Pro Ser Ala Ser Gly Val Tyr Ala Val Tyr Asp Lys Ser  
85 90 95  
Asp Glu Leu Gln Phe Val Gly Ile Ser Arg Asn Ile Ala Ala Ser Val  
100 105 110  
Ser Ala His Leu Lys Ser Val Pro Glu Leu Cys Gly Ser Val Lys Val  
115 120 125  
Gly Ile Val Glu Glu Pro Asp Lys Ala Val Leu Thr Gln Ala Trp Lys  
130 135 140  
Leu Trp Ile Glu Glu His Ile Lys Val Thr Gly Lys Val Pro Pro Gly  
145 150 155 160  
Asn Lys Ser Gly Asn Asn Thr Phe Val Lys Gln Thr Pro Arg Lys Lys  
165 170 175  
Ile Arg Tyr Pro Ser His Ser Arg Ser Pro Cys Leu Ser Ser Arg Phe  
180 185 190  
Xaa Trp Arg Asn  
195

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

00000000-00000000

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1569525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

Met Phe Glu Leu Thr Val Xaa Leu Glu Glu Leu Ile Asp Arg Leu Val  
1 5 10 15  
Lys Glu Ser Lys Val Val Ala Phe Ile Lys Gly Ser Arg Ser Ala Pro  
20 25 30  
Gln Cys Gly Phe Ser Gln Arg Val Val Gly Ile Leu Glu Ser Gln Gly  
35 40 45  
Val Asp Tyr Glu Thr Val Asp Val Leu Asp Asp Glu Tyr Asn His Gly  
50 55 60  
Leu Arg Glu Thr Leu Lys Asn Tyr Ser Asn Trp Pro Thr Phe Pro Gln  
65 70 75 80  
Ile Phe Val Lys Gly Glu Leu Val Gly Gly Cys Asp Ile Leu Thr Ser  
85 90 95  
Met Tyr Glu Asn Gly Glu Leu Ala Asn Ile Leu Asn  
100 105

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..654

(D) OTHER INFORMATION: / Ceres Seq. ID 1569526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

atatttgaag ttcgtggatt ttgaaggatt tgattggttt ccatgatcta gagttttgag 60  
aatggcgatg gtatcaggaa gacgatctac tctaaacccc gacgcaccto tttttattcc 120  
ggcagctgta cgacaagtgg aagatttctc accggagtgg tggcaattgg tgacaacttc 180  
gacttggtac cctgattact ggatcagtcg gcagcagcaa ggcgcgatg gtttctatga 240  
caacggagag aatgagaatg gtggaggatc tatcgatgta gctgatcttc ttccagaatc 300  
attttatttt gatgatatgg aagatttctt tgacactgat gctgctgagt ttgatcaagg 360  
attcgatgga agaattgtatt accaagcacc ttccgaattt ggctttggaa agaattggtga 420  
gatgggttaag aaatcaagtg gaaacaggag cccgagatcg attgtggaac cagctaagta 480  
tcgggaaaag ccagcgaaat ggggaaacca gagggttgct gctgctccga gaaacatcca 540  
ccagcctcgc tgaagagata tgttgttaac tagtcagaga agtcagagca gttcgggtctg 600  
tgtatcttta gccaccactg tacctttgta atYYYYtttta gtatttgctt ccac

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1569527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

Met Ala Met Val Ser Gly Arg Arg Ser Thr Leu Asn Pro Asp Ala Pro  
1 5 10 15  
Leu Phe Ile Pro Ala Ala Val Arg Gln Val Glu Asp Phe Ser Pro Glu  
20 25 30  
Trp Trp Gln Leu Val Thr Thr Ser Thr Trp Tyr Pro Asp Tyr Trp Ile  
35 40 45  
Ser Gln Gln Gln Gln Gly Ala Asp Gly Phe Tyr Asp Asn Gly Glu Asn  
50 55 60  
Glu Asn Gly Gly Gly His Ile Asp Val Ala Asp Leu Leu Pro Glu Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Tyr | Phe | Asp | Asp | Met | Glu | Asp | Phe | Phe | Asp | Thr | Asp | Ala | Ala | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Asp | Gln | Gly | Phe | Asp | Gly | Arg | Met | Tyr | Tyr | Gln | Ala | Pro | Ser | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Phe | Gly | Lys | Asn | Gly | Glu | Met | Val | Lys | Lys | Ser | Ser | Gly | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Ser | Pro | Arg | Ser | Ile | Val | Glu | Pro | Ala | Lys | Tyr | Ala | Glu | Lys | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Lys | Trp | Gly | Asn | Gln | Arg | Val | Ala | Ala | Ala | Pro | Arg | Asn | Ile | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Pro | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1569528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Gly | Arg | Arg | Ser | Thr | Leu | Asn | Pro | Asp | Ala | Pro | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Pro | Ala | Ala | Val | Arg | Gln | Val | Glu | Asp | Phe | Ser | Pro | Glu | Trp | Trp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Val | Thr | Thr | Ser | Thr | Trp | Tyr | Pro | Asp | Tyr | Trp | Ile | Ser | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gln | Gln | Gln | Gly | Ala | Asp | Gly | Phe | Tyr | Asp | Asn | Gly | Glu | Asn | Glu | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Gly | His | Ile | Asp | Val | Ala | Asp | Leu | Leu | Pro | Glu | Ser | Phe | Tyr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Asp | Asp | Met | Glu | Asp | Phe | Phe | Asp | Thr | Asp | Ala | Ala | Glu | Phe | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gln | Gly | Phe | Asp | Gly | Arg | Met | Tyr | Tyr | Gln | Ala | Pro | Ser | Glu | Phe | Gly |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Gly | Lys | Asn | Gly | Glu | Met | Val | Lys | Lys | Ser | Ser | Gly | Asn | Arg | Ser |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Arg | Ser | Ile | Val | Glu | Pro | Ala | Lys | Tyr | Ala | Glu | Lys | Pro | Ala | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Gly | Asn | Gln | Arg | Val | Ala | Ala | Ala | Pro | Arg | Asn | Ile | His | Gln | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1569529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Trp | Lys | Ile | Ser | Leu | Thr | Leu | Met | Leu | Leu | Ser | Leu | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Asp Ser Met Glu Glu Cys Ile Thr Lys His Leu Pro Asn Leu Ala Leu  
20 25 30  
Glu Arg Met Val Arg Trp Leu Arg Asn Gln Val Glu Thr Gly Ala Arg  
35 40 45  
Asp Arg Leu Trp Asn Gln Leu Ser Met Arg Lys Ser Gln Arg Asn Gly  
50 55 60  
Glu Thr Arg Gly Leu Leu Leu Leu Arg Glu Thr Ser Thr Ser Leu Ala  
65 70 75 80  
Glu Glu Ile Cys Cys  
85

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ttttcggtt caacggaacc gccggaatat ggagaatagc ggcgataaat gaagctgggtg  | 60   |
| ggttgaaaga tcggaccacc gtggaagata tggatctcgc cgtccgagca agtcttcgcg  | 120  |
| gctggaaatt tctctacctc ggtgaccttc aggtgaaaag tgagcttcca agtactttta  | 180  |
| gagccttcog ttttcagcaa catagatggt cttgtggacc tgcaaatctc tttaggaaaa  | 240  |
| tggttatgga gatcgtaaga aacaagaaag tgagattctg gaagaaagtg tacgtgatat  | 300  |
| acagcttctt ctttgtgagg aaaatcattg cacattgggt cacattttgt ttctactgcg  | 360  |
| ttgttcttcc tctcacaatt ctcgctcccg aggttaaagt tccgatttgg gggtcgggtt  | 420  |
| atatcccatc catcatcact atcctcaatt ccgtcggtag tcCaaggtca attcatctgc  | 480  |
| tgttctattg gattctattc gagaatgtga tgtcgctgca ccggacaaaag gccactctca | 540  |
| ttggtctggt tgaggcagga agggctaacg agttggtagt gactgctaag cttggaagcg  | 600  |
| gtcagagcgc taaaggaaac actaaaggga tcaaaagggt cccaagaatc ttcaaattgc  | 660  |
| ctgatcgatt gaatacattg gagcttggat ttgcggcttt cttgttcgtg tgcggatgct  | 720  |
| atgactttgt gcacgggaag aacaattact tcatctacct gtttcttcag acaatgtctt  | 780  |
| tcttcatcag tgggctgggc tggatcggga cttatgtccc gagttagtag ttgtgttgtt  | 840  |
| tcagagagaa aagagaatgt tattaatttt cttgagaaat aaagacaatt ttcattgaaa  | 900  |
| tgacaaagga aaattgatag gggagataga gacgtaccgg taacaacaag taggaagaaa  | 960  |
| ggagaagact tttatcaaag accaggaaag aggagaagct ccaagggttc ttttgattta  | 1020 |
| tttttatttt ttctgtgttt tatttatata gctatgggat ttgtgattca gttgttgtga  | 1080 |
| gattttaatt ttcgttcttt gttttttatt ttggtttttg ggtatttttt cgttttgaaa  | 1140 |
| gtgttagtct ttttgttttg tttttaaatt aaattccaag taaaaattaa attcc       |      |

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..274
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Phe Gly Phe Asn Gly Thr Ala Gly Ile Trp Arg Ile Ala Ala Ile Asn  
1 5 10 15  
Glu Ala Gly Gly Trp Lys Asp Arg Thr Thr Val Glu Asp Met Asp Leu  
20 25 30  
Ala Val Arg Ala Ser Leu Arg Gly Trp Lys Phe Leu Tyr Leu Gly Asp  
35 40 45  
Leu Gln Val Lys Ser Glu Leu Pro Ser Thr Phe Arg Ala Phe Arg Phe

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Gln Gln His Arg Trp Ser Cys Gly Pro Ala Asn Leu Phe Arg Lys Met |     |     |
| 65                                                              | 70  | 75  |
| Val Met Glu Ile Val Arg Asn Lys Lys Val Arg Phe Trp Lys Lys Val |     | 80  |
|                                                                 | 85  | 90  |
| Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Ile Ile Ala His Trp |     | 95  |
|                                                                 | 100 | 105 |
| Val Thr Phe Cys Phe Tyr Cys Val Val Leu Pro Leu Thr Ile Leu Val |     | 110 |
|                                                                 | 115 | 120 |
| Pro Glu Val Lys Val Pro Ile Trp Gly Ser Val Tyr Ile Pro Ser Ile |     | 125 |
|                                                                 | 130 | 135 |
| Ile Thr Ile Leu Asn Ser Val Gly Thr Pro Arg Ser Ile His Leu Leu |     | 140 |
|                                                                 | 145 | 150 |
| Phe Tyr Trp Ile Leu Phe Glu Asn Val Met Ser Leu His Arg Thr Lys |     | 155 |
|                                                                 | 165 | 170 |
| Ala Thr Leu Ile Gly Leu Phe Glu Ala Gly Arg Ala Asn Glu Leu Val |     | 175 |
|                                                                 | 180 | 185 |
| Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly Asn Thr Lys |     | 190 |
|                                                                 | 195 | 200 |
| Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp Arg Leu Asn |     | 205 |
|                                                                 | 210 | 215 |
| Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys Gly Cys Tyr |     | 220 |
|                                                                 | 225 | 230 |
| Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu Phe Leu Gln |     | 235 |
|                                                                 | 245 | 250 |
| Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly Thr Tyr Val |     | 255 |
|                                                                 | 260 | 265 |
|                                                                 |     | 270 |
| Pro Ser                                                         |     |     |

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1569532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Asp Leu Ala Val Arg Ala Ser Leu Arg Gly Trp Lys Phe Leu Tyr |     |
| 1                                                               | 15  |
| Leu Gly Asp Leu Gln Val Lys Ser Glu Leu Pro Ser Thr Phe Arg Ala |     |
|                                                                 | 30  |
| Phe Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala Asn Leu Phe |     |
|                                                                 | 45  |
| Arg Lys Met Val Met Glu Ile Val Arg Asn Lys Lys Val Arg Phe Trp |     |
|                                                                 | 60  |
| Lys Lys Val Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Ile Ile |     |
|                                                                 | 75  |
| Ala His Trp Val Thr Phe Cys Phe Tyr Cys Val Val Leu Pro Leu Thr |     |
|                                                                 | 90  |
| Ile Leu Val Pro Glu Val Lys Val Pro Ile Trp Gly Ser Val Tyr Ile |     |
|                                                                 | 105 |
| Pro Ser Ile Ile Thr Ile Leu Asn Ser Val Gly Thr Pro Arg Ser Ile |     |
|                                                                 | 120 |
| His Leu Leu Phe Tyr Trp Ile Leu Phe Glu Asn Val Met Ser Leu His |     |
|                                                                 | 135 |
| Arg Thr Lys Ala Thr Leu Ile Gly Leu Phe Glu Ala Gly Arg Ala Asn |     |
|                                                                 | 150 |
|                                                                 | 160 |

Glu Leu Val Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly  
165 170 175  
Asn Thr Lys Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp  
180 185 190  
Arg Leu Asn Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys  
195 200 205  
Gly Cys Tyr Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu  
210 215 220  
Phe Leu Gln Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly  
225 230 235 240  
Thr Tyr Val Pro Ser  
245

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

Met Val Met Glu Ile Val Arg Asn Lys Lys Val Arg Phe Trp Lys Lys  
1 5 10 15  
Val Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Ile Ile Ala His  
20 25 30  
Trp Val Thr Phe Cys Phe Tyr Cys Val Val Leu Pro Leu Thr Ile Leu  
35 40 45  
Val Pro Glu Val Lys Val Pro Ile Trp Gly Ser Val Tyr Ile Pro Ser  
50 55 60  
Ile Ile Thr Ile Leu Asn Ser Val Gly Thr Pro Arg Ser Ile His Leu  
65 70 75 80  
Leu Phe Tyr Trp Ile Leu Phe Glu Asn Val Met Ser Leu His Arg Thr  
85 90 95  
Lys Ala Thr Leu Ile Gly Leu Phe Glu Ala Gly Arg Ala Asn Glu Leu  
100 105 110  
Val Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly Asn Thr  
115 120 125  
Lys Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp Arg Leu  
130 135 140  
Asn Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys Gly Cys  
145 150 155 160  
Tyr Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu Phe Leu  
165 170 175  
Gln Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly Thr Tyr  
180 185 190  
Val Pro Ser  
195

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569538

2025 RELEASE UNDER E.O. 14176



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| gcagacattt | tagacaaagt  | tactctcttt | ctttctcatg | ttcttttcgg  | acagaacaaa | 60   |
| aactcccta  | ccaaatgtca  | attcctttgg | tctctctctg | aataatcacc  | tctcttcaaa | 120  |
| ccctattcaa | ttttaactat  | cgatcttcgg | ctaagttctc | aatggcggcg  | gcgtttgcct | 180  |
| ctcttccac  | atttagtgtc  | gtcaattcct | ccagatttcc | cagaagaaga  | atcggttttt | 240  |
| cttgctccaa | aaagcccctc  | gaagttcggt | gttcttccgg | caatactcgt  | tacactaagc | 300  |
| agagaggggc | atttacatca  | ttgaaagaat | gtgcgatttc | attagcttta  | tcggttggtt | 360  |
| taatggtttc | agtaccttcg  | attgctttgc | ctcccaatgc | tcacgcagtg  | gcgaatccag | 420  |
| tgattccaga | tgtttcagtg  | ttgatctccg | gtcctccgat | taaagatccg  | gaagctttac | 480  |
| taagatatgc | attgcctatt  | gacaacaaag | ccatcaggga | agtcgagaag  | cctcttgagg | 540  |
| atatcactga | tagcctcaag  | attgctggcg | ttaaggctct | agattctggt  | gaacggaatg | 600  |
| tgaggcaggc | aagtagaaca  | ttgcagcaag | ggaaaagtat | aattgtggca  | ggttttgctg | 660  |
| aatcgaagaa | ggatcatggt  | aatgaaatga | ttgaaaagtt | ggaagctggg  | atgcaagata | 720  |
| tgcttaagat | agtggaagat  | cgaaaaagag | acgcagttgc | tccaaaacag  | aaagaaattc | 780  |
| tcaaataatg | tggcgggaata | gaagaggata | tggttgatgg | ctttccatat  | gaagtgcggg | 840  |
| aagagtatcg | Cgaacatgcc  | tctcctcaag | ggaagagcta | gtgtggacat  | gaaggtcaag | 900  |
| atcaaggaca | atcccaacat  | cgaggactgt | gtgttccgca | ttgttcttga  | tggttataac | 960  |
| gcccctgtta | ccgccggaaa  | ctttgtggac | ttggtagaga | ggcattttcta | cgatgctctt | 1020 |
| ccggcacttc | atatggaaag  | ccatcaacca | tatcctcctc | tattccatgt  | ttctgttttt | 1080 |
| tggtttctac | tcggtattca  | atacaatttg | tcttttccct | tctgtcattt  | ttgtcagatg | 1140 |
| ttatttagtt | ttgttcaagt  | taactcttgt | tggttatctt | actttaagag  | ctcatatgga | 1200 |
| tctcgttctt | cc          |            |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Phe | Ala | Ser | Leu | Pro | Thr | Phe | Ser | Val | Val | Asn | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Arg | Phe | Pro | Arg | Arg | Arg | Ile | Gly | Phe | Ser | Cys | Ser | Lys | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Val | Arg | Cys | Ser | Ser | Gly | Asn | Thr | Arg | Tyr | Thr | Lys | Gln | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Phe | Thr | Ser | Leu | Lys | Glu | Cys | Ala | Ile | Ser | Leu | Ala | Leu | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Gly | Leu | Met | Val | Ser | Val | Pro | Ser | Ile | Ala | Leu | Pro | Pro | Asn | Ala |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| His | Ala | Val | Ala | Asn | Pro | Val | Ile | Pro | Asp | Val | Ser | Val | Leu | Ile | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Pro | Pro | Ile | Lys | Asp | Pro | Glu | Ala | Leu | Leu | Arg | Tyr | Ala | Leu | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asp | Asn | Lys | Ala | Ile | Arg | Glu | Val | Gln | Lys | Pro | Leu | Glu | Asp | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asp | Ser | Leu | Lys | Ile | Ala | Gly | Val | Lys | Ala | Leu | Asp | Ser | Val | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Arg | Asn | Val | Arg | Gln | Ala | Ser | Arg | Thr | Leu | Gln | Gln | Gly | Lys | Ser | Ile |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Val | Ala | Gly | Phe | Ala | Glu | Ser | Lys | Lys | Asp | His | Gly | Asn | Glu | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Glu | Lys | Leu | Glu | Ala | Gly | Met | Gln | Asp | Met | Leu | Lys | Ile | Val | Glu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Arg | Lys | Arg | Asp | Ala | Val | Ala | Pro | Lys | Gln | Lys | Glu | Ile | Leu | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Val | Gly | Gly | Ile | Glu | Glu | Asp | Met | Val | Asp | Gly | Phe | Pro | Tyr | Glu |

210 215 220  
Val Pro Glu Glu Tyr Arg Glu His Ala Ser Pro Gln Gly Lys Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala His Ala Val  
1 5 10 15  
Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser Gly Pro Pro  
20 25 30  
Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro Ile Asp Asn  
35 40 45  
Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile Thr Asp Ser  
50 55 60  
Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu Arg Asn Val  
65 70 75 80  
Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile Ile Val Ala  
85 90 95  
Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met Ile Glu Lys  
100 105 110  
Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu Asp Arg Lys  
115 120 125  
Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys Tyr Val Gly  
130 135 140  
Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu Val Pro Glu  
145 150 155 160  
Glu Tyr Arg Glu His Ala Ser Pro Gln Gly Lys Ser  
165 170

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

Met Ala Phe His Met Lys Cys Arg Lys Ser Ile Ala Asn Met Pro Leu  
1 5 10 15  
Leu Lys Gly Arg Ala Ser Val Asp Met Lys Val Lys Ile Lys Asp Asn  
20 25 30  
Pro Asn Ile Glu Asp Cys Val Phe Arg Ile Val Leu Asp Gly Tyr Asn  
35 40 45  
Ala Pro Val Thr Ala Gly Asn Phe Val Asp Leu Val Glu Arg His Phe  
50 55 60  
Tyr Asp Ala Leu Pro Ala Leu His Met Glu Ser His Gln Pro Tyr Pro  
65 70 75 80  
Pro Leu Phe His Val Ser Val Phe Trp Phe Leu Leu Gly Ile Gln Tyr  
85 90 95

Asn Leu Ser Phe Pro Phe Cys His Phe Cys Gln Met Leu Phe Ser Phe  
100 105 110  
Val Gln Val Asn Ser Cys Trp Leu Ser Tyr Phe Lys Ser Ser Tyr Gly  
115 120 125  
Ser Arg Ser Ser  
130

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..684
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| acatctcact | gctcactact  | ctcactgtaa  | tccctTagat | ctTcttttca | aattTcaatg | 60  |
| gcgtccCggt | gatgttgagt  | atcgggtgctt | cgttggaggt | ctagcatggg | ccactgatga | 120 |
| cagagctctt | gagactgcct  | tcgctcaata  | cggcgacgtt | attgattcca | agatcattaa | 180 |
| cgatcgtgag | actggaagat  | caaggggatt  | cggattcgtc | accttcaagg | atgagaaagc | 240 |
| catgaaggat | gcgattgagg  | gaatgaacgg  | acaagatctc | gatggccgta | gcatactgt  | 300 |
| taacgaggct | cagtcacgag  | gaagcgggtg  | cggcggaggg | caccgtggag | gtggtggcgg | 360 |
| tggataccgc | agcggcgggtg | gtggaagacg  | tgagggagga | ggaggatacg | gtggtggtga | 420 |
| aggaggaggt | tacggaggaa  | gcgggtggtg  | tggaggatgg | taattccttt | aattaggttt | 480 |
| gggattacca | atgaatgttc  | tctctctcgc  | ttgttatgct | tctacttggt | tttgtgtgtt | 540 |
| ctctattttg | ttctggttct  | gcttttagatt | tgatgtaaca | gttcgtgatt | aggtattttg | 600 |
| gtatctggaa | acgtaatgtt  | aagtcacttg  | tcattctcta | aataacaaat | ttcttcggag | 660 |
| atattatctc | tggtgattga  | ttct        |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Thr | Ala | His | Tyr | Ser | His | Cys | Asn | Pro | Leu | Asp | Leu | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Phe | Gln | Trp | Arg | Pro | Gly | Asp | Val | Glu | Tyr | Arg | Cys | Phe | Val | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Ala | Trp | Ala | Thr | Asp | Asp | Arg | Ala | Leu | Glu | Thr | Ala | Phe | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Tyr | Gly | Asp | Val | Ile | Asp | Ser | Lys | Ile | Ile | Asn | Asp | Arg | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Arg | Ser | Arg | Gly | Phe | Gly | Phe | Val | Thr | Phe | Lys | Asp | Glu | Lys | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | Lys | Asp | Ala | Ile | Glu | Gly | Met | Asn | Gly | Gln | Asp | Leu | Asp | Gly | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Ile | Thr | Val | Asn | Glu | Ala | Gln | Ser | Arg | Gly | Ser | Gly | Gly | Gly | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | His | Arg | Gly | Gly | Gly | Gly | Gly | Gly | Tyr | Arg | Ser | Gly | Gly | Gly | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Arg | Glu | Gly | Gly | Gly | Gly | Tyr | Gly | Gly | Gly | Glu | Gly | Gly | Gly | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Ser | Gly | Gly | Gly | Gly | Gly | Trp |     |     |     |     |     |     |     |

145

150

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..773
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tccatataaa | ttgttccaaa | tttcattcgt | atcctttccg | ctgctgccgt | cttcgtctct | 60  |
| gagataataa | ggacttggtg | atctttccat | cgttaaaagg | catttcaaag | agacaatatg | 120 |
| tcaggatgat | aggctgcccc | tggtgttggt | cctccccccg | ttgctgagcc | agcggccatc | 180 |
| ccagaggaca | tggacttaat | gactgcattg | gagttgactc | ttaggaaagc | tcgtgcttat | 240 |
| ggtggtggtg | ttcgtgggtc | ccatgagtg  | gctaagctta | ttgagaagcg | tgtggctcaa | 300 |
| ctcgttgtct | tggttgaaga | ctgcaaccag | cctgattatg | tcaagcttgt | gaaggctctc | 360 |
| tgtgctgata | acgaagtcag | gttgctaaca | gttccaagt  | ccaagaccct | tggcgaatgg | 420 |
| gctggtctct | gcaagattga | ttctgagggt | aatgccagga | agggtgttgg | atgctcatgt | 480 |
| cttggtgtca | aggacttcgg | cgaggagaca | actgccctca | gtatcgtcaa | taagcatatt | 540 |
| gcttctcaat | aaaatgccat | gaagcatatc | taaactcgga | tttcatatgt | tttccacccc | 600 |
| caatgctgtt | Attctcttgg | ttttgatata | ttatctaata | tttagcggac | agctcttgag | 660 |
| atttstttgg | aacatgatca | agttttgttg | ttatctagac | tttactcttc | caaggccaaa | 720 |
| tttgcttgag | atttatttgg | ctcattactc | ttcatcataa | tttttttttt | cct        |     |

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Asp | Glu | Ala | Ala | Pro | Val | Val | Val | Pro | Pro | Pro | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Glu | Pro | Ala | Ala | Ile | Pro | Glu | Asp | Met | Asp | Leu | Met | Thr | Ala | Leu | Glu |
|     |     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |
| Leu | Thr | Leu | Arg | Lys | Ala | Arg | Ala | Tyr | Gly | Gly | Val | Val | Arg | Gly | Leu |
|     |     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |
| His | Glu | Cys | Ala | Lys | Leu | Ile | Glu | Lys | Arg | Val | Ala | Gln | Leu | Val | Val |
|     |     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |
| Leu | Ala | Glu | Asp | Cys | Asn | Gln | Pro | Asp | Tyr | Val | Lys | Leu | Val | Lys | Ala |
|     |     |     |     | 65  |     |     |     |     |     | 70  |     |     |     | 75  | 80  |
| Leu | Cys | Ala | Asp | His | Glu | Val | Arg | Leu | Leu | Thr | Val | Pro | Ser | Ala | Lys |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Thr | Leu | Gly | Glu | Trp | Ala | Gly | Leu | Cys | Lys | Ile | Asp | Ser | Glu | Gly | Asn |
|     |     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |
| Ala | Arg | Lys | Val | Val | Gly | Cys | Ser | Cys | Leu | Val | Val | Lys | Asp | Phe | Gly |
|     |     |     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |
| Glu | Glu | Thr | Thr | Ala | Leu | Ser | Ile | Val | Asn | Lys | His | Ile | Ala | Ser | Gln |
|     |     |     |     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
```

(A) NAME/KEY: -  
(B) LOCATION: 1..1141  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

|            |             |            |            |             |             |      |
|------------|-------------|------------|------------|-------------|-------------|------|
| atttagccct | ttgtttctct  | acacacatct | cacatcccc  | tatctctctc  | tctcttcaaa  | 60   |
| cgttttagtt | ccccaaaaaa  | atatcaaaag | aactaaaaga | aaaaccctag  | aagccgaaga  | 120  |
| atctcctact | cgttgtcgat  | cggatcacct | aactaattac | tcgttgataa  | tcattataatc | 180  |
| gagaaatatg | attaattttg  | aggccacgga | gctgagatta | gggctaccgg  | gtgggaatca  | 240  |
| cggaggagaa | atggctggaa  | aaaataatgg | taaaagagga | ttttctgaga  | ctggtgatct  | 300  |
| caaactgaat | ctttcatcga  | cggctatgga | ttcagtttcc | aaagtcgatt  | tagagaatat  | 360  |
| gaaggagaag | gtcgtaaaac  | caccagccaa | ggcacaagtt | gtgggatggc  | caccggtagc  | 420  |
| atctttccgc | aagaacgtca  | tgtccggcca | aaaaccgacc | accggagatg  | ccaccgaagg  | 480  |
| aaacgataag | acttctggca  | gcagtggagc | cacctcatcc | gcctccgcac  | gtgccaccgt  | 540  |
| ggcttatgtg | aaggttagca  | tggacggtgc | accgtaccta | cggaaaattg  | acttgaaact  | 600  |
| ctacaaaact | taccaagatc  | tctccaacgc | cttaagcaaa | atgttttagct | cttttaccat  | 660  |
| aggcaactat | ggaccacaag  | gaatgaaaga | tttcatgaat | gagagtaa    | tgatcgatct  | 720  |
| tctaaacgga | tcagattatg  | ttccaacata | tgaagataaa | gatggcgact  | ggatgcttgt  | 780  |
| aggagacgta | cogtgggaga  | tgtttgttga | ttcatgcaaa | cgtatacgaa  | taatgaagg   | 840  |
| atcagaagca | atcggacttg  | ctccaagggc | attagaaaag | tgcaagaaca  | gaagttgagt  | 900  |
| tctcgacgac | atttcgtgtt  | cttacctaaa | aaaggaagaa | agcctgtttc  | gatcggtttg  | 960  |
| atatctcgaa | ccgagaaaagc | taaaccggct | cgaactatt  | gttccgagca  | aggagtttgc  | 1020 |
| ttataatatt | aattaataat  | aatattaata | ttgtCggtgt | attacatttt  | aaaaaattaa  | 1080 |
| atcgtttttg | ttatatgtat  | tatatacata | tattaatatg | tatattta    | taggttgcat  | 1140 |

c

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..298  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Pro | Leu | Phe | Leu | Tyr | Thr | His | Leu | Thr | Ser | Pro | Tyr | Leu | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Asn | Val | Leu | Val | Pro | Gln | Lys | Asn | Ile | Lys | Arg | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Lys | Thr | Leu | Glu | Ala | Glu | Glu | Ser | Pro | Thr | Arg | Cys | Arg | Ser | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| His | Leu | Thr | Asn | Tyr | Ser | Leu | Ile | Ile | Ile | Ile | Ser | Arg | Asn | Met | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Phe | Glu | Ala | Thr | Glu | Leu | Arg | Leu | Gly | Leu | Pro | Gly | Gly | Asn | His |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Gly | Glu | Met | Ala | Gly | Lys | Asn | Asn | Gly | Lys | Arg | Gly | Phe | Ser | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Val | Asp | Leu | Lys | Leu | Asn | Leu | Ser | Ser | Thr | Ala | Met | Asp | Ser | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Ser | Lys | Val | Asp | Leu | Glu | Asn | Met | Lys | Glu | Lys | Val | Val | Lys | Pro | Pro |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Lys | Ala | Gln | Val | Val | Gly | Trp | Pro | Pro | Val | Arg | Ser | Phe | Arg | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Val | Met | Ser | Gly | Gln | Lys | Pro | Thr | Thr | Gly | Asp | Ala | Thr | Glu | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Asp | Lys | Thr | Ser | Gly | Ser | Ser | Gly | Ala | Thr | Ser | Ser | Ala | Ser | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Cys | Ala | Thr | Val | Ala | Tyr | Val | Lys | Val | Ser | Met | Asp | Gly | Ala | Pro | Tyr |
|     | 180 |     |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Leu | Arg | Lys | Ile | Asp | Leu | Lys | Leu | Tyr | Lys | Thr | Tyr | Gln | Asp | Leu | Ser |

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..215  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569582  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

Met Ala Gly Lys Asn Asn Gly Lys Arg Gly Phe Ser Glu Thr Val Asp  
1                  5                  10                  15  
Leu Lys Leu Asn Leu Ser Ser Thr Ala Met Asp Ser Val Ser Lys Val  
                  20                  25                  30  
Asp Leu Glu Asn Met Lys Glu Lys Val Val Lys Pro Pro Ala Lys Ala  
                  35                  40                  45  
Gln Val Val Gly Trp Pro Pro Val Arg Ser Phe Arg Lys Asn Val Met  
50                  55                  60  
Ser Gly Gln Lys Pro Thr Thr Gly Asp Ala Thr Glu Gly Asn Asp Lys  
65                  70                  75                  80  
Thr Ser Gly Ser Ser Gly Ala Thr Ser Ser Ala Ser Ala Cys Ala Thr  
                  85                  90                  95  
Val Ala Tyr Val Lys Val Ser Met Asp Gly Ala Pro Tyr Leu Arg Lys  
100                 105                 110  
Ile Asp Leu Lys Leu Tyr Lys Thr Tyr Gln Asp Leu Ser Asn Ala Leu  
115                 120                 125  
Ser Lys Met Phe Ser Ser Phe Thr Ile Gly Asn Tyr Gly Pro Gln Gly  
130                 135                 140  
Met Lys Asp Phe Met Asn Glu Ser Lys Leu Ile Asp Leu Leu Asn Gly  
145                 150                 155                 160  
Ser Asp Tyr Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp Trp Met Leu  
                  165                 170                 175  
Val Gly Asp Val Pro Trp Glu Met Phe Val Asp Ser Cys Lys Arg Ile  
180                 185                 190  
Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro Arg Ala Leu  
195                 200                 205  
Glu Lys Cys Lys Asn Arg Ser  
210                 215

(2) INFORMATION FOR SEQ ID NO:1304:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 929 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..929  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

aaaaacatta gttacagtcg gaatttcgaa aaaccctaata tcagctaaag gttgatcggt 60  
gatctaaaag ctcgagtgat gaagggaat tggtcgatcg tacgaaagg tcttcatcgc 120  
cagttctcca ctctccgttc ctgcacacca tcgtcgcgat tatctacttc catccgaccg 180  
cttgttctgg ccccaaactc gatatcgtcg ctaatcgcta gaaactcatt gtttactgcc 240  
tccaacattg gtccatccat cgattttaac ttctccaaca cttcgcttcc tcatcgga 300  
agcctctgct cggaagctgg aggtgaaaat ggtgttggtc tagtgaaatc agaggaagag 360  
ttcatcaatg caatgagcaa agctcaagat ggatctttac catcggtctt ctatttcact 420  
gccgcctggt gtggaccatg caggtttatc tctcctgtaa tcgtggagct tagtaaacaa 480  
tatcccgatg taactacgta taaagtcgac attgatgagg gcgggatttc gaacactatc 540  
agcaagttga atatcacggc tgtgccaaaca ctgcatttct tcaaaggagg ctccaagcaa 600  
ggcgaggttg tgggtgcaga tgtcacgaag ctgaagaatc tcatggaaca gctctacaag 660  
tgaagaccta atccgtccta gtaaagaacg tggtgaatag ttgcaagata gtttaagact 720  
gaaaatttga aatcaatcta aaaataatga atgcgctgaa ccagtttcgt ctttgttccc 780  
ccctcgttgt tcaggattgt aattgccctt ttgttttggt tgttttctcc atttcctttg 840  
ggcttagttt cctgagattt gtttggtgtcc gtcggtgaca acttcaaaaa atatcgacaa 900



gtcataactt tttatcaaaa ttttGsmcc

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

Met Lys Gly Asn Trp Ser Ile Val Arg Lys Val Leu His Arg Gln Phe  
1 5 10 15  
Ser Thr Leu Arg Ser Ser Thr Pro Ser Ser Arg Leu Ser Thr Ser Ile  
20 25 30  
Arg Pro Leu Val Leu Ala Pro Asn Ser Ile Ser Ser Leu Ile Ala Arg  
35 40 45  
Asn Ser Leu Phe Thr Ala Ser Asn Ile Gly Pro Ser Ile Asp Phe Asn  
50 55 60  
Phe Ser Asn Thr Ser Leu Pro His Arg Arg Ser Leu Cys Ser Glu Ala  
65 70 75 80  
Gly Gly Glu Asn Gly Val Val Leu Val Lys Ser Glu Glu Glu Phe Ile  
85 90 95  
Asn Ala Met Ser Lys Ala Gln Asp Gly Ser Leu Pro Ser Val Phe Tyr  
100 105 110  
Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Phe Ile Ser Pro Val Ile  
115 120 125  
Val Glu Leu Ser Lys Gln Tyr Pro Asp Val Thr Thr Tyr Lys Val Asp  
130 135 140  
Ile Asp Glu Gly Gly Ile Ser Asn Thr Ile Ser Lys Leu Asn Ile Thr  
145 150 155 160  
Ala Val Pro Thr Leu His Phe Phe Lys Gly Gly Ser Lys Gln Gly Glu  
165 170 175  
Val Val Gly Ala Asp Val Thr Lys Leu Lys Asn Leu Met Glu Gln Leu  
180 185 190  
Tyr Lys

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

gccgcagagt gttgatgctg ttacgttttag tacttttgatg aatgggtatc ttcaggtttc 60  
taagaaagcg ttggcttttg atttgttttag gattatgaga aaaagtgagg tggctcgtaa 120  
tgtcagtacg ttgcttagct ttctttcggc tattagtgat ctaggagatt tgtctggagc 180  
agaatctgct catgtgttat gcatcaagat tggccttgat ttagacttgc atttaacac 240  
agcttttgata gggatgtacg gcaaaaactgg gggatatcagt tcagcacgca ggatctttga 300  
ttgcgccatt cgaaaggatg ttgttacatg gaactgtatg atagaccaat atgcaaaaac 360  
gggtctcctt gaagagtgtg tatggctact gaggcagatg aagtatgaaa aaatgaaacc 420  
gaattcatct acgtttgttg ggctgttgct ttctgtgctg tacagtgaag cagcattcgt 480  
aggacgtact gttTgctgat ctattggaag aggaaagaat agctttggat gcaatacttg 540  
gaactgcact cgttgatatg tatgcaaaag taggattgct tgaaaaagct gttgagattt 600

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| tcaatagaat  | gaaggataag | gatgtaaagt | cctggaccgc | gatgatctcg | ggttatggag  | 660  |
| ctcatggact  | agcaagagaa | gcagtaacac | tattcaataa | gatggaggaa | gagaactgca  | 720  |
| aagtgaagacc | caatgagatt | accttcttgg | ttgtgctgaa | tgcttgtagc | catggagggt  | 780  |
| tggtaatgga  | aggaatcaga | tgctttaaga | ggatgggtga | ggcttacagc | ttcacgcccc  | 840  |
| aagttgaaca  | ttatggttgt | gtggttgatc | ttttaggtcg | agcggggcag | ttagaggaag  | 900  |
| cgtatgagtt  | aataaggaac | ttaccgatca | caagtgattc | aacggccttg | cgtgctctgc  | 960  |
| tagctgcttg  | tagagtatac | gggaatgcag | atttggggga | aagtgtgatg | atgagattgg  | 1020 |
| ctgaaatggg  | tgagacacat | cggcagatg  | caattcttct | agctgggaca | cacgctgttg  | 1080 |
| cagggaaaccc | acaaaaatca | ttagataatg | agttgaataa | agggagaaaa | gaagctggat  | 1140 |
| acagcgccat  | tgaaatagaa | tagagtagac | aatctctggc | gttcattcac | ctctgacctt  | 1200 |
| tttgttgaaa  | actatatcag | caaaatgttg | ttcaataagg | taaacccttg | tatttactct  | 1260 |
| ttctttatgc  | tttaaaacag | taacttatgt | ataaagaaag | gagacaattg | atcttaatatg | 1320 |
| aacagttttg  | atggattgtg |            |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Tyr | Ala | Lys | Val | Gly | Leu | Leu | Glu | Lys | Ala | Val | Glu | Ile | Phe | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Met | Lys | Asp | Lys | Asp | Val | Lys | Ser | Trp | Thr | Ala | Met | Ile | Ser | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Gly | Ala | His | Gly | Leu | Ala | Arg | Glu | Ala | Val | Thr | Leu | Phe | Asn | Lys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Met | Glu | Glu | Glu | Asn | Cys | Lys | Val | Arg | Pro | Asn | Glu | Ile | Thr | Phe | Leu |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Val | Val | Leu | Asn | Ala | Cys | Ser | His | Gly | Gly | Leu | Val | Met | Glu | Gly | Ile |  |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Arg | Cys | Phe | Lys | Arg | Met | Val | Glu | Ala | Tyr | Ser | Phe | Thr | Pro | Lys | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | His | Tyr | Gly | Cys | Val | Val | Asp | Leu | Leu | Gly | Arg | Ala | Gly | Gln | Leu |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Glu | Glu | Ala | Tyr | Glu | Leu | Ile | Arg | Asn | Leu | Pro | Ile | Thr | Ser | Asp | Ser |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |  |
| Thr | Ala | Trp | Arg | Ala | Leu | Leu | Ala | Ala | Cys | Arg | Val | Tyr | Gly | Asn | Ala |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Asp | Leu | Gly | Glu | Ser | Val | Met | Met | Arg | Leu | Ala | Glu | Met | Gly | Glu | Thr |  |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |  |
| His | Pro | Ala | Asp | Ala | Ile | Leu | Leu | Ala | Gly | Thr | His | Ala | Val | Ala | Gly |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Asn | Pro | Gln | Lys | Ser | Leu | Asp | Asn | Glu | Leu | Asn | Lys | Gly | Arg | Lys | Glu |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Ala | Gly | Tyr | Ser | Ala | Ile | Glu | Ile | Glu |     |     |     |     |     |     |     |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1569587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

Met Lys Asp Lys Val Lys Ser Trp Thr Ala Met Ile Ser Gly Tyr  
1 5 10 15  
Gly Ala His Gly Leu Ala Arg Glu Ala Val Thr Leu Phe Asn Lys Met  
20 25 30  
Glu Glu Glu Asn Cys Lys Val Arg Pro Asn Glu Ile Thr Phe Leu Val  
35 40 45  
Val Leu Asn Ala Cys Ser His Gly Gly Leu Val Met Glu Gly Ile Arg  
50 55 60  
Cys Phe Lys Arg Met Val Glu Ala Tyr Ser Phe Thr Pro Lys Val Glu  
65 70 75 80  
His Tyr Gly Cys Val Val Asp Leu Leu Gly Arg Ala Gly Gln Leu Glu  
85 90 95  
Glu Ala Tyr Glu Leu Ile Arg Asn Leu Pro Ile Thr Ser Asp Ser Thr  
100 105 110  
Ala Trp Arg Ala Leu Leu Ala Ala Cys Arg Val Tyr Gly Asn Ala Asp  
115 120 125  
Leu Gly Glu Ser Val Met Met Arg Leu Ala Glu Met Gly Glu Thr His  
130 135 140  
Pro Ala Asp Ala Ile Leu Leu Ala Gly Thr His Ala Val Ala Gly Asn  
145 150 155 160  
Pro Gln Lys Ser Leu Asp Asn Glu Leu Asn Lys Gly Arg Lys Glu Ala  
165 170 175  
Gly Tyr Ser Ala Ile Glu Ile Glu  
180

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1569588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

Met Ile Ser Gly Tyr Gly Ala His Gly Leu Ala Arg Glu Ala Val Thr  
1 5 10 15  
Leu Phe Asn Lys Met Glu Glu Glu Asn Cys Lys Val Arg Pro Asn Glu  
20 25 30  
Ile Thr Phe Leu Val Val Leu Asn Ala Cys Ser His Gly Gly Leu Val  
35 40 45  
Met Glu Gly Ile Arg Cys Phe Lys Arg Met Val Glu Ala Tyr Ser Phe  
50 55 60  
Thr Pro Lys Val Glu His Tyr Gly Cys Val Val Asp Leu Leu Gly Arg  
65 70 75 80  
Ala Gly Gln Leu Glu Glu Ala Tyr Glu Leu Ile Arg Asn Leu Pro Ile  
85 90 95  
Thr Ser Asp Ser Thr Ala Trp Arg Ala Leu Leu Ala Ala Cys Arg Val  
100 105 110  
Tyr Gly Asn Ala Asp Leu Gly Glu Ser Val Met Met Arg Leu Ala Glu  
115 120 125  
Met Gly Glu Thr His Pro Ala Asp Ala Ile Leu Leu Ala Gly Thr His  
130 135 140  
Ala Val Ala Gly Asn Pro Gln Lys Ser Leu Asp Asn Glu Leu Asn Lys  
145 150 155 160  
Gly Arg Lys Glu Ala Gly Tyr Ser Ala Ile Glu Ile Glu  
165 170

(2) INFORMATION FOR SEQ ID NO:1310:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1666 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1666  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569589  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

aaatataatt tcacgcagct gctctctttt cttcttccga tcctccttcc gccgagtcaa 60  
gccgcgactg tgaaatcatg agaggagtaa aacgcgccgc catctccgaa tcgaatgact 120  
ctccctttta gaatgcaaaa ccggtgggag gaatcttttt tggtagctag aagaatgtgg 180  
ccccgatgca gcagagtcca ttaacatcag catcattgga taaacagagg gctgagttag 240  
ctaggaagca tgtgagagct ctttaataacc aatttgtaag ttgggtgcag ttacagctga 300  
agaatcatcc tgatgaactt tgggaagatg ggatgaatga ctacattacg catgcttcaa 360  
acattctgga aaagtttaag gatgtgggtca gctggcttaa agaaaataag ggaaaggggg 420  
agaatttatc ccctgaatct cgtggagcag aaaagaaatt agtggctgaa gtcaagaata 480  
ccaatgttaa atcattttca aacaatatc cttttgcttc aaacaatcaa cctgggatct 540  
tctcaaaaca tcaatcttcc gatttttcca gtagtcagtc tggtttcttt tcaagccaat 600  
ctggagcatt ctccagcagt ccttctgggt taatatccaa tagccagact ggatctttta 660  
gcagtggcca gtgttggtacg acaaaaagca gccaaccaag cctatttttc ggtagtcaag 720  
ccggagcaat ctctaatagc caacctggaa ctttctccag cagtcttctt ggtataacat 780  
ctaatagcca gacgggatct tttagtagtg gccaatttgg tcagacaaaa agcagccaac 840  
caagcctact ttccggcagt caagcaggag taatctctag tagccaacct tcttttcaat 900  
tttctaacag tcaatcccct tttacatctg cagtacctcc agtgtccata ccggcaaagc 960  
aggatcactc agatgatgag gatggtggag acgaacaatc tcaaccgagc agcccactctg 1020  
tcaaaaagac ggaagaaaaag ggtattactg tggttcatga agtcaaagtc aaactttatg 1080  
tcaagtcaag tgaccagca gataaagggg ggaagataa aggaactggg aatctctaca 1140  
taaaatgcaa agaaggagtc gacaagggGg aaaaagaatc aaaaccaca attcttgtcc 1200  
gaaacgatgt tggaaaactg cttctgaatg cactactgta cgctggaatg aagacaagcc 1260  
cacagaagaa cgctcttgtt gcaatatctc actcctcgga tgattccaac gagaatgtaa 1320  
caccgagaac ctttctgata aggacaaaga acgcagaagc tagagataat ttagcaacgg 1380  
ccatccaaga atacgcccct tcttcataga ttgccaaaag ccagggttag atcttctactg 1440  
taacttttaa aagccttctc gagtcgtcct ctctctatat ttttttctg atttgtaata 1500  
ttaggaaggg tcttaagagt aacgtaaagc ttgataaagg gcacaaaaat gttgtatgat 1560  
tgtgagagag agagagggcc aaaggagttc gtagcttatt agagaatgtt gtgccaatct 1620  
tctttgtaac ttaaaaacca gaaacaataa aatcacttct ttttat

(2) INFORMATION FOR SEQ ID NO:1311:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 443 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..443  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

Met Arg Gly Val Lys Arg Ala Ala Ile Ser Glu Ser Asn Asp Ser Pro  
1                   5                   10                   15  
Phe Lys Asn Ala Lys Pro Val Gly Gly Ile Phe Phe Gly Thr Gln Lys  
                  20                   25                   30  
Asn Val Ala Pro Met Gln Gln Ser Pro Leu Thr Ser Ala Ser Leu Asp  
                  35                   40                   45  
Lys Gln Arg Ala Glu Leu Ala Arg Lys His Val Arg Ala Leu Asn Asn  
                  50                   55                   60  
Gln Phe Val Ser Trp Val Gln Leu Gln Leu Lys Asn His Pro Asp Glu  
65                   70                   75                   80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Glu | Asp | Gly | Met | Asn | Asp | Tyr | Ile | Thr | His | Ala | Ser | Asn | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Lys | Phe | Lys | Asp | Val | Val | Ser | Trp | Leu | Lys | Glu | Asn | Lys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Gly | Glu | Asn | Leu | Ser | Pro | Glu | Ser | Arg | Gly | Ala | Glu | Lys | Lys | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ala | Glu | Val | Lys | Asn | Thr | Asn | Val | Lys | Ser | Phe | Ser | Asn | Asn | Ile |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Pro | Phe | Ala | Ser | Asn | Asn | Gln | Pro | Gly | Ile | Phe | Ser | Asn | Asn | Gln | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Asp | Phe | Ser | Ser | Ser | Gln | Ser | Gly | Phe | Phe | Ser | Ser | Gln | Ser | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Phe | Ser | Ser | Ser | Pro | Ser | Gly | Leu | Ile | Ser | Asn | Ser | Gln | Thr | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Phe | Ser | Ser | Gly | Gln | Phe | Gly | Thr | Thr | Lys | Ser | Ser | Gln | Pro | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Phe | Ser | Gly | Ser | Gln | Ala | Gly | Ala | Ile | Ser | Asn | Ser | Gln | Pro | Gly |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Phe | Ser | Ser | Ser | Pro | Ser | Gly | Ile | Thr | Ser | Asn | Ser | Gln | Thr | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Phe | Ser | Ser | Gly | Gln | Phe | Gly | Gln | Thr | Lys | Ser | Ser | Gln | Pro | Ser |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Leu | Ser | Gly | Ser | Gln | Ala | Gly | Val | Ile | Ser | Ser | Ser | Gln | Pro | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Gln | Phe | Ser | Asn | Ser | Gln | Ser | Pro | Phe | Thr | Ser | Ala | Val | Pro | Pro |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Ser | Ile | Pro | Ala | Lys | Gln | Asp | His | Ser | Asp | Asp | Ala | Asp | Gly | Gly |
|     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Asp | Glu | Gln | Ser | Gln | Pro | Ser | Ser | Pro | Ser | Val | Lys | Lys | Thr | Glu | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Gly | Ile | Thr | Val | Val | His | Glu | Val | Lys | Cys | Lys | Leu | Tyr | Val | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Ser | Asp | Pro | Ala | Asp | Lys | Gly | Trp | Lys | Asp | Lys | Gly | Thr | Gly | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Tyr | Ile | Lys | Cys | Lys | Glu | Gly | Val | Asp | Lys | Gly | Thr | Lys | Glu | Ser |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Pro | Thr | Ile | Leu | Val | Arg | Asn | Asp | Val | Gly | Lys | Leu | Leu | Leu | Asn |
|     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Leu | Leu | Tyr | Ala | Gly | Met | Lys | Thr | Ser | Pro | Gln | Lys | Asn | Ala | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Ala | Ile | Phe | His | Ser | Ser | Asp | Asp | Ser | Asn | Glu | Asn | Val | Thr | Pro |
|     |     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |
| Arg | Thr | Phe | Leu | Ile | Arg | Thr | Lys | Asn | Ala | Glu | Ala | Arg | Asp | Asn | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Thr | Ala | Ile | Gln | Glu | Tyr | Ala | Pro | Ser | Ser |     |     |     |     |     |
|     |     |     | 435 |     |     |     | 440 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1569591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Gln | Ser | Pro | Leu | Thr | Ser | Ala | Ser | Leu | Asp | Lys | Gln | Arg | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Leu | Ala | Arg | Lys | His | Val | Arg | Ala | Leu | Asn | Asn | Gln | Phe | Val | Ser |

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |
| Trp | Val | Gln | Leu | Gln | Leu | Trp | Glu | Asp |     |
|     | 35  |     |     |     | 40  |     | 45  |     |     |
| Gly | Met | Asn | Asp | Tyr | Ile | Thr | His | Ala | Ser |
|     | 50  |     |     |     | 55  |     |     |     | 60  |
| Lys | Asp | Val | Val | Ser | Trp | Leu | Lys | Glu | Asn |
|     | 65  |     |     |     | 70  |     |     | 75  |     |
| Leu | Ser | Pro | Glu | Ser | Arg | Gly | Ala | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |
| Lys | Asn | Thr | Asn | Val | Lys | Ser | Phe | Ser | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |
| Asn | Asn | Gln | Pro | Gly | Ile | Phe | Ser | Asn | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |
| Ser | Ser | Gln | Ser | Gly | Phe | Phe | Ser | Ser | Gln |
|     | 130 |     |     |     |     | 135 |     |     | 140 |
| Ser | Pro | Ser | Gly | Leu | Ile | Ser | Asn | Ser | Gln |
|     | 145 |     |     |     | 150 |     |     | 155 |     |
| Gly | Gln | Phe | Gly | Thr | Thr | Lys | Ser | Ser | Gln |
|     |     |     |     | 165 |     |     |     | 170 |     |
| Ser | Gln | Ala | Gly | Ala | Ile | Ser | Asn | Ser | Gln |
|     |     | 180 |     |     |     |     |     | 185 |     |
| Ser | Pro | Ser | Gly | Ile | Thr | Ser | Asn | Ser | Gln |
|     | 195 |     |     |     |     |     | 200 |     |     |
| Gly | Gln | Phe | Gly | Gln | Thr | Lys | Ser | Ser | Gln |
|     | 210 |     |     |     |     | 215 |     |     | 220 |
| Ser | Gln | Ala | Gly | Val | Ile | Ser | Ser | Ser | Gln |
|     | 225 |     |     |     | 230 |     |     |     | 235 |
| Asn | Ser | Gln | Ser | Pro | Phe | Thr | Ser | Ala | Val |
|     |     |     |     | 245 |     |     |     | 250 |     |
| Ala | Lys | Gln | Asp | His | Ser | Asp | Asp | Ala | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |
| Gln | Pro | Ser | Ser | Pro | Ser | Val | Lys | Lys | Thr |
|     |     | 275 |     |     |     |     | 280 |     | 285 |
| Val | Val | His | Glu | Val | Lys | Cys | Lys | Leu | Tyr |
|     | 290 |     |     |     |     | 295 |     |     | 300 |
| Ala | Asp | Lys | Gly | Trp | Lys | Asp | Lys | Gly | Thr |
|     | 305 |     |     |     | 310 |     |     |     | 315 |
| Cys | Lys | Glu | Gly | Val | Asp | Lys | Gly | Thr | Lys |
|     |     |     |     | 325 |     |     |     | 330 |     |
| Leu | Val | Arg | Asn | Asp | Val | Gly | Lys | Leu | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |
| Ala | Gly | Met | Lys | Thr | Ser | Pro | Gln | Lys | Asn |
|     |     | 355 |     |     |     |     | 360 |     | 365 |
| His | Ser | Ser | Asp | Asp | Ser | Asn | Glu | Asn | Val |
|     | 370 |     |     |     |     | 375 |     |     | 380 |
| Ile | Arg | Thr | Lys | Asn | Ala | Glu | Ala | Arg | Asp |
|     | 385 |     |     |     | 390 |     |     | 395 |     |
| Gln | Glu | Tyr | Ala | Pro | Ser | Ser |     |     |     |
|     |     |     |     | 405 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1569592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

|    | Age | Gender | Height | Weight | Body mass index | Waist circumference | Waist-hip ratio | Trunk muscle strength | Trunk muscle endurance | Trunk muscle power | Trunk muscle endurance power | Trunk muscle endurance power index |
|----|-----|--------|--------|--------|-----------------|---------------------|-----------------|-----------------------|------------------------|--------------------|------------------------------|------------------------------------|
| 1  | 20  | M      | 1.75   | 75     | 24.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 2  | 20  | F      | 1.65   | 60     | 22.0            | 75                  | 0.80            | 80                    | 80                     | 80                 | 80                           | 80                                 |
| 3  | 20  | M      | 1.80   | 80     | 24.7            | 90                  | 0.88            | 110                   | 110                    | 110                | 110                          | 110                                |
| 4  | 20  | F      | 1.70   | 65     | 22.6            | 80                  | 0.82            | 90                    | 90                     | 90                 | 90                           | 90                                 |
| 5  | 20  | M      | 1.75   | 70     | 22.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 6  | 20  | F      | 1.65   | 55     | 20.5            | 70                  | 0.78            | 75                    | 75                     | 75                 | 75                           | 75                                 |
| 7  | 20  | M      | 1.80   | 85     | 26.0            | 95                  | 0.90            | 120                   | 120                    | 120                | 120                          | 120                                |
| 8  | 20  | F      | 1.70   | 70     | 24.1            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 9  | 20  | M      | 1.75   | 75     | 24.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 10 | 20  | F      | 1.65   | 60     | 22.0            | 75                  | 0.80            | 80                    | 80                     | 80                 | 80                           | 80                                 |
| 11 | 20  | M      | 1.80   | 80     | 24.7            | 90                  | 0.88            | 110                   | 110                    | 110                | 110                          | 110                                |
| 12 | 20  | F      | 1.70   | 65     | 22.6            | 80                  | 0.82            | 90                    | 90                     | 90                 | 90                           | 90                                 |
| 13 | 20  | M      | 1.75   | 70     | 22.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 14 | 20  | F      | 1.65   | 55     | 20.5            | 70                  | 0.78            | 75                    | 75                     | 75                 | 75                           | 75                                 |
| 15 | 20  | M      | 1.80   | 85     | 26.0            | 95                  | 0.90            | 120                   | 120                    | 120                | 120                          | 120                                |
| 16 | 20  | F      | 1.70   | 70     | 24.1            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 17 | 20  | M      | 1.75   | 75     | 24.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 18 | 20  | F      | 1.65   | 60     | 22.0            | 75                  | 0.80            | 80                    | 80                     | 80                 | 80                           | 80                                 |
| 19 | 20  | M      | 1.80   | 80     | 24.7            | 90                  | 0.88            | 110                   | 110                    | 110                | 110                          | 110                                |
| 20 | 20  | F      | 1.70   | 65     | 22.6            | 80                  | 0.82            | 90                    | 90                     | 90                 | 90                           | 90                                 |
| 21 | 20  | M      | 1.75   | 70     | 22.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 22 | 20  | F      | 1.65   | 55     | 20.5            | 70                  | 0.78            | 75                    | 75                     | 75                 | 75                           | 75                                 |
| 23 | 20  | M      | 1.80   | 85     | 26.0            | 95                  | 0.90            | 120                   | 120                    | 120                | 120                          | 120                                |
| 24 | 20  | F      | 1.70   | 70     | 24.1            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 25 | 20  | M      | 1.75   | 75     | 24.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 26 | 20  | F      | 1.65   | 60     | 22.0            | 75                  | 0.80            | 80                    | 80                     | 80                 | 80                           | 80                                 |
| 27 | 20  | M      | 1.80   | 80     | 24.7            | 90                  | 0.88            | 110                   | 110                    | 110                | 110                          | 110                                |
| 28 | 20  | F      | 1.70   | 65     | 22.6            | 80                  | 0.82            | 90                    | 90                     | 90                 | 90                           | 90                                 |
| 29 | 20  | M      | 1.75   | 70     | 22.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 30 | 20  | F      | 1.65   | 55     | 20.5            | 70                  | 0.78            | 75                    | 75                     | 75                 | 75                           | 75                                 |
| 31 | 20  | M      | 1.80   | 85     | 26.0            | 95                  | 0.90            | 120                   | 120                    | 120                | 120                          | 120                                |
| 32 | 20  | F      | 1.70   | 70     | 24.1            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 33 | 20  | M      | 1.75   | 75     | 24.2            | 85                  | 0.85            | 100                   | 100                    | 100                | 100                          | 100                                |
| 34 | 20  | F      | 1.65   | 60     | 22.0            | 75                  | 0.80            |                       |                        |                    |                              |                                    |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1569603

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| aaccaacaag | aagaatccaa | agacatgaaa  | cttctcttta | ttgtttctcat | ctctttttctt | 60  |
| tccctcctcc | aagcatcaaa | aggattcgat  | ttcgacgaaa | aagaattaga  | aaccgaagag  | 120 |
| aacctatgga | agctctatga | gagggtggaga | ggccaccact | ctgtatccCa  | gagctttctca | 180 |

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tgaggcaata  | aagcgggttca | acgttttttag | acacaatgtc  | cttcatgtcc  | acaggactaa  | 240  |
| caagaagaac  | aagccttaca  | aactcaagat  | caatagattc  | gccgacaacg  | caccacgagt  | 300  |
| ttagaagctc  | ctacgttggc  | tctaattgtta | agcatcaccg  | aatgcttcgt  | ggaccgaagc  | 360  |
| gcggtatctgg | tggtttcatg  | tatgagaatg  | tgaccagagt  | tccgagttct  | gttgattggc  | 420  |
| gagagaaaagg | agctgtcact  | gaagtcaaga  | atcaacagga  | ttgtggaagt  | tgctgggcgt  | 480  |
| tttcgacggt  | tgcagcagtg  | gaagggataa  | acaagatcgg  | aacaaacaaa  | ctagtttcat  | 540  |
| tgtctgaaca  | agagcttgtg  | gattgtgaca  | ctgaagagaa  | tcaaggttgt  | gcaggaggtc  | 600  |
| tcatggaacc  | tgcgtttgaa  | tttataaaga  | acaatggtgg  | catcaaaacc  | gaagagactt  | 660  |
| atccttacga  | ttccagtgac  | gttcaattct  | gtagagctaa  | gagtattggt  | ggagaaaactg | 720  |
| taaccatcga  | tggacacgaa  | cacgtccctg  | agaatgatga  | ggaagaactt  | ctcaaagctg  | 780  |
| ttgtccacca  | gcctgtctct  | gtagctattg  | atgctgggag  | ctcagatttc  | cagctttact  | 840  |
| ctgagggtgt  | gtttatcggg  | gaatgcggga  | ctcagttgaa  | ccacggggtg  | gtgattggtg  | 900  |
| ggtatggaga  | gaccaaaaat  | ggaacaaaat  | attggatagt  | aaggaaactca | tggggacctg  | 960  |
| aatggggaga  | aggaggctat  | gttcggatag  | aaagagggaat | atcgggagaat | gaaggacgtt  | 1020 |
| gcggtatagc  | catggaggct  | tcttatccca  | ccaagctctc  | ttcgactcct  | tctactcatg  | 1080 |
| agtcagtagt  | tcgatgatgat | gttaaagacg  | agctctagag  | actttaagtc  | attgaaaact  | 1140 |
| gaatttcgaa  | ccattcttct  | agtgagctta  | cactgagttt  | attattyyaA  | tggattgagg  | 1200 |
| ttcatgggtt  | tcaattttaca | catctatcgt  | gtattcatct  | taagttgaga  | cgatttttat  | 1260 |
| ctccttgtaa  | tattggccag  | catttgcttt  | gcggaaaaat  | ggcggtt     |             |      |

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1569604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Met | Ser | Thr | Gly | Leu | Thr | Arg | Arg | Thr | Ser | Leu | Thr | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Arg | Ser | Ile | Asp | Ser | Pro | Thr | Thr | His | His | Glu | Phe | Arg | Ser | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ala | Gly | Ser | Asn | Val | Lys | His | Arg | Met | Leu | Arg | Gly | Pro | Lys |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Gly | Ser | Gly | Gly | Phe | Met | Tyr | Glu | Asn | Val | Thr | Arg | Val | Pro | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Asp | Trp | Arg | Glu | Lys | Gly | Ala | Val | Thr | Glu | Val | Lys | Asn | Gln |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Asp | Cys | Gly | Ser | Cys | Trp | Ala | Phe | Ser | Thr | Val | Ala | Ala | Val | Glu |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ile | Asn | Lys | Ile | Gly | Thr | Asn | Lys | Leu | Val | Ser | Leu | Ser | Glu | Gln |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Leu | Val | Asp | Cys | Asp | Thr | Glu | Asn | Gln | Gly | Cys | Ala | Gly | Gly |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Met | Glu | Pro | Ala | Phe | Glu | Phe | Ile | Lys | Asn | Asn | Gly | Gly | Ile | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Glu | Glu | Thr | Tyr | Pro | Tyr | Asp | Ser | Ser | Asp | Val | Gln | Phe | Cys | Arg |
|     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Lys | Ser | Ile | Gly | Gly | Glu | Thr | Val | Thr | Ile | Asp | Gly | His | Glu | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Pro | Glu | Asn | Asp | Glu | Glu | Glu | Leu | Lys | Ala | Val | Ala | His | Gln |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Pro | Val | Ser | Val | Ala | Ile | Asp | Ala | Gly | Ser | Ser | Asp | Phe | Gln | Leu | Tyr |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ser | Glu | Gly | Val | Phe | Ile | Gly | Glu | Cys | Gly | Thr | Gln | Leu | Asn | His | Gly |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Val | Ile | Val | Gly | Tyr | Gly | Glu | Thr | Lys | Asn | Gly | Thr | Lys | Tyr | Trp |
|     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |



Ile Val Arg Asn Ser Trp Gly Pro Glu Trp Gly Glu Gly Tyr Val  
245 250 255  
Arg Ile Glu Arg Gly Ile Ser Glu Asn Glu Gly Arg Cys Gly Ile Ala  
260 265 270  
Met Glu Ala Ser Tyr Pro Thr Lys Leu Ser Ser Thr Pro Ser Thr His  
275 280 285  
Glu Ser Val Val Arg Asp Asp Val Lys Asp Glu Leu  
290 295 300

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1569605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

Met Ser Thr Gly Leu Thr Arg Arg Thr Ser Leu Thr Asn Ser Arg Ser  
1 5 10 15  
Ile Asp Ser Pro Thr Thr His His Glu Phe Arg Ser Ser Tyr Ala Gly  
20 25 30  
Ser Asn Val Lys His His Arg Met Leu Arg Gly Pro Lys Arg Gly Ser  
35 40 45  
Gly Gly Phe Met Tyr Glu Asn Val Thr Arg Val Pro Ser Ser Val Asp  
50 55 60  
Trp Arg Glu Lys Gly Ala Val Thr Glu Val Lys Asn Gln Gln Asp Cys  
65 70 75 80  
Gly Ser Cys Trp Ala Phe Ser Thr Val Ala Ala Val Glu Gly Ile Asn  
85 90 95  
Lys Ile Gly Thr Asn Lys Leu Val Ser Leu Ser Glu Gln Glu Leu Val  
100 105 110  
Asp Cys Asp Thr Glu Glu Asn Gln Gly Cys Ala Gly Gly Leu Met Glu  
115 120 125  
Pro Ala Phe Glu Phe Ile Lys Asn Asn Gly Gly Ile Lys Thr Glu Glu  
130 135 140  
Thr Tyr Pro Tyr Asp Ser Ser Asp Val Gln Phe Cys Arg Ala Lys Ser  
145 150 155 160  
Ile Gly Gly Glu Thr Val Thr Ile Asp Gly His Glu His Val Pro Glu  
165 170 175  
Asn Asp Glu Glu Glu Leu Leu Lys Ala Val Ala His Gln Pro Val Ser  
180 185 190  
Val Ala Ile Asp Ala Gly Ser Ser Asp Phe Gln Leu Tyr Ser Glu Gly  
195 200 205  
Val Phe Ile Gly Glu Cys Gly Thr Gln Leu Asn His Gly Val Val Ile  
210 215 220  
Val Gly Tyr Gly Glu Thr Lys Asn Gly Thr Lys Tyr Trp Ile Val Arg  
225 230 235 240  
Asn Ser Trp Gly Pro Glu Trp Gly Glu Gly Gly Tyr Val Arg Ile Glu  
245 250 255  
Arg Gly Ile Ser Glu Asn Glu Gly Arg Cys Gly Ile Ala Met Glu Ala  
260 265 270  
Ser Tyr Pro Thr Lys Leu Ser Ser Thr Pro Ser Thr His Glu Ser Val  
275 280 285  
Val Arg Asp Asp Val Lys Asp Glu Leu  
290 295

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..258  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569606  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

Met Leu Arg Gly Pro Lys Arg Gly Ser Gly Gly Phe Met Tyr Glu Asn  
1 5 10 15  
Val Thr Arg Val Pro Ser Ser Val Asp Trp Arg Glu Lys Gly Ala Val  
20 25 30  
Thr Glu Val Lys Asn Gln Gln Asp Cys Gly Ser Cys Trp Ala Phe Ser  
35 40 45  
Thr Val Ala Ala Val Glu Gly Ile Asn Lys Ile Gly Thr Asn Lys Leu  
50 55 60  
Val Ser Leu Ser Glu Gln Glu Leu Val Asp Cys Asp Thr Glu Glu Asn  
65 70 75 80  
Gln Gly Cys Ala Gly Gly Leu Met Glu Pro Ala Phe Glu Phe Ile Lys  
85 90 95  
Asn Asn Gly Gly Ile Lys Thr Glu Glu Thr Tyr Pro Tyr Asp Ser Ser  
100 105 110  
Asp Val Gln Phe Cys Arg Ala Lys Ser Ile Gly Gly Glu Thr Val Thr  
115 120 125  
Ile Asp Gly His Glu His Val Pro Glu Asn Asp Glu Glu Glu Leu Leu  
130 135 140  
Lys Ala Val Ala His Gln Pro Val Ser Val Ala Ile Asp Ala Gly Ser  
145 150 155 160  
Ser Asp Phe Gln Leu Tyr Ser Glu Gly Val Phe Ile Gly Glu Cys Gly  
165 170 175  
Thr Gln Leu Asn His Gly Val Val Ile Val Gly Tyr Gly Glu Thr Lys  
180 185 190  
Asn Gly Thr Lys Tyr Trp Ile Val Arg Asn Ser Trp Gly Pro Glu Trp  
195 200 205  
Gly Glu Gly Gly Tyr Val Arg Ile Glu Arg Gly Ile Ser Glu Asn Glu  
210 215 220  
Gly Arg Cys Gly Ile Ala Met Glu Ala Ser Tyr Pro Thr Lys Leu Ser  
225 230 235 240  
Ser Thr Pro Ser Thr His Glu Ser Val Val Arg Asp Asp Val Lys Asp  
245 250 255  
Glu Leu

(2) INFORMATION FOR SEQ ID NO:1318:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2081 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..2081  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569611  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

aaaagcttct tcatcaatgg agaagcaagg atgtgagatc gaagcttttag atattgatta 60  
caacatcttt gtaaggaaga ttaatgttaa tccctttgga atcttttaggc ggaaaccgcg 120  
gccggaagct gaccagccgg taaagacaga ggaagagtca ttgaagctag aggatgaaac 180  
cggtaacaaa gtcaagcatg tactaaaagg agtgacttgc agagccaaac catgggagat 240  
tcttgctatt gttggcccaa gtggtgcagg gaagtcgtct ttgcttgaaa ttctagctgc 300  
tagactcatc cctcaaaccg ggtcggttta tgtcaacaag agcccggtgg atagagccaa 360

tttcaagaaa atctctgggt atgtcactca gaaggatact ctgttttcctt tgcttacggt 420  
ggaggaaaacc cttctgttca gtgctaagct gcgtttaaaag ctccctgcag atgaactgag 480  
atcacggggtt aagtcctttgg tccatgagct tgggcttgaa gctgttgcca cggctcgtgt 540  
tggcgatgat agtgtcagag gtatatcggtg tggagagaga cgtcgtgtct ccataggagt 600  
tgaagttatt cacgacctta aagttctgat ccttgatgag ccaacctctg gtcttgatag 660  
tacttcgggt ctgctgatca tagacatgct caaacacatg gctgaaacac gaggcaggac 720  
cataattctg actatccacc aaccgggatt tcggatagtc aaacagttca attctgttct 780  
cttgttggcc aatggctcga ccttgaagca ggggtcgggtg gatcagcttg gcgtttactt 840  
aaggtcaaat ggtttgacc ctcctctcca tgaaaacatc gttgaatttg ccattgaatc 900  
aatcgaatcc atcacaaaa agcaacggct acaggaaagc agaagagcag ctcatgtcct 960  
aacaccacaa acaacattac aagagaagag atcagaagat agtcaagggg agagcaaaag 1020  
tggcaaatcc acactacaac agctgtttca acaacaagg gtcgctgatg taggaacgat 1080  
gaacatagca acagagttca caagagattt tgcaaatcca agattagaag aaactatgat 1140  
actcacacat aggtttctcca agaacatttt cagaaccaag gagctttttg cgtgcaggac 1200  
ggttcagatg ttaggttcag gaattgtcct agtctgattt ttcataatct caaagacgat 1260  
ttaaagggtg cggagaaaag agtcggcctc tttgcattca tattgacctt tctgctaact 1320  
tcgacaatag aggcactccc tatatttctg caagaaagag agattctgat gaaggagacc 1380  
tctagtggaa gctacagagt gtcttcatat gccgtcgcta atggactagt ttacttgcca 1440  
tttctgctca tctagctat tctatttctca accccagtgt actggctggt gggactgaac 1500  
cccagtttca ttgogtttct acacttttctg ctcctcattt ggtaaatcct ctacacagca 1560  
aactcgggtg ttgtgtgctt tagtgcactg gttcctaatt tcatagtgg aaactcagtg 1620  
atttccgggtg tgatgggttc cttcttttctg ttctccggct acttcatatc gaaccatgag 1680  
atccctgggt actggatttt catgcactac atctccttgt tcaagtaccc gttcgaagga 1740  
tttctgatta acgagttctc aaaatcaaac aagtgtttgg agtatggatt cggaaaatgt 1800  
ttggtgaccg aggaggatct actcaaagaa gaaaggtagc gagaggaaag tagatggaga 1860  
aatgttgtga tcatgctatg ttttgtcttg ctctacaggt tcatttccta tgtgattctg 1920  
aggtgtagat gttcccaacg aagtttcaaa accactctcg cttaataaat gtggtagcaa 1980  
taatgtcctt tctgaaaaac attgggttac aggtttgttc atgtgtttaa ttatttactT 2040  
cgtacagcaa ccgaagatgt gaaagaaaat gttgtttctg c

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

Lys Ala Ser Ser Ser Met Glu Lys Gln Gly Cys Glu Ile Glu Ala Leu  
1 5 10 15  
Asp Ile Asp Tyr Asn Ile Phe Val Arg Lys Ile Asn Val Asn Pro Phe  
20 25 30  
Gly Ile Phe Arg Arg Lys Pro Arg Pro Glu Ala Asp Gln Pro Val Lys  
35 40 45  
Thr Glu Glu Glu Ser Leu Lys Leu Glu Asp Glu Thr Gly Asn Lys Val  
50 55 60  
Lys His Val Leu Lys Gly Val Thr Cys Arg Ala Lys Pro Trp Glu Ile  
65 70 75 80  
Leu Ala Ile Val Gly Pro Ser Gly Ala Gly Lys Ser Ser Leu Leu Glu  
85 90 95  
Ile Leu Ala Ala Arg Leu Ile Pro Gln Thr Gly Ser Val Tyr Val Asn  
100 105 110  
Lys Ser Pro Val Asp Arg Ala Asn Phe Lys Lys Ile Ser Gly Tyr Val  
115 120 125  
Thr Gln Lys Asp Thr Leu Phe Pro Leu Leu Thr Val Glu Glu Thr Leu  
130 135 140  
Leu Phe Ser Ala Lys Leu Arg Leu Lys Leu Pro Ala Asp Glu Leu Arg  
145 150 155 160

Ser Arg Val Lys Ser Leu Val His Glu Leu Gly Leu Glu Ala Val Ala  
165 170 175  
Thr Ala Arg Val Gly Asp Asp Ser Val Arg Gly Ile Ser Gly Gly Glu  
180 185 190  
Arg Arg Arg Val Ser Ile Gly Val Glu Val Ile His Asp Pro Lys Val  
195 200 205  
Leu Ile Leu Asp Glu Pro Thr Ser Gly Leu Asp Ser Thr Ser Ala Leu  
210 215 220  
Leu Ile Ile Asp Met Leu Lys His Met Ala Glu Thr Arg Gly Arg Thr  
225 230 235 240  
Ile Ile Leu Thr Ile His Gln Pro Gly Phe Arg Ile Val Lys Gln Phe  
245 250 255  
Asn Ser Val Leu Leu Leu Ala Asn Gly Ser Thr Leu Lys Gln Gly Ser  
260 265 270  
Val Asp Gln Leu Gly Val Tyr Leu Arg Ser Asn Gly Leu His Pro Pro  
275 280 285  
Leu His Glu Asn Ile Val Glu Phe Ala Ile Glu Ser Ile Glu Ser Ile  
290 295 300  
Thr Lys Gln Gln Arg Leu Gln Glu Ser Arg Arg Ala Ala His Val Leu  
305 310 315 320  
Thr Pro Gln Thr Thr Leu Gln Glu Lys Arg Ser Glu Asp Ser Gln Gly  
325 330 335  
Glu Ser Lys Ser Gly Lys Phe Thr Leu Gln Gln Leu Phe Gln Gln Thr  
340 345 350  
Arg Val Ala Asp Val Gly Thr Met Asn Ile Ala Thr Glu Phe Thr Arg  
355 360 365  
Asp Phe Ala Asn Ser Arg Leu Glu Glu Thr Met Ile Leu Thr His Arg  
370 375 380  
Phe Ser Lys Asn Ile Phe Arg Thr Lys Glu Leu Phe Ala Cys Arg Thr  
385 390 395 400  
Val Gln Met Leu Gly Ser Gly Ile Val Leu Val  
405 410

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1569613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Glu Lys Gln Gly Cys Glu Ile Glu Ala Leu Asp Ile Asp Tyr Asn  
1 5 10 15  
Ile Phe Val Arg Lys Ile Asn Val Asn Pro Phe Gly Ile Phe Arg Arg  
20 25 30  
Lys Pro Arg Pro Glu Ala Asp Gln Pro Val Lys Thr Glu Glu Glu Ser  
35 40 45  
Leu Lys Leu Glu Asp Glu Thr Gly Asn Lys Val Lys His Val Leu Lys  
50 55 60  
Gly Val Thr Cys Arg Ala Lys Pro Trp Glu Ile Leu Ala Ile Val Gly  
65 70 75 80  
Pro Ser Gly Ala Gly Lys Ser Ser Leu Leu Glu Ile Leu Ala Ala Arg  
85 90 95  
Leu Ile Pro Gln Thr Gly Ser Val Tyr Val Asn Lys Ser Pro Val Asp  
100 105 110  
Arg Ala Asn Phe Lys Lys Ile Ser Gly Tyr Val Thr Gln Lys Asp Thr  
115 120 125  
Leu Phe Pro Leu Leu Thr Val Glu Glu Thr Leu Leu Phe Ser Ala Lys

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Leu Arg Leu Lys Leu Pro Ala Asp Glu Leu Arg Ser Arg Val Lys Ser |     |     |
| 145                                                             | 150 | 155 |
| Leu Val His Glu Leu Gly Leu Glu Ala Val Ala Thr Ala Arg Val Gly |     |     |
|                                                                 | 165 | 170 |
| Asp Asp Ser Val Arg Gly Ile Ser Gly Gly Glu Arg Arg Arg Val Ser |     |     |
|                                                                 | 180 | 185 |
| Ile Gly Val Glu Val Ile His Asp Pro Lys Val Leu Ile Leu Asp Glu |     |     |
|                                                                 | 195 | 200 |
| Pro Thr Ser Gly Leu Asp Ser Thr Ser Ala Leu Leu Ile Ile Asp Met |     |     |
|                                                                 | 210 | 215 |
| Leu Lys His Met Ala Glu Thr Arg Gly Arg Thr Ile Ile Leu Thr Ile |     |     |
| 225                                                             | 230 | 235 |
| His Gln Pro Gly Phe Arg Ile Val Lys Gln Phe Asn Ser Val Leu Leu |     |     |
|                                                                 | 245 | 250 |
| Leu Ala Asn Gly Ser Thr Leu Lys Gln Gly Ser Val Asp Gln Leu Gly |     |     |
|                                                                 | 260 | 265 |
| Val Tyr Leu Arg Ser Asn Gly Leu His Pro Pro Leu His Glu Asn Ile |     |     |
|                                                                 | 275 | 280 |
| Val Glu Phe Ala Ile Glu Ser Ile Glu Ser Ile Thr Lys Gln Gln Arg |     |     |
|                                                                 | 290 | 295 |
| Leu Gln Glu Ser Arg Arg Ala Ala His Val Leu Thr Pro Gln Thr Thr |     |     |
| 305                                                             | 310 | 315 |
| Leu Gln Glu Lys Arg Ser Glu Asp Ser Gln Gly Glu Ser Lys Ser Gly |     |     |
|                                                                 | 325 | 330 |
| Lys Phe Thr Leu Gln Gln Leu Phe Gln Gln Thr Arg Val Ala Asp Val |     |     |
|                                                                 | 340 | 345 |
| Gly Thr Met Asn Ile Ala Thr Glu Phe Thr Arg Asp Phe Ala Asn Ser |     |     |
|                                                                 | 355 | 360 |
| Arg Leu Glu Glu Thr Met Ile Leu Thr His Arg Phe Ser Lys Asn Ile |     |     |
|                                                                 | 370 | 375 |
| Phe Arg Thr Lys Glu Leu Phe Ala Cys Arg Thr Val Gln Met Leu Gly |     |     |
| 385                                                             | 390 | 395 |
| Ser Gly Ile Val Leu Val                                         |     |     |
|                                                                 | 405 |     |

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acgatctggt gctggataag ccttttgctt cattctcact tccttctccta tccaaaaaag | 60  |
| ctcctccatt tcaatggcga cagCatcatc tctctcatca ctctcttcac tctcactcca  | 120 |
| caccggaacc tcttctctca tctctctctc ctccacaaaa tccatcgtct ctttctcctc  | 180 |
| cttctctcaac cgccgcttct catctctcac tctcgtcaaa gcctcatoga ccgataccga | 240 |
| aaccatcttc ttccaagacg aaacaccaga aataaccgca aatgctgtct tcgaccacc   | 300 |
| aattgctccc gaaggattcg tctctctctc gtatttcgac gaaggaagcg acgagacaga  | 360 |
| ggaagagatc gCtaccgctt ttgaagagct ctatggacct gcgtatagtg gtgagagtat  | 420 |
| gctttgagtc catcacataa atatctttcc caagcatact ctcaccagtc             |     |

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..127
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569615
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

Thr Ile Trp Cys Trp Ile Ser Leu Leu Leu His Ser His Phe Leu Pro  
1 5 10 15  
His Pro Lys Lys Leu Leu His Phe Asn Gly Asp Ser Ile Ile Ser Leu  
20 25 30  
Ile Thr Leu Phe Thr Leu Thr Pro His Pro Asn Leu Phe Ser His Leu  
35 40 45  
Leu Phe Leu His Lys Ile His Arg Leu Phe Leu Leu Leu Pro Gln Pro  
50 55 60  
Pro Leu Leu Ile Ser His Ser Arg Gln Ser Leu Ile Asp Arg Tyr Arg  
65 70 75 80  
Asn His Leu Leu Arg Arg Arg Asn Thr Arg Asn Asn Arg Lys Cys Arg  
85 90 95  
Leu Arg Pro Thr Asn Cys Ser Arg Arg Ile Arg Leu Ser Ser Val Phe  
100 105 110  
Arg Arg Arg Lys Arg Arg Asp Arg Gly Arg Asp Arg Tyr Arg Phe  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..90
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569616
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Asp Leu Val Leu Asp Lys Pro Phe Ala Ser Phe Ser Leu Pro Ser Ser  
1 5 10 15  
Ser Lys Lys Lys Ala Pro Pro Phe Gln Trp Arg Gln His His Leu Ser His  
20 25 30  
His Ser Leu His Ser His Ser Thr Pro Glu Pro Leu Leu Ser Ser Pro  
35 40 45  
Leu Pro Pro Gln Asn Pro Ser Ser Leu Ser Pro Pro Ser Ser Thr Ala  
50 55 60  
Ala Ser His Leu Ser Leu Ser Ser Lys Pro His Arg Pro Ile Pro Lys  
65 70 75 80  
Pro Ser Ser Ser Lys Thr Lys His Gln Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:1324:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..117
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569617
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

Met Ala Thr Ala Ser Ser Leu Ser Ser Leu Ser Ser Leu Ser Leu His  
1 5 10 15  
Thr Arg Thr Ser Ser Leu Ile Ser Ser Ser Ser Thr Lys Ser Ile Val

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|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |
| Ser | Phe | Ser | Ser | Phe | Leu | Val |
|     | 35  |     | 40  |     | 45  |     |
| Lys | Ala | Ser | Ser | Thr | Asp | Thr |
|     | 50  |     | 55  |     | 60  |     |
| Pro | Glu | Ile | Thr | Ala | Asn | Val |
|     | 65  |     | 70  |     | 75  |     |
| Gly | Phe | Val | Ser | Pro | Tyr | Phe |
|     |     | 85  |     | 90  |     |     |
| Glu | Glu | Ile | Ala | Thr | Ala | Phe |
|     | 100 |     | 105 |     | 110 |     |
| Gly | Glu | Ser | Met | Leu |     |     |
|     | 115 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| aaacccaaac  | atcttttcgat | tttccccgac  | tttctccgac | gatgcatgg  | cgatagCgat | 60   |
| ggtgatccg   | gtgacttatg  | ctccgacgat  | tgacacgac  | atttgaggca | gtctcctttg | 120  |
| tccagatttt  | cttcttcaac  | ctctttctct  | tgcttacc   | ccaaattcat | catctttgaa | 180  |
| actgcttcat  | ccctttcgct  | ttggtgattc  | tgaagactcc | gctttatacc | cattttgatc | 240  |
| tggagaagga  | tatagatgaa  | gtgctacagt  | cgcatactgt | ttattcaaat | gtttcgaaag | 300  |
| gagttcttgc  | aaaatcgaaa  | gacttgatga  | agtcgtttgg | atcagatgat | catacgaaaa | 360  |
| tatgcatcga  | tattttggag  | aaaggagagc  | ttcaagttgc | tggaaaagaa | agagaatcac | 420  |
| agttctcaag  | ccagtttcgg  | gatatagcaa  | cgattgttat | gcagaaaact | atcaaccctg | 480  |
| aaacacaacg  | accttatacc  | atcagcatgg  | tagagcgcct | aatgcatgaa | attcattttg | 540  |
| ctgttgatcc  | tcatagtaat  | tccaagaagc  | aggcacttga | tgtcatccgt | gagctgcaaa | 600  |
| agcacttccc  | tataaagcgt  | tctccaatga  | gactgcgtct | tactgttcct | gttcaaaatt | 660  |
| tcccctcgct  | tctggagaag  | ctaaaagaat  | gggatggtag | tggtgtctcc | aaagacgaat | 720  |
| ctggaacaca  | gatgtccact  | gtctgcgaga  | tggaaccggg | cctattccga | gagtgatgat | 780  |
| cccatgtgag  | gagtatccag  | ggaagactag  | aaatactcgc | tgtatcagtt | catgcagaag | 840  |
| gtgacacaag  | catggatcat  | tacgatgagc  | atgatgat   | ggcattgcaa | accacaagc  | 900  |
| cgttgttacc  | tgctgagact  | gagactaagg  | atttgaccga | tcccgtcgtt | gaacttagca | 960  |
| agaaactgca  | gaagcaagag  | ataagtacta  | cagataacat | aaagcaagaa | ggtggagaag | 1020 |
| aaaagaaggg  | gaccaagtgc  | agcacttgca  | acacgttcgt | tggagaggct | aagcaataca | 1080 |
| gagagcactg  | taagagtgat  | tggcacaac   | acaaccttaa | gcgtaagact | cggaaactcc | 1140 |
| ctcctattag  | tgctgacgaa  | tgcatgtctg  | agattgacat | ggacgactct | agagcagatt | 1200 |
| tgaaagacta  | ctctttctga  | aactacaatt  | ttctcctttt | gtgcttttaa | ttttgtcaat | 1260 |
| gtgttaaaatc | tcgtagtcat  | atgtgagtat  | gaatacacaa | aacttggtga | atgaaatttt | 1320 |
| gcgcgaaactt | taagagtaaa  | aacttggtgtt | taagag     |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

```

1 5 10 15
Leu Glu Lys Gly Glu Leu Gln Val Ala Gly Lys Glu Arg Glu Ser Gln
20 25 30
Phe Ser Ser Gln Phe Arg Asp Ile Ala Thr Ile Val Met Gln Lys Thr
35 40 45
Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser Met Val Glu Arg
50 55 60
Leu Met His Glu Ile His Phe Ala Val Asp Pro His Ser Asn Ser Lys
65 70 75 80
Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys His Phe Pro Ile
85 90 95
Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro Val Gln Asn Phe
100 105 110
Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly Ser Val Val Ser
115 120 125
Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys Glu Met Glu Pro
130 135 140
Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser Ile Gln Gly Arg
145 150 155 160
Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly Asp Thr Ser Met
165 170 175
Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln Thr His Lys Pro
180 185 190
Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr Asp Pro Val Val
195 200 205
Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser Thr Thr Asp Asn
210 215 220
Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr Lys Cys Ser Thr
225 230 235 240
Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg Glu His Cys Lys
245 250 255
Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr Arg Lys Leu Pro
260 265 270
Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp Met Asp Asp Ser
275 280 285
Arg Ala Asp Leu Lys Asp Tyr Ser Phe
290 295

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(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

```

Met Gln Lys Thr Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser
1 5 10 15
Met Val Glu Arg Leu Met His Glu Ile His Phe Ala Val Asp Pro His
20 25 30
Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys
35 40 45
His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro
50 55 60
Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly
65 70 75 80
Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys
85 90 95

```



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Met | Glu | Pro | Gly | Leu | Phe | Arg | Glu | Cys | Asp | Ser | His | Val | Arg | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gln | Gly | Arg | Leu | Glu | Ile | Leu | Ala | Val | Ser | Val | His | Ala | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Thr | Ser | Met | Asp | His | Tyr | Asp | Glu | His | Asp | Asp | Met | Ala | Leu | Gln |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | His | Lys | Pro | Leu | Leu | Pro | Ala | Glu | Thr | Glu | Thr | Lys | Asp | Leu | Thr |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Pro | Val | Val | Glu | Leu | Ser | Lys | Lys | Leu | Gln | Lys | Gln | Glu | Ile | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Thr | Thr | Asp | Asn | Ile | Lys | Gln | Glu | Gly | Glu | Glu | Lys | Lys | Gly | Thr |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Cys | Ser | Thr | Cys | Asn | Thr | Phe | Val | Gly | Glu | Ala | Lys | Gln | Tyr | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | His | Cys | Lys | Ser | Asp | Trp | His | Lys | His | Asn | Leu | Lys | Arg | Lys | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Lys | Leu | Pro | Pro | Ile | Ser | Ala | Asp | Glu | Cys | Met | Ser | Glu | Ile | Asp |
|     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Asp | Asp | Ser | Arg | Ala | Asp | Leu | Lys | Asp | Tyr | Ser | Phe |     |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1569621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Arg | Leu | Met | His | Glu | Ile | His | Phe | Ala | Val | Asp | Pro | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asn | Ser | Lys | Lys | Gln | Ala | Leu | Asp | Val | Ile | Arg | Glu | Leu | Gln | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Phe | Pro | Ile | Lys | Arg | Ser | Pro | Met | Arg | Leu | Arg | Leu | Thr | Val | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Gln | Asn | Phe | Pro | Ser | Leu | Leu | Glu | Lys | Leu | Lys | Glu | Trp | Asp | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Val | Ser | Lys | Asp | Glu | Ser | Gly | Thr | Gln | Met | Ser | Thr | Val | Cys |
|     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Met | Glu | Pro | Gly | Leu | Phe | Arg | Glu | Cys | Asp | Ser | His | Val | Arg | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Gln | Gly | Arg | Leu | Glu | Ile | Leu | Ala | Val | Ser | Val | His | Ala | Glu | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Thr | Ser | Met | Asp | His | Tyr | Asp | Glu | His | Asp | Asp | Met | Ala | Leu | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | His | Lys | Pro | Leu | Leu | Pro | Ala | Glu | Thr | Glu | Thr | Lys | Asp | Leu | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Asp | Pro | Val | Val | Glu | Leu | Ser | Lys | Lys | Leu | Gln | Lys | Gln | Glu | Ile | Ser |
|     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Thr | Asp | Asn | Ile | Lys | Gln | Glu | Gly | Gly | Glu | Glu | Lys | Lys | Gly | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Cys | Ser | Thr | Cys | Asn | Thr | Phe | Val | Gly | Glu | Ala | Lys | Gln | Tyr | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | His | Cys | Lys | Ser | Asp | Trp | His | Lys | His | Asn | Leu | Lys | Arg | Lys | Thr |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Lys | Leu | Pro | Pro | Ile | Ser | Ala | Asp | Glu | Cys | Met | Ser | Glu | Ile | Asp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Asp | Asp | Ser | Arg | Ala | Asp | Leu | Lys | Asp | Tyr | Ser | Phe |     |     |     |

225 230 235

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| aaattcaaaa  | tttaacacac | aaacacaaac  | acacacacca | aaaaaaaaa  | cagaccttaa | 60   |
| aaaaataaaa  | atggttgata | tggattggaa  | gaggaagatg | gtatcatcag | atttaccaaa | 120  |
| ctcacctaag  | ctttcttcaa | agcttcacgt  | aactattcca | tcaccgttca | aaatcgtccc | 180  |
| tgtttcatct  | cggatctcat | gttcagcacc  | tgctctttgc | tctgcttacg | agctttacct | 240  |
| tcgtctccct  | gagctaagaa | agctctggtc  | atctcgtgat | tttcctcaat | ggacatcaga | 300  |
| gccgattctc  | aaaccagctc | ttcaagcttt  | ggagatcagt | ttcagattag | ttttcgccgt | 360  |
| ttgttctgat  | actagaccgt | acatcaacca  | ccgtgaatgg | aaccggaggc | tagattctct | 420  |
| catcacgaag  | cagatccagc | ttgtagcagc  | gatctgcgaa | gatgaagaag | aagaaggtat | 480  |
| atcagcggag  | gctccgggtc | gcggtagcag  | gagttcgttg | agtttgttac | cgcagctagc | 540  |
| tacgtggagg  | agatcagagg | ctttggggaa  | gaagatctta | tatacgatcg | ataacgagat | 600  |
| gagtcggtgt  | aagtacacgc | tggactcgg   | tgaacaaaac | atcgccggaa | aaccaaattc | 660  |
| ccggtacgat  | gcgatttgcc | gaccaaacga  | gatctatagc | ctcaaggata | atccatacgc | 720  |
| agatcatatc  | gataatcacg | agaatcaaac  | tctctatatc | attcaccaga | tcctcgaatc | 780  |
| gtggatctac  | gcatctggaa | atctttctgaa | tgaatcgtc  | tcaagtatcg | aagaagagaa | 840  |
| attcgaaaaa  | gcttcaaacg | atgtttactt  | gctggagaag | atctggaaaa | ttttagcggg | 900  |
| gattgaagat  | cttcatatgt | tgatggatcc  | ggaagatttt | ttgaaattga | agaaacagtt | 960  |
| acagatcaaaa | tgcacgggta | aaaacgatgc  | gttttgtttc | agatctaaag | gattagtggg | 1020 |
| gatgatgaag  | atgtcgaaag | atctgagaca  | gaaagtaccg | gcggtccttg | cggttgaggt | 1080 |
| agatccaacc  | ggaggaccga | gattAcaaga  | ggcggcgatg | aagctttacg | cgaggaagac | 1140 |
| agagtgcgat  | aagattcatt | tgcttcaggg  | gatgcaagcg | gtggaagcgg | cggcgaagag | 1200 |
| tttcttcttt  | gggtataggc | agtttagtgg  | ggctatgatg | ggaagtgcgg | agatgaacgc | 1260 |
| gacggcgagt  | caagagtcgt | gtgactcact  | gagtcagata | tttatggagc | cgacgtattt | 1320 |
| cccgagcctt  | gacgcggcaa | agacgtttct  | gggagagttt | tggagtcatt | tgggatgatt | 1380 |
| aaattttta   | ttctgctgg  | ataattat    | aatataaatt | taaattggtg | gtttggttta | 1440 |
| atttactttg  | taagatagt  | aaatttttgg  | aacatttgac | gatccatatt | tgaatacaaa | 1500 |
| ttcattttta  | c          |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Lys | Phe | Asn | Thr | Gln | Thr | Gln | Thr | His | Thr | Pro | Lys | Lys | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asp | Leu | Lys | Lys | Ile | Lys | Met | Val | Asp | Met | Asp | Trp | Lys | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Val | Ser | Ser | Asp | Leu | Pro | Asn | Ser | Pro | Lys | Leu | Ser | Ser | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Val | Thr | Ile | Pro | Ser | Pro | Phe | Lys | Ile | Val | Pro | Val | Ser | Ser | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Ser | Cys | Ser | Ala | Pro | Ala | Leu | Cys | Ser | Ala | Tyr | Glu | Leu | Tyr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEO ID NO:1331:

(A) LENGTH: 435 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1569654

Met Val Asp Met Asp Trp Lys Arg Lys Met Val Ser Ser Asp Leu Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Asn | Ser | Pro | Lys | Leu | Ser | Ser | Lys | Leu | His | Val | Thr | Ile | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Phe | Lys | Ile | Val | Pro | Val | Ser | Ser | Pro | Ile | Ser | Cys | Ser | Ala | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Cys | Ser | Ala | Tyr | Glu | Leu | Tyr | Leu | Arg | Leu | Pro | Glu | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Leu | Trp | Ser | Ser | Arg | Asp | Phe | Pro | Gln | Trp | Thr | Ser | Glu | Pro | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Lys | Pro | Ala | Leu | Gln | Ala | Leu | Glu | Ile | Ser | Phe | Arg | Leu | Val | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Val | Cys | Ser | Asp | Thr | Arg | Pro | Tyr | Ile | Asn | His | Arg | Glu | Trp | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Arg | Leu | Asp | Ser | Leu | Ile | Thr | Lys | Gln | Ile | Gln | Leu | Val | Ala | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Cys | Glu | Asp | Glu | Glu | Glu | Glu | Gly | Ile | Ser | Ala | Glu | Ala | Pro | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gly | Gly | Arg | Ser | Ser | Leu | Ser | Leu | Leu | Pro | Gln | Leu | Ala | Thr | Trp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Arg | Ser | Glu | Ala | Leu | Gly | Lys | Lys | Ile | Leu | Tyr | Thr | Ile | Asp | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Met | Ser | Arg | Cys | Lys | Tyr | Thr | Leu | Gly | Leu | Gly | Glu | Gln | Asn | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Gly | Lys | Pro | Asn | Leu | Arg | Tyr | Asp | Ala | Ile | Cys | Arg | Pro | Asn | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Tyr | Ser | Leu | Lys | Asp | Asn | Pro | Tyr | Ala | Asp | His | Ile | Asp | Asn | His |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Asn | Gln | Thr | Leu | Tyr | Ile | Ile | His | Gln | Ile | Leu | Glu | Ser | Trp | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ala | Ser | Gly | Asn | Leu | Asn | Arg | Ile | Val | Ser | Ser | Ile | Glu | Glu | Glu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Phe | Glu | Lys | Ala | Ser | Asn | Asp | Val | Tyr | Leu | Leu | Glu | Lys | Ile |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Lys | Ile | Leu | Ala | Glu | Ile | Glu | Asp | Leu | His | Met | Leu | Met | Asp | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Asp | Phe | Leu | Lys | Leu | Lys | Lys | Gln | Leu | Gln | Ile | Lys | Ser | Thr | Gly |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Asn | Asp | Ala | Phe | Cys | Phe | Arg | Ser | Lys | Gly | Leu | Val | Glu | Met | Met |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |
| Met | Ser | Lys | Asp | Leu | Arg | Gln | Lys | Val | Pro | Ala | Val | Leu | Ala | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Asp | Pro | Thr | Gly | Gly | Pro | Arg | Leu | Gln | Glu | Ala | Ala | Met | Lys |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |
| Tyr | Ala | Arg | Lys | Thr | Glu | Cys | Asp | Lys | Ile | His | Leu | Leu | Gln | Gly |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |
| Gln | Ala | Val | Glu | Ala | Ala | Ala | Lys | Ser | Phe | Phe | Phe | Gly | Tyr | Arg |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |
| Leu | Val | Ala | Ala | Met | Met | Gly | Ser | Ala | Glu | Met | Asn | Ala | Thr | Ala |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     | 400 |
| Gln | Glu | Ser | Cys | Asp | Ser | Leu | Ser | Gln | Ile | Phe | Met | Glu | Pro | Thr |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Pro | Ser | Leu | Asp | Ala | Ala | Lys | Thr | Phe | Leu | Gly | Glu | Phe | Trp |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |
| His | Leu | Gly |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 435 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..432  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569655  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Trp | Lys | Arg | Lys | Met | Val | Ser | Ser | Asp | Leu | Pro | Asn | Ser | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Leu | Ser | Ser | Lys | Leu | His | Val | Thr | Ile | Pro | Ser | Pro | Phe | Lys | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Pro | Val | Ser | Ser | Pro | Ile | Ser | Cys | Ser | Ala | Pro | Ala | Leu | Cys | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Tyr | Glu | Leu | Tyr | Leu | Arg | Leu | Pro | Glu | Leu | Arg | Lys | Leu | Trp | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Arg | Asp | Phe | Pro | Gln | Trp | Thr | Ser | Glu | Pro | Ile | Leu | Lys | Pro | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Leu | Gln | Ala | Leu | Glu | Ile | Ser | Phe | Arg | Leu | Val | Phe | Ala | Val | Cys | Ser |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | Thr | Arg | Pro | Tyr | Ile | Asn | His | Arg | Glu | Trp | Asn | Arg | Arg | Leu | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Leu | Ile | Thr | Lys | Gln | Ile | Gln | Leu | Val | Ala | Ala | Ile | Cys | Glu | Asp |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Glu | Glu | Glu | Glu | Gly | Ile | Ser | Ala | Glu | Ala | Pro | Val | Gly | Gly | Gly | Arg |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Ser | Leu | Ser | Leu | Leu | Pro | Gln | Leu | Ala | Thr | Trp | Arg | Arg | Ser | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Ala | Leu | Gly | Lys | Lys | Ile | Leu | Tyr | Thr | Ile | Asp | Asn | Glu | Met | Ser | Arg |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Cys | Lys | Tyr | Thr | Leu | Gly | Leu | Gly | Glu | Gln | Asn | Ile | Ala | Gly | Lys | Pro |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asn | Leu | Arg | Tyr | Asp | Ala | Ile | Cys | Arg | Pro | Asn | Glu | Ile | Tyr | Ser | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Lys | Asp | Asn | Pro | Tyr | Ala | Asp | His | Ile | Asp | Asn | His | Glu | Asn | Gln | Thr |  |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |
| Leu | Tyr | Ile | Ile | His | Gln | Ile | Leu | Glu | Ser | Trp | Ile | Tyr | Ala | Ser | Gly |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Asn | Leu | Leu | Asn | Arg | Ile | Val | Ser | Ser | Ile | Glu | Glu | Glu | Lys | Phe | Glu |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Lys | Ala | Ser | Asn | Asp | Val | Tyr | Leu | Leu | Glu | Lys | Ile | Trp | Lys | Ile | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ala | Glu | Ile | Glu | Asp | Leu | His | Met | Leu | Met | Asp | Pro | Glu | Asp | Phe | Leu |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Lys | Leu | Lys | Lys | Gln | Leu | Gln | Ile | Lys | Ser | Thr | Gly | Lys | Asn | Asp | Ala |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |
| Phe | Cys | Phe | Arg | Ser | Lys | Gly | Leu | Val | Glu | Met | Met | Lys | Met | Ser | Lys |  |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |  |
| Asp | Leu | Arg | Gln | Lys | Val | Pro | Ala | Val | Leu | Ala | Val | Glu | Val | Asp | Pro |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Thr | Gly | Gly | Pro | Arg | Leu | Gln | Glu | Ala | Ala | Met | Lys | Leu | Tyr | Ala | Arg |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Lys | Thr | Glu | Cys | Asp | Lys | Ile | His | Leu | Leu | Gln | Gly | Met | Gln | Ala | Val |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Glu | Ala | Ala | Ala | Lys | Ser | Phe | Phe | Phe | Gly | Tyr | Arg | Gln | Leu | Val | Ala |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Ala | Met | Met | Gly | Ser | Ala | Glu | Met | Asn | Ala | Thr | Ala | Ser | Gln | Glu | Ser |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |  |
| Cys | Asp | Ser | Leu | Ser | Gln | Ile | Phe | Met | Glu | Pro | Thr | Tyr | Phe | Pro | Ser |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Leu | Asp | Ala | Ala | Lys | Thr | Phe | Leu | Gly | Glu | Phe | Trp | Ser | His | Leu | Gly |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |  |

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(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

|            |             |            |            |             |             |      |
|------------|-------------|------------|------------|-------------|-------------|------|
| acttaaagcc | ctcaaaatct  | cagagaacgc | tcgctgatca | aatccgtcgt  | ccttcaaccg  | 60   |
| tcgcctcctc | cgatcatgaca | attgagtgcg | ttaatcccga | aggtcttcga  | ttcaacccaaa | 120  |
| tgaaaagctc | ctctcatcaa  | accctagaaa | cgaggatgag | gccgattttg  | atgaagggac  | 180  |
| atgaacgtcc | attgacgttc  | ctgaggtaca | acagaaatgg | tgatctgctt  | ttctcctgcg  | 240  |
| ccaaagacca | cactcccaca  | gtctggtttg | ccgataacgg | cgagcgtcct  | ggcacttacc  | 300  |
| gtggccacag | tggtgctgtt  | tggtgctgtg | atatctccag | agactcgtct  | agattgatca  | 360  |
| ctggtagtgc | tgatcagact  | gcaaagctgt | gggatgtgaa | atctggcaaa  | gaattgttca  | 420  |
| ctttcaagtt | tggtgcccct  | gcaaGgtctg | tggatttctc | tggttggtgat | catcttgacg  | 480  |
| tgattaccac | tgatcacttc  | gtgggaactt | cctctgctat | tcatgtcaaa  | cgcattgcag  | 540  |
| aagatcccga | agaccaggtt  | ggtgattctg | tgcttgtcct | tcaaagtcct  | gatggaaaga  | 600  |
| agaagatcaa | tagagctgtt  | tggggtcccc | tgaaccaaac | cattgttagt  | ggtggtgaag  | 660  |
| atgctgctat | cagaatctgg  | gatgcagaga | ctagaaaatt | gcttaagcaa  | tcagatgagg  | 720  |
| aagtgggtca | caaggaggcc  | attacatccc | tctgcaaagc | agctgatgac  | tctcacttCc  | 780  |
| ttacaggttc | acatgacaaa  | actgcaaagc | tttgggacat | gagaacgctg  | actcttatta  | 840  |
| agacttacac | cactgtggtg  | cctgtaaatG | ctgtcgccat | gtctccactt  | ctcaaccatg  | 900  |
| ttgtgcttgg | aggtggtcaa  | gatgcacacg | ctgtgactac | cactgatcat  | cgtgctggga  | 960  |
| agtttgaagc | taagttttac  | gacacgattc | tgcaagagga | aattggtggc  | gtgaaaggtc  | 1020 |
| attttggacc | tattaatgct  | ttggcattca | gtcctgatgg | gaagagtttc  | tctagtggag  | 1080 |
| gtgaagacgg | ctacgtgaga  | ctgcacattt | ttgactccaa | ttacttcaac  | atcaagattt  | 1140 |
| agattctttg | aacatgtcct  | tccatttttt | catcattcca | cataatattt  | tctctctttt  | 1200 |
| taacattttc | agaattgatg  | tactaccaaa | ttaccaatat | actactttga  | tgataaagct  | 1260 |
| tggtgtttgt | cttttc      |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Lys | Pro | Ser | Lys | Ser | Gln | Arg | Thr | Leu | Ala | Asp | Gln | Ile | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Thr | Val | Ala | Ser | Ser | Val | Met | Thr | Ile | Glu | Cys | Val | Asn | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Leu | Arg | Phe | Asn | Gln | Met | Lys | Ser | Ser | Ser | His | Gln | Thr | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Thr | Arg | Met | Arg | Pro | Ile | Leu | Met | Lys | Gly | His | Glu | Arg | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Phe | Leu | Arg | Tyr | Asn | Arg | Asn | Gly | Asp | Leu | Leu | Phe | Ser | Cys | Ala |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Asp | His | Thr | Pro | Thr | Val | Trp | Phe | Ala | Asp | Asn | Gly | Glu | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Thr | Tyr | Arg | Gly | His | Ser | Gly | Ala | Val | Trp | Cys | Cys | Asp | Ile | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Arg Asp Ser Ser Arg Leu Ile Thr Gly Ser Ala Asp Gln Thr Ala Lys  
115 120 125  
Leu Trp Asp Val Lys Ser Gly Lys Glu Leu Phe Thr Phe Lys Phe Gly  
130 135 140  
Ala Pro Ala Arg Ser Val Asp Phe Ser Val Gly Asp His Leu Ala Val  
145 150 155 160  
Ile Thr Thr Asp His Phe Val Gly Thr Ser Ser Ala Ile His Val Lys  
165 170 175  
Arg Ile Ala Glu Asp Pro Glu Asp Gln Val Gly Asp Ser Val Leu Val  
180 185 190  
Leu Gln Ser Pro Asp Gly Lys Lys Lys Ile Asn Arg Ala Val Trp Gly  
195 200 205  
Pro Leu Asn Gln Thr Ile Val Ser Gly Gly Glu Asp Ala Ala Ile Arg  
210 215 220  
Ile Trp Asp Ala Glu Thr Arg Lys Leu Leu Lys Gln Ser Asp Glu Glu  
225 230 235 240  
Val Gly His Lys Glu Ala Ile Thr Ser Leu Cys Lys Ala Ala Asp Asp  
245 250 255  
Ser His Phe Leu Thr Gly Ser His Asp Lys Thr Ala Lys Leu Trp Asp  
260 265 270  
Met Arg Thr Leu Thr Leu Ile Lys Thr Tyr Thr Thr Val Val Pro Val  
275 280 285  
Asn Ala Val Ala Met Ser Pro Leu Leu Asn His Val Val Leu Gly Gly  
290 295 300  
Gly Gln Asp Ala Ser Ala Val Thr Thr Thr Asp His Arg Ala Gly Lys  
305 310 315 320  
Phe Glu Ala Lys Phe Tyr Asp Thr Ile Leu Gln Glu Glu Ile Gly Gly  
325 330 335  
Val Lys Gly His Phe Gly Pro Ile Asn Ala Leu Ala Phe Ser Pro Asp  
340 345 350  
Gly Lys Ser Phe Ser Ser Gly Gly Glu Asp Gly Tyr Val Arg Leu His  
355 360 365  
His Phe Asp Ser Asn Tyr Phe Asn Ile Lys Ile  
370 375

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1569658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

Met Thr Ile Glu Cys Val Asn Pro Glu Gly Leu Arg Phe Asn Gln Met  
1 5 10 15  
Lys Ser Ser Ser His Gln Thr Leu Glu Thr Arg Met Arg Pro Ile Leu  
20 25 30  
Met Lys Gly His Glu Arg Pro Leu Thr Phe Leu Arg Tyr Asn Arg Asn  
35 40 45  
Gly Asp Leu Leu Phe Ser Cys Ala Lys Asp His Thr Pro Thr Val Trp  
50 55 60  
Phe Ala Asp Asn Gly Glu Arg Leu Gly Thr Tyr Arg Gly His Ser Gly  
65 70 75 80  
Ala Val Trp Cys Cys Asp Ile Ser Arg Asp Ser Ser Arg Leu Ile Thr  
85 90 95  
Gly Ser Ala Asp Gln Thr Ala Lys Leu Trp Asp Val Lys Ser Gly Lys  
100 105 110  
Glu Leu Phe Thr Phe Lys Phe Gly Ala Pro Ala Arg Ser Val Asp Phe

SEQUENCE: 1569658

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1569659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Ser | Ser | His | Gln | Thr | Leu | Glu | Thr | Arg | Met | Arg | Pro | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Met | Lys | Gly | His | Glu | Arg | Pro | Leu | Thr | Phe | Leu | Arg | Tyr | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Gly | Asp | Leu | Leu | Phe | Ser | Cys | Ala | Lys | Asp | His | Thr | Pro | Thr | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Phe | Ala | Asp | Asn | Gly | Glu | Arg | Leu | Gly | Thr | Tyr | Arg | Gly | His | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Val | Trp | Cys | Cys | Asp | Ile | Ser | Arg | Asp | Ser | Ser | Arg | Leu | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Gly | Ser | Ala | Asp | Gln | Thr | Ala | Lys | Leu | Trp | Asp | Val | Lys | Ser | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Glu | Leu | Phe | Thr | Phe | Lys | Phe | Gly | Ala | Pro | Ala | Arg | Ser | Val | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Val | Gly | Asp | His | Leu | Ala | Val | Ile | Thr | Thr | Asp | His | Phe | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Thr | Ser | Ser | Ala | Ile | His | Val | Lys | Arg | Ile | Ala | Glu | Asp | Pro | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |



Asp Gln Val Gly Asp Ser Val Leu Val Leu Gln Ser Pro Asp Gly Lys  
145 150 155 160  
Lys Lys Ile Asn Arg Ala Val Trp Gly Pro Leu Asn Gln Thr Ile Val  
165 170 175  
Ser Gly Gly Glu Asp Ala Ala Ile Arg Ile Trp Asp Ala Glu Thr Arg  
180 185 190  
Lys Leu Leu Lys Gln Ser Asp Glu Glu Val Gly His Lys Glu Ala Ile  
195 200 205  
Thr Ser Leu Cys Lys Ala Ala Asp Asp Ser His Phe Leu Thr Gly Ser  
210 215 220  
His Asp Lys Thr Ala Lys Leu Trp Asp Met Arg Thr Leu Thr Leu Ile  
225 230 235 240  
Lys Thr Tyr Thr Thr Val Val Pro Val Asn Ala Val Ala Met Ser Pro  
245 250 255  
Leu Leu Asn His Val Val Leu Gly Gly Gly Gln Asp Ala Ser Ala Val  
260 265 270  
Thr Thr Thr Asp His Arg Ala Gly Lys Phe Glu Ala Lys Phe Tyr Asp  
275 280 285  
Thr Ile Leu Gln Glu Glu Ile Gly Gly Val Lys Gly His Phe Gly Pro  
290 295 300  
Ile Asn Ala Leu Ala Phe Ser Pro Asp Gly Lys Ser Phe Ser Ser Gly  
305 310 315 320  
Gly Glu Asp Gly Tyr Val Arg Leu His His Phe Asp Ser Asn Tyr Phe  
325 330 335  
Asn Ile Lys Ile  
340

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| atcttcttct  | ctctaaacct  | ctccttcaat | ggcgcgcgat | gctcaccatc  | tctttctttc  | 60   |
| tcctcctcaa  | ctcttctcca  | acagagaatt | aacgatgaat | aataacacta  | tggaaccaac  | 120  |
| tagtggcggg  | ttctgcaata  | acaatcaaac | cggttacggc | gtcgtttcac  | ctttctccgt  | 180  |
| tccaaaccat  | acatcaacaa  | caacaacagc | aacgcctcct | cttcttcata  | tgtacggcgg  | 240  |
| ctctgatact  | attcccacca  | ccgcgcgtta | ctacgcgat  | ggtgctacta  | atctcgactg  | 300  |
| tgaatttttc  | cctttaccaa  | cgagaaaacg | ctcaagagat | tcttcaagat  | caaattatca  | 360  |
| tcactttctt  | cttcagaacc  | cgagatcatc | atcatgtgtt | aacgctgcta  | ctacaacaac  | 420  |
| tacaacaact  | ccgttctcgt  | ttcttggcca | agacattgat | atctcctctc  | acatgaatca  | 480  |
| acaacaacac  | gaaatagatc  | gattcgtctc | ccttcactta | tatcagatgg  | agagagtga   | 540  |
| atatgagata  | gaagagaaga  | ggaaaagaca | agcgagaacg | ataatggagg  | cgatagagca  | 600  |
| aggactggtt  | aaaaggcttc  | gtgtcaaaga | agaagaaaga | gagaggatcg  | gcaagggtta  | 660  |
| ccacgcgctt  | gaggagcgag  | tgaagtcact | ttctatagag | aaccaaactc  | ggagagacct  | 720  |
| tgctcagacg  | aacgaagcca  | cggctaacca | cctccgaacc | aacctcgagc  | atgtttctggc | 780  |
| gcaggttaag  | gacgtatcac  | gcggcgcagg | attagagaaa | aacatgaacg  | aagaggacga  | 840  |
| tgccggagtgc | tgctgcggaa  | gcagctgtgg | tggtgtgtgt | gaagaaacgg  | taaggcgcag  | 900  |
| ggtaggatta  | gaaagggagg  | cgaggataaa | ggcggagagg | aggaggagga  | ggatgtgtag  | 960  |
| aaactgtggg  | gaggaggaat  | cgtgtgtgtt | gctgttaccg | tgcagacact  | tgtgtttgtg  | 1020 |
| tggagtatgc  | gggtccagtgc | tgcacacgtg | tcccatctgt | acatctccta  | aaaacgctag  | 1080 |
| cgttcatgtc  | aacatgtcat  | cttgaccccg | tcccgtttat | ggaatactcc  | tcttcttctt  | 1140 |
| tttttWtttt  | tttttttgtt  | ctttagaaaa | tttgaagga  | tatttttagtt | gaatattatt  | 1200 |
| attatttttta | gct         |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Asp | Ala | His | His | Leu | Phe | Leu | Ser | Pro | Pro | Gln | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asn | Arg | Glu | Leu | Thr | Met | Asn | Asn | Asn | Thr | Met | Glu | Pro | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Phe | Cys | Asn | Asn | Asn | Gln | Thr | Gly | Tyr | Gly | Val | Val | Ser | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Val | Pro | Asn | His | Thr | Ser | Thr | Thr | Thr | Thr | Ala | Thr | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | His | Met | Tyr | Gly | Gly | Ser | Asp | Thr | Ile | Pro | Thr | Thr | Ala | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Tyr | Ala | Asp | Gly | Ala | Thr | Asn | Leu | Asp | Cys | Glu | Phe | Phe | Pro | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Thr | Arg | Lys | Arg | Ser | Arg | Asp | Ser | Ser | Arg | Ser | Asn | Tyr | His | His |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Leu | Leu | Gln | Asn | Pro | Arg | Ser | Ser | Ser | Cys | Val | Asn | Ala | Ala | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Thr | Thr | Thr | Thr | Thr | Pro | Phe | Ser | Phe | Leu | Gly | Gln | Asp | Ile | Asp |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Ser | Ser | His | Met | Asn | Gln | Gln | Gln | His | Glu | Ile | Asp | Arg | Phe | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Leu | His | Leu | Tyr | Gln | Met | Glu | Arg | Val | Lys | Tyr | Glu | Ile | Glu | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Arg | Lys | Arg | Gln | Ala | Arg | Thr | Ile | Met | Glu | Ala | Ile | Glu | Gln | Gly |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Leu | Val | Lys | Arg | Leu | Arg | Val | Lys | Glu | Glu | Glu | Arg | Glu | Arg | Ile | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Val | Asn | His | Ala | Leu | Glu | Glu | Arg | Val | Lys | Ser | Leu | Ser | Ile | Glu |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Asn | Gln | Ile | Trp | Arg | Asp | Leu | Ala | Gln | Thr | Asn | Glu | Ala | Thr | Ala | Asn |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Leu | Arg | Thr | Asn | Leu | Glu | His | Val | Leu | Ala | Gln | Val | Lys | Asp | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Arg | Gly | Ala | Gly | Leu | Glu | Lys | Asn | Met | Asn | Glu | Glu | Asp | Asp | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Ser | Cys | Cys | Gly | Ser | Ser | Cys | Gly | Gly | Gly | Gly | Glu | Glu | Thr | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Arg | Arg | Val | Gly | Leu | Glu | Arg | Glu | Ala | Gln | Asp | Lys | Ala | Glu | Arg |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Arg | Arg | Arg | Arg | Met | Cys | Arg | Asn | Cys | Gly | Glu | Glu | Glu | Ser | Cys | Val |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Leu | Leu | Pro | Cys | Arg | His | Leu | Cys | Leu | Cys | Gly | Val | Cys | Gly | Ser |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Ser | Val | His | Thr | Cys | Pro | Ile | Cys | Thr | Ser | Pro | Lys | Asn | Ala | Ser | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| His | Val | Asn | Met | Ser | Ser |     |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

|            |            |            |            |            |     |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asn        | Asn        | Asn        | Thr<br>5   | Met | Glu        | Pro        | Thr        | Ser<br>10  | Gly        | Gly        | Phe        | Cys        | Asn<br>15  | Asn        |
| Asn        | Gln        | Thr        | Gly<br>20  | Tyr        | Gly | Val        | Val        | Ser<br>25  | Pro        | Phe        | Ser        | Val        | Pro<br>30  | Asn        | His        |
| Thr        | Ser        | Thr        | Thr<br>35  | Thr        | Thr | Ala        | Thr<br>40  | Pro        | Pro        | Leu        | Leu        | His<br>45  | Met        | Tyr        | Gly        |
| Gly        | Ser<br>50  | Asp        | Thr        | Ile        | Pro | Thr<br>55  | Ala        | Gly        | Tyr        | Tyr<br>60  | Ala        | Asp        | Gly        | Ala        |            |
| Thr<br>65  | Asn        | Leu        | Asp        | Cys<br>70  | Glu | Phe        | Phe        | Pro        | Leu        | Pro<br>75  | Thr        | Arg        | Lys        | Arg        | Ser<br>80  |
| Arg        | Asp        | Ser        | Ser<br>85  | Arg        | Ser | Asn        | Tyr        | His<br>90  | His        | Leu        | Leu        | Leu        | Gln<br>95  | Asn        | Pro        |
| Arg        | Ser        | Ser        | Ser<br>100 | Cys        | Val | Asn        | Ala        | Ala<br>105 | Thr        | Thr        | Thr        | Thr        | Thr<br>110 | Thr        | Thr        |
| Pro        | Phe        | Ser<br>115 | Phe        | Leu        | Gly | Gln        | Asp<br>120 | Ile        | Asp        | Ile        | Ser        | Ser<br>125 | His        | Met        | Asn        |
| Gln        | Gln<br>130 | Gln        | His        | Glu        | Ile | Asp<br>135 | Arg        | Phe        | Val        | Ser        | Leu<br>140 | His        | Leu        | Tyr        | Gln        |
| Met<br>145 | Glu        | Arg        | Val        | Lys<br>150 | Tyr | Glu        | Ile        | Glu        | Glu        | Lys<br>155 | Arg        | Lys        | Arg        | Gln        | Ala<br>160 |
| Arg        | Thr        | Ile        | Met<br>165 | Glu        | Ala | Ile        | Glu        | Gln        | Gly<br>170 | Leu        | Val        | Lys        | Arg        | Leu<br>175 | Arg        |
| Val        | Lys        | Glu        | Glu<br>180 | Glu        | Arg | Glu        | Arg        | Ile<br>185 | Gly        | Lys        | Val        | Asn        | His<br>190 | Ala        | Leu        |
| Glu        | Glu        | Arg<br>195 | Val        | Lys        | Ser | Leu        | Ser<br>200 | Ile        | Glu        | Asn        | Gln        | Ile<br>205 | Trp        | Arg        | Asp        |
| Leu        | Ala<br>210 | Gln        | Thr        | Asn        | Glu | Ala<br>215 | Thr        | Ala        | Asn        | His        | Leu<br>220 | Arg        | Thr        | Asn        | Leu        |
| Glu<br>225 | His        | Val        | Leu        | Ala<br>230 | Gln | Val        | Lys        | Asp        | Val        | Ser<br>235 | Arg        | Gly        | Ala        | Gly        | Leu<br>240 |
| Glu        | Lys        | Asn        | Met<br>245 | Asn        | Glu | Glu        | Asp        | Asp        | Ala<br>250 | Glu        | Ser        | Cys        | Cys        | Gly<br>255 | Ser        |
| Ser        | Cys        | Gly        | Gly<br>260 | Gly        | Gly | Glu        | Glu        | Thr<br>265 | Val        | Arg        | Arg        | Arg        | Val<br>270 | Gly        | Leu        |
| Glu        | Arg<br>275 | Glu        | Ala        | Gln        | Asp | Lys        | Ala<br>280 | Glu        | Arg        | Arg        | Arg        | Arg        | Arg<br>285 | Met        | Cys        |
| Arg        | Asn<br>290 | Cys        | Gly        | Glu        | Glu | Glu        | Ser<br>295 | Cys        | Val        | Leu        | Leu        | Leu        | Pro        | Cys        | Arg        |
| His<br>305 | Leu        | Cys        | Leu        | Cys<br>310 | Gly | Val        | Cys        | Gly        | Ser        | Ser<br>315 | Val        | His        | Thr        | Cys        | Pro<br>320 |
| Ile        | Cys        | Thr        | Ser<br>325 | Pro        | Lys | Asn        | Ala        | Ser        | Val<br>330 | His        | Val        | Asn        | Met        | Ser        | Ser        |

```
(2) INFORMATION FOR SEQ ID NO:1340:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..331
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1569670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met Glu Pro Thr Ser Gly Gly Phe Cys Asn Asn Gln Thr Gly Tyr  
1 5 10 15  
Gly Val Val Ser Pro Phe Ser Val Pro Asn His Thr Ser Thr Thr Thr  
20 25 30  
Thr Ala Thr Pro Pro Leu Leu His Met Tyr Gly Gly Ser Asp Thr Ile  
35 40 45  
Pro Thr Thr Ala Gly Tyr Tyr Ala Asp Gly Ala Thr Asn Leu Asp Cys  
50 55 60  
Glu Phe Phe Pro Leu Pro Thr Arg Lys Arg Ser Arg Asp Ser Ser Arg  
65 70 75 80  
Ser Asn Tyr His His Leu Leu Leu Gln Asn Pro Arg Ser Ser Ser Cys  
85 90 95  
Val Asn Ala Ala Thr Thr Thr Thr Thr Thr Thr Pro Phe Ser Phe Leu  
100 105 110  
Gly Gln Asp Ile Asp Ile Ser Ser His Met Asn Gln Gln Gln His Glu  
115 120 125  
Ile Asp Arg Phe Val Ser Leu His Leu Tyr Gln Met Glu Arg Val Lys  
130 135 140  
Tyr Glu Ile Glu Glu Lys Arg Lys Arg Gln Ala Arg Thr Ile Met Glu  
145 150 155 160  
Ala Ile Glu Gln Gly Leu Val Lys Arg Leu Arg Val Lys Glu Glu Glu  
165 170 175  
Arg Glu Arg Ile Gly Lys Val Asn His Ala Leu Glu Glu Arg Val Lys  
180 185 190  
Ser Leu Ser Ile Glu Asn Gln Ile Trp Arg Asp Leu Ala Gln Thr Asn  
195 200 205  
Glu Ala Thr Ala Asn His Leu Arg Thr Asn Leu Glu His Val Leu Ala  
210 215 220  
Gln Val Lys Asp Val Ser Arg Gly Ala Gly Leu Glu Lys Asn Met Asn  
225 230 235 240  
Glu Glu Asp Asp Ala Glu Ser Cys Cys Gly Ser Ser Cys Gly Gly Gly  
245 250 255  
Gly Glu Glu Thr Val Arg Arg Arg Val Gly Leu Glu Arg Glu Ala Gln  
260 265 270  
Asp Lys Ala Glu Arg Arg Arg Arg Arg Met Cys Arg Asn Cys Gly Glu  
275 280 285  
Glu Glu Ser Cys Val Leu Leu Pro Cys Arg His Leu Cys Leu Cys  
290 295 300  
Gly Val Cys Gly Ser Ser Val His Thr Cys Pro Ile Cys Thr Ser Pro  
305 310 315 320  
Lys Asn Ala Ser Val His Val Asn Met Ser Ser  
325 330

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1169

(D) OTHER INFORMATION: / Ceres Seq. ID 1569671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| acacccaaac acgcgacgcg agcgaaAgaa gacgatgacg aacaaggaga aagctcgaga | 60  |
| gagaagggag aaaaaaatgc aggagatctc tctccttoga actattcctt actctgacca | 120 |
| ccataggtgG tggctctgtg aaaatgtagc agtagtgact ggttcaaacc gcgggattgg | 180 |
| attcgagatt gcaagacagc ttgcggttca cggattgacg gttgttctta cagctagaaa | 240 |
| cgtgaatgct ggtcttgaag cagttaaatc tttgaggcac caagaagaag gtctcaaggt | 300 |

|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| ttatttttcat | caacttgatg  | tcacagactc  | ttcctcgatt  | agagagtttg | gttgctggct | 360  |
| taagcaaaca  | tttggagggt  | tagatatctt  | cgtgaataat  | Ygcagggtgt | aactacaatc | 420  |
| tcggctcaga  | taatacgggt  | gaatttgctg  | aaacagttat  | atctactaac | taccaaggaa | 480  |
| ccaaaaacat  | gacaaaagct  | atgataacc   | Ct          | tgatgagacc | atctcctcat | 540  |
| tagtcaatgt  | tagttctcgg  | ctaggtagag  | taaatggaag  | acgtaataga | ctggcaaagt | 600  |
| tagagttgag  | agatcagcta  | agcagtcag   | atttgctgac  | cgaggaactt | atagacagaa | 660  |
| ctgtctctaa  | attcatcaac  | caagtaaaaag | acggaacttg  | ggaatcaggc | gggtggcctc | 720  |
| agacattcac  | tgactactcc  | atgtctaagc  | ttgcagtcaa  | tgcttacacg | agactaatgg | 780  |
| caaaagaact  | tgagagacga  | ggagaggaag  | agaagattta  | tgtaaacagc | ttttgccctg | 840  |
| gttgggtgaa  | gactgcgatg  | aNctgGCTac  | gccggaaata  | tgccacctga | agatgcagct | 900  |
| gatactggag  | tttggccttag | cctggtcctt  | tccgaagagt  | cagtaaccgg | aaaattcttc | 960  |
| gcagagagac  | gtgagatcaa  | cttctgaggg  | ttgttgaaatg | tttgtaaacg | ttggaataga | 1020 |
| ttgtgtcgtc  | ttcgttttagt | gccatagttt  | tagtcaaagg  | tttacaaaat | caattgtaat | 1080 |
| tggtaaagtga | atggtttag   | tcatgatacg  | cgtcagattt  | gccacaaaac | taggagttta | 1140 |
| taatttaaat  | ataattaatt  | tttaattgc   |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1569672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Asn | Thr | Arg | Arg | Glu | Arg | Lys | Lys | Thr | Met | Thr | Asn | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Arg | Glu | Arg | Arg | Glu | Lys | Lys | Met | Gln | Glu | Ile | Ser | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Thr | Ile | Pro | Tyr | Ser | Asp | His | His | Arg | Trp | Trp | Ser | Cys | Glu | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ala | Val | Val | Thr | Gly | Ser | Asn | Arg | Gly | Ile | Gly | Phe | Glu | Ile | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Gln | Leu | Ala | Val | His | Gly | Leu | Thr | Val | Val | Leu | Thr | Ala | Arg | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Asn | Ala | Gly | Leu | Glu | Ala | Val | Lys | Ser | Leu | Arg | His | Gln | Glu | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Leu | Lys | Val | Tyr | Phe | His | Gln | Leu | Asp | Val | Thr | Asp | Ser | Ser | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Arg | Glu | Phe | Gly | Cys | Trp | Leu | Lys | Gln | Thr | Phe | Gly | Gly | Leu | Asp |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu | Val | Asn | Asn | Xaa | Arg | Cys |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1569673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Ala | Met | Ile | Pro | Leu | Met | Arg | Pro | Ser | Pro | His | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Val | Asn | Val | Ser | Ser | Arg | Leu | Gly | Arg | Val | Asn | Gly | Arg | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Asn Arg Leu Ala Asn Val Glu Leu Arg Asp Gln Leu Ser Ser Pro Asp  
35 40 45  
Leu Leu Thr Glu Glu Leu Ile Asp Arg Thr Val Ser Lys Phe Ile Asn  
50 55 60  
Gln Val Lys Asp Gly Thr Trp Glu Ser Gly Gly Trp Pro Gln Thr Phe  
65 70 75 80  
Thr Asp Tyr Ser Met Ser Lys Leu Ala Val Asn Ala Tyr Thr Arg Leu  
85 90 95  
Met Ala Lys Glu Leu Glu Arg Arg Gly Glu Glu Glu Lys Ile Tyr Val  
100 105 110  
Asn Ser Phe Cys Pro Gly Trp Val Lys Thr Ala Met Xaa Trp Leu Arg  
115 120 125  
Arg Lys Tyr Ala Thr  
130

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Met Ile Pro Leu Met Arg Pro Ser Pro His Gly Ala Arg Val Val Asn  
1 5 10 15  
Val Ser Ser Arg Leu Gly Arg Val Asn Gly Arg Arg Asn Arg Leu Ala  
20 25 30  
Asn Val Glu Leu Arg Asp Gln Leu Ser Ser Pro Asp Leu Leu Thr Glu  
35 40 45  
Glu Leu Ile Asp Arg Thr Val Ser Lys Phe Ile Asn Gln Val Lys Asp  
50 55 60  
Gly Thr Trp Glu Ser Gly Gly Trp Pro Gln Thr Phe Thr Asp Tyr Ser  
65 70 75 80  
Met Ser Lys Leu Ala Val Asn Ala Tyr Thr Arg Leu Met Ala Lys Glu  
85 90 95  
Leu Glu Arg Arg Gly Glu Glu Glu Lys Ile Tyr Val Asn Ser Phe Cys  
100 105 110  
Pro Gly Trp Val Lys Thr Ala Met Xaa Trp Leu Arg Arg Lys Tyr Ala  
115 120 125  
Thr

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aatcaaaaag gcaaaaagca aagagagaga gagagagaag aagaagtgag acttgtgttc  | 60  |
| ttacgggtgtt tatagcttct ttgttttgct ttttaggttc ttgccttttt ccgatcaatc | 120 |
| agaccaatcc ctcttcaact tttagcatct tattctcttt cgttcttctt atatttctgg  | 180 |
| gaattttctt caatcgattc ctctttgttg taatctcaca attAgagaga gagatrtgta  | 240 |
| Gtaatcagtt ggcgatatct tcgtcttctt catcttsttc gtactatgaa tctttgaagg  | 300 |

(2) INFORMATION FOR SEO ID NO:1346:

(A) LENGTH: 338 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1569686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Arg | Gln | Lys | Ala | Lys | Arg | Glu | Arg | Glu | Arg | Arg | Arg | Ser | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Cys | Val | Leu | Thr | Val | Phe | Ile | Ala | Ser | Leu | Phe | Cys | Leu | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Cys | Leu | Phe | Pro | Ile | Asn | Gln | Thr | Asn | Pro | Ser | Phe | Thr | Phe | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Leu | Phe | Ser | Phe | Val | Leu | Leu | Ile | Phe | Leu | Gly | Ile | Phe | Phe | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Phe | Leu | Phe | Val | Val | Ile | Ser | Gln | Leu | Glu | Arg | Glu | Xaa | Cys | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Gln | Leu | Ala | Ile | Ser | Ser | Ser | Ser | Ser | Ser | Xaa | Ser | Tyr | Tyr | Glu |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |
| Ser | Leu | Lys | Val | Leu | Glu | Ala | Asp | Val | Gln | His | Ala | Asn | Ser | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Ile | Pro | Met | Gly | Lys | Asn | Asn | Val | Arg | Leu | Gln | Met | Lys | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | His | Ser | Asn | Phe | Ala | Ser | Leu | Leu | Leu | Phe | Leu | Leu | Arg | Trp | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Leu | Ser | Ser | Ser | Cys | Leu | Ile | Pro | Arg | Tyr | Leu | Asn | Leu | Phe | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Leu | Val | Tyr | Lys | Val | Gln | Ser | Asp | Gly | Gln | Pro | Lys | Leu | Thr | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Gly | Arg | Lys | Ala | Thr | Ile | Ser | Glu | Phe | Tyr | Gly | Val | Ile | Leu | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Leu | Gln | Leu | Leu | His | Ser | Asn | Leu | Asp | Glu | Leu | Glu | Thr | Thr | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Gly | Phe | Asp | Leu | Lys | Arg | Leu | Ser | Lys | Lys | Ile | Thr | Lys | Glu | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Ser | Ser | Arg | Phe | Ser | Asn | Ala | Gly | Leu | Glu | Arg | Glu | Glu | Glu | Cys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ile | Cys | Leu | Glu | Thr | Cys | Thr | Lys | Met | Val | Leu | Pro | Asn | Cys | Cys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Ser | Met | Cys | Ile | Lys | Cys | Tyr | Arg | Asn | Trp | Asn | Leu | Lys | Ser | Gln |

260 265 270  
Ser Cys Pro Phe Cys Arg Gly Ser Met Lys Arg Val Asn Ser Glu Asp  
275 280 285  
Leu Trp Val Leu Ala Gly Asp Asn Asp Val Val Asp Thr Arg Thr Ala  
290 295 300  
Ser Arg Glu Asp Leu Phe Arg Phe Tyr Leu Tyr Ile Asn Ser Leu Pro  
305 310 315 320  
Lys Asp Tyr Pro Glu Ala Leu Phe Val Val Tyr Tyr Glu Tyr Ser Asn  
325 330 335  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Met Gly Lys Asn Asn Val Arg Leu Gln Met Lys Leu Val His Ser Asn  
1 5 10 15  
Phe Ala Ser Leu Leu Leu Phe Leu Leu Arg Trp Ile Asp Leu Ser Ser  
20 25 30  
Ser Cys Leu Ile Pro Arg Tyr Leu Asn Leu Phe His Val Leu Val Tyr  
35 40 45  
Lys Val Gln Ser Asp Gly Gln Pro Lys Leu Thr Thr His Gly Arg Lys  
50 55 60  
Ala Thr Ile Ser Glu Phe Tyr Gly Val Ile Leu Pro Ser Leu Gln Leu  
65 70 75 80  
Leu His Ser Asn Leu Asp Glu Leu Glu Thr Thr Asp Ile Gly Phe Asp  
85 90 95  
Leu Lys Arg Leu Ser Lys Lys Ile Thr Lys Glu Ala Arg Ser Ser Arg  
100 105 110  
Phe Ser Asn Ala Gly Leu Glu Arg Glu Glu Glu Cys Gly Ile Cys Leu  
115 120 125  
Glu Thr Cys Thr Lys Met Val Leu Pro Asn Cys Cys His Ser Met Cys  
130 135 140  
Ile Lys Cys Tyr Arg Asn Trp Asn Leu Lys Ser Gln Ser Cys Pro Phe  
145 150 155 160  
Cys Arg Gly Ser Met Lys Arg Val Asn Ser Glu Asp Leu Trp Val Leu  
165 170 175  
Ala Gly Asp Asn Asp Val Val Asp Thr Arg Thr Ala Ser Arg Glu Asp  
180 185 190  
Leu Phe Arg Phe Tyr Leu Tyr Ile Asn Ser Leu Pro Lys Asp Tyr Pro  
195 200 205  
Glu Ala Leu Phe Val Val Tyr Tyr Glu Tyr Ser Asn Leu Leu  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

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(D) OTHER INFORMATION: / Ceres Seq. ID 1569688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met Lys Leu Val His Ser Asn Phe Ala Ser Leu Leu Leu Phe Leu Leu  
1 5 10 15  
Arg Trp Ile Asp Leu Ser Ser Ser Cys Leu Ile Pro Arg Tyr Leu Asn  
20 25 30  
Leu Phe His Val Leu Val Tyr Lys Val Gln Ser Asp Gly Gln Pro Lys  
35 40 45  
Leu Thr Thr His Gly Arg Lys Ala Thr Ile Ser Glu Phe Tyr Gly Val  
50 55 60  
Ile Leu Pro Ser Leu Gln Leu Leu His Ser Asn Leu Asp Glu Leu Glu  
65 70 75 80  
Thr Thr Asp Ile Gly Phe Asp Leu Lys Arg Leu Ser Lys Lys Ile Thr  
85 90 95  
Lys Glu Ala Arg Ser Ser Arg Phe Ser Asn Ala Gly Leu Glu Arg Glu  
100 105 110  
Glu Glu Cys Gly Ile Cys Leu Glu Thr Cys Thr Lys Met Val Leu Pro  
115 120 125  
Asn Cys Cys His Ser Met Cys Ile Lys Cys Tyr Arg Asn Trp Asn Leu  
130 135 140  
Lys Ser Gln Ser Cys Pro Phe Cys Arg Gly Ser Met Lys Arg Val Asn  
145 150 155 160  
Ser Glu Asp Leu Trp Val Leu Ala Gly Asp Asn Asp Val Val Asp Thr  
165 170 175  
Arg Thr Ala Ser Arg Glu Asp Leu Phe Arg Phe Tyr Leu Tyr Ile Asn  
180 185 190  
Ser Leu Pro Lys Asp Tyr Pro Glu Ala Leu Phe Val Val Tyr Tyr Glu  
195 200 205  
Tyr Ser Asn Leu Leu  
210

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..792

(D) OTHER INFORMATION: / Ceres Seq. ID 1569697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

gattcagagt ttgtcagcga gagagacgaa gaaagaaaga gaggagaggt ggaagatgat 60  
taaggcagtg atgatgatga acacacaagg caaaccacgt ctagctaaat tctacgatta 120  
catgcctgtg gagaagcagc aggagcttat tcgcggcgtg ttttcagtat tgtgcagtag 180  
acctgagaac gtaagcaatt ttctggagat cgaatcattg tttggaccgg actcgcggct 240  
tgtatacaag cattatgcta cactctatgt tgttcttgta tttgatgggt cagaaaatga 300  
gcttgctatg cttgatctca ttttaagttct tgttgaaaca ctggacaaat gcttcagcaa 360  
tgtctgcgaa ctgcacattg Gtgttcaact acagcaagat gcacgcggtg ttagGatgag 420  
attgtatttg gaggacaaAg tactggaaac tagttctgct gaagtcatga aggctggtga 480  
agaaatatca aaattagaag ctgcctcaaa ttcgatttca cttgtcccca agtctgtttc 540  
cgggtggcgt ggccgttagc ttcgaaaaaa cttgcctgaa taagtcagag aacatgtaac 600  
aaaagcttat ccaagtcttg atccaaacat gtttgtttaa tgagcgtgga atgttgctg 660  
gatgggctca gtagtctaac gtgggcctgt gaattgtaac tgggtaacgg acggaactgc 720  
ttgctatttt tgagaatgta acaaaaacga cgagaagtta agatctataa atgataaatg 780  
atgtccaaat cc

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1350:

(2) INFORMATION FOR SEO ID NO:1351:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

(2) INFORMATION FOR SEQ ID NO:1352:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..84  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Met | Asn | Thr | Gln | Gly | Lys | Pro | Arg | Leu | Ala | Lys | Phe | Tyr | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Met | Pro | Val | Glu | Lys | Gln | Gln | Glu | Leu | Ile | Arg | Gly | Val | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:1353:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

(2) INFORMATION FOR SEQ ID NO:1354:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Lys | Glu | Gly | Ser | Lys | Met | Asn | Ile | Ala | Ile | Ile | His | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Gly | Ile | Gly | Gly | Ala | Glu | Arg | Leu | Ile | Val | Asp | Ala | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Ala | Ser | His | Gly | His | Lys | Val | His | Ile | Phe | Thr | Ser | His | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

```

Asp Lys Ser Arg Cys Phe Glu Glu Thr Leu Ser Gly Ile Phe Gln Val
 50 55 60
Thr Val Tyr Gly Ser Phe Leu Pro Arg His Ile Phe Tyr Arg Leu His
 65 70 75 80
Ala Xaa Val Ala Tyr Leu Arg Cys Leu Phe Val Ala Leu Cys Val Leu
 85 90 95
Leu Gly Trp Ser Ser Phe Asp Val Val Leu Ala Asp Gln Val Ser Val
 100 105 110
Val Val Pro Leu Leu Lys Leu Lys Arg Ser Ser Lys Val Val Phe Tyr
 115 120 125
Cys His Phe Pro Asp Leu Leu Leu Ala Lys His Thr Thr Thr Leu Arg
 130 135 140
Arg Met Tyr Arg Lys Pro Ile Asp Phe Ile Glu Glu Gln Thr Thr Gly
 145 150 155 160
Met Ala Asp Met Ile Leu Val Asn Ser Asn Phe Thr Ala Ser Thr Phe
 165 170 175
Ala Asn Thr Phe Lys Arg Leu Asn Ala Gln Gly Ser Arg Pro Ala Val
 180 185 190
Leu Tyr Pro Ala Val Asn Ile Asp Gln Phe Ile Glu Pro His Thr Tyr
 195 200 205
Lys Leu Asn Phe Leu Ser Ile Asn Arg Phe Glu Arg Lys Lys Asn Ile
 210 215 220
Asp Leu Ala Val Ser Ala Phe Ala Ile Leu Cys Lys His Lys Gln Asn
 225 230 235 240
Leu Ser Asp Val Thr Leu Thr Val Ala Gly Gly Tyr Asp Glu Arg Leu
 245 250 255
Lys Glu Asn Val Glu Tyr Leu Glu Glu Leu Arg Ser Leu Ala Glu Lys
 260 265 270
Glu Gly Val Ser Asp Arg Val Asn Phe Ile Thr Ser Cys Ser Thr Ala
 275 280 285
Glu Arg Asn Glu Leu Leu Ser Ser Cys Leu Cys Val Leu Tyr Thr Pro
 290 295 300
Thr Asp Glu His Phe Gly Ile Val Pro Leu Glu Ala Met Ala Ala Tyr
 305 310 315 320
Lys Pro Val Ile Ala Cys Asn Ser Gly Gly Pro Val Glu Thr Val Lys
 325 330 335
Asn Gly Val Thr Gly Tyr Leu Cys Glu Pro Thr Pro Glu Asp Phe Ser
 340 345 350
Ser Ala Met Ala Arg Phe Ile Glu Asn Pro Glu Leu Ala Asn Arg Met
 355 360 365
Gly Ala Glu Ala Arg Asn His Val Val Glu Ser Phe Ser Val Lys Thr
 370 375 380
Phe Gly Gln Lys Leu Asn Gln Tyr Leu Val Asp Val Val Ser Ser Pro
 385 390 395 400
Lys Glu Asp

```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```

Met Asn Ile Ala Ile Ile His Pro Asp Leu Gly Ile Gly Gly Ala Glu
 1 5 10 15
Arg Leu Ile Val Asp Ala Ala Val Glu Leu Ala Ser His Gly His Lys

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Val | His | Ile | Phe | Thr | Ser | His | His | Asp | Lys | Ser | Arg | Cys | Phe | Glu | Glu |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Ser | Gly | Ile | Phe | Gln | Val | Thr | Val | Tyr | Gly | Ser | Phe | Leu | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | His | Ile | Phe | Tyr | Arg | Leu | His | Ala | Xaa | Val | Ala | Tyr | Leu | Arg | Cys |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Phe | Val | Ala | Leu | Cys | Val | Leu | Leu | Gly | Trp | Ser | Ser | Phe | Asp | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Ala | Asp | Gln | Val | Ser | Val | Val | Val | Pro | Leu | Leu | Lys | Leu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Ser | Lys | Val | Val | Phe | Tyr | Cys | His | Phe | Pro | Asp | Leu | Leu | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Lys | His | Thr | Thr | Thr | Leu | Arg | Arg | Met | Tyr | Arg | Lys | Pro | Ile | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ile | Glu | Glu | Gln | Thr | Thr | Gly | Met | Ala | Asp | Met | Ile | Leu | Val | Asn |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Asn | Phe | Thr | Ala | Ser | Thr | Phe | Ala | Asn | Thr | Phe | Lys | Arg | Leu | Asn |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Gln | Gly | Ser | Arg | Pro | Ala | Val | Leu | Tyr | Pro | Ala | Val | Asn | Ile | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Phe | Ile | Glu | Pro | His | Thr | Tyr | Lys | Leu | Asn | Phe | Leu | Ser | Ile | Asn |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Phe | Glu | Arg | Lys | Lys | Asn | Ile | Asp | Leu | Ala | Val | Ser | Ala | Phe | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Leu | Cys | Lys | His | Lys | Gln | Asn | Leu | Ser | Asp | Val | Thr | Leu | Thr | Val |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Gly | Gly | Tyr | Asp | Glu | Arg | Leu | Lys | Glu | Asn | Val | Glu | Tyr | Leu | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Leu | Arg | Ser | Leu | Ala | Glu | Lys | Glu | Gly | Val | Ser | Asp | Arg | Val | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     | 270 |     |     |     |
| Phe | Ile | Thr | Ser | Cys | Ser | Thr | Ala | Glu | Arg | Asn | Glu | Leu | Leu | Ser | Ser |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Leu | Cys | Val | Leu | Tyr | Thr | Pro | Thr | Asp | Glu | His | Phe | Gly | Ile | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Leu | Glu | Ala | Met | Ala | Ala | Tyr | Lys | Pro | Val | Ile | Ala | Cys | Asn | Ser |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gly | Gly | Pro | Val | Glu | Thr | Val | Lys | Asn | Gly | Val | Thr | Gly | Tyr | Leu | Cys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Pro | Thr | Pro | Glu | Asp | Phe | Ser | Ser | Ala | Met | Ala | Arg | Phe | Ile | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Pro | Glu | Leu | Ala | Asn | Arg | Met | Gly | Ala | Glu | Ala | Arg | Asn | His | Val |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Val | Glu | Ser | Phe | Ser | Val | Lys | Thr | Phe | Gly | Gln | Lys | Leu | Asn | Gln | Tyr |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Val | Asp | Val | Val | Ser | Pro | Lys | Glu | Asp |     |     |     |     |     |     |
|     | 385 |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Arg | Lys | Pro | Ile | Asp | Phe | Ile | Glu | Glu | Gln | Thr | Thr | Gly | Met |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

Ala Asp Met Ile Leu Val Asn Ser Asn Phe Thr Ala Ser Thr Phe Ala  
20 25 30  
Asn Thr Phe Lys Arg Leu Asn Ala Gln Gly Ser Arg Pro Ala Val Leu  
35 40 45  
Tyr Pro Ala Val Asn Ile Asp Gln Phe Ile Glu Pro His Thr Tyr Lys  
50 55 60  
Leu Asn Phe Leu Ser Ile Asn Arg Phe Glu Arg Lys Lys Asn Ile Asp  
65 70 75 80  
Leu Ala Val Ser Ala Phe Ala Ile Leu Cys Lys His Lys Gln Asn Leu  
85 90 95  
Ser Asp Val Thr Leu Thr Val Ala Gly Tyr Asp Glu Arg Leu Lys  
100 105 110  
Glu Asn Val Glu Tyr Leu Glu Glu Leu Arg Ser Leu Ala Glu Lys Glu  
115 120 125  
Gly Val Ser Asp Arg Val Asn Phe Ile Thr Ser Cys Ser Thr Ala Glu  
130 135 140  
Arg Asn Glu Leu Leu Ser Ser Cys Leu Cys Val Leu Tyr Thr Pro Thr  
145 150 155 160  
Asp Glu His Phe Gly Ile Val Pro Leu Glu Ala Met Ala Ala Tyr Lys  
165 170 175  
Pro Val Ile Ala Cys Asn Ser Gly Gly Pro Val Glu Thr Val Lys Asn  
180 185 190  
Gly Val Thr Gly Tyr Leu Cys Glu Pro Thr Pro Glu Asp Phe Ser Ser  
195 200 205  
Ala Met Ala Arg Phe Ile Glu Asn Pro Glu Leu Ala Asn Arg Met Gly  
210 215 220  
Ala Glu Ala Arg Asn His Val Val Glu Ser Phe Ser Val Lys Thr Phe  
225 230 235 240  
Gly Gln Lys Leu Asn Gln Tyr Leu Val Asp Val Val Ser Ser Pro Lys  
245 250 255  
Glu Asp

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..662
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

```
actcgatcat agaataaaaa accaaaaccc ttgaagtcac taagttgatt caaaatgggt 60
gcgagaagtg aggaagttga gatagtggaa gatacggcgg cgaaatgttt gatgttggtt 120
tcaagagttg gagaaggcgg cggaggagga gagaaacgag ttttccgatg caagacttgt 180
cttaaagagt tttcgtcgtt tcaagctttg ggaggtcatt gtgcaagcca caacaaactc 240
attaacagta gcgatccatc acttctttgga tcctttgtcta acaagaaaac taaaacggcg 300
acgtctcatt cttgtccgat atgtggcgtg gagtttccga tggggcaagc tcttggtggt 360
cacatgagga gacataggag tgagaaagcc tcaccaggca cgttggGtta cacgttcttt 420
tttaccggag acgacgacgg tgacgacttt gaagaaatcg agtagtggga agagagtggc 480
ttgtttggac ttagattcga tggagagttt agtcaattgg aagttggagt tgggaagaac 540
gatttcttga ttogttttat ttcttcatat tcgttatagg gttttaacat attttcatac 600
agtttcatat tgtaatcttt gtgatccat ttatcttacc gatcgatgtg aatattattt 660
tg
```

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Arg | Ser | Glu | Glu | Val | Glu | Ile | Val | Glu | Asp | Thr | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Cys | Leu | Met | Leu | Leu | Ser | Arg | Val | Gly | Glu | Gly | Gly | Gly | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Arg | Val | Phe | Arg | Cys | Lys | Thr | Cys | Leu | Lys | Glu | Phe | Ser | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Gln | Ala | Leu | Gly | Gly | His | Arg | Ala | Ser | His | Asn | Lys | Leu | Ile | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Asp | Pro | Ser | Leu | Leu | Gly | Ser | Leu | Ser | Asn | Lys | Lys | Thr | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ala | Thr | Ser | His | Pro | Cys | Pro | Ile | Cys | Gly | Val | Glu | Phe | Pro | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gln | Ala | Leu | Gly | Gly | His | Met | Arg | Arg | His | Arg | Ser | Glu | Lys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Gly | Thr | Leu | Gly | Tyr | Thr | Phe | Phe | Phe | Thr | Gly | Asp | Asp | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Asp | Asp | Phe | Glu | Glu | Ile | Glu |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(D) OTHER INFORMATION: / Ceres Seq. ID 1569723

[illegible]

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

(2) INFORMATION FOR SEQ ID NO:1361:

(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1569725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ser | Ile | Glu | Asp | Glu | Leu | Phe | Pro | Ser | Thr | Pro | Gly | Lys | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ile | Asp | Arg | Ser | Asn | Arg | Gln | Leu | His | Arg | Cys | Phe | Ala | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Met | Phe | Leu | Trp | Ala | Leu | Phe | Leu | Ile | Ala | Leu | Thr | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Leu | Ser | Phe | Gln | Ser | Phe | Val | Asp | Ser | Gly | Ser | Arg | Tyr | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ser | Trp | Gly | Gly | Ile | Gln | Trp | Glu | Lys | Gln | Val | Arg | Thr | Ser | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Ile | His | Arg | Ser | Gly | Gly | Ile | Ser | Val | Leu | Val | Thr | Gly | Ala | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Phe | Val | Gly | Ser | His | Val | Ser | Leu | Ala | Leu | Arg | Lys | Arg | Gly | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Val | Val | Gly | Leu | Asp | Asn | Phe | Asn | Asn | Tyr | Tyr | Asp | Pro | Ser | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Arg | Ala | Arg | Arg | Ser | Leu | Ser | Ser | Arg | Gly | Ile | Phe | Val | Val |     |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Gly | Asp | Leu | Asn | Asp | Ala | Lys | Leu | Leu | Ala | Lys | Leu | Phe | Asp | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Trp | Ala | Leu | Phe | Leu | Ile | Ala | Leu | Thr | Ala | Ser | Tyr | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Phe | Gln | Ser | Phe | Val | Asp | Ser | Gly | Ser | Arg | Tyr | Leu | Thr | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Gly | Gly | Ile | Gln | Trp | Glu | Lys | Gln | Val | Arg | Thr | Ser | Ala | Gln | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Arg | Ser | Gly | Gly | Ile | Ser | Val | Leu | Val | Thr | Gly | Ala | Thr | Gly | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Gly | Ser | His | Val | Ser | Leu | Ala | Leu | Arg | Lys | Arg | Gly | Asp | Gly | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Gly | Leu | Asp | Asn | Phe | Asn | Asn | Tyr | Tyr | Asp | Pro | Ser | Leu | Lys | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | Arg | Ser | Leu | Leu | Ser | Ser | Arg | Gly | Ile | Phe | Val | Val | Glu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Asn | Asp | Ala | Lys | Leu | Leu | Ala | Lys | Leu | Phe | Asp | Val | Val | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Thr | His | Val | Met | His | Leu | Ala | Ala | Gln | Ala | Gly | Val | Arg | Tyr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Glu | Asn | Pro | Gln | Ser | Tyr | Val | His | Ser | Asn | Ile | Ala | Gly | Leu | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Leu | Leu | Glu | Ile | Cys | Lys | Ala | Ala | Asn | Pro | Gln | Pro | Ala | Ile | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Trp | Ala | Ser | Ser | Ser | Ser | Val | Tyr | Gly | Leu | Asn | Glu | Lys | Val | Pro | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Glu | Ser | Asp | Arg | Thr | Asp | Gln | Pro | Ala | Ser | Leu | Tyr | Ala | Ala | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Lys | Ala | Gly | Glu | Glu | Ile | Thr | His | Thr | Tyr | Asn | His | Ile | Tyr | Gly |

210 215 220  
Leu Ala Ile Thr Gly Leu Arg Phe Phe Thr Val Tyr Gly Pro Trp Gly  
225 230 235 240  
Arg Pro Asp Met Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu Gln Gly  
245 250 255  
Lys Pro Ile Thr Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu Ala Arg  
260 265 270  
Asp Phe Thr Tyr Ile Asp Asp Ile Val Lys Gly Cys Leu Gly Ser Leu  
275 280 285  
Asp Ser Ser Gly Lys Ser Thr Gly Ser Gly  
290 295

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

Met His Leu Ala Ala Gln Ala Gly Val Arg Tyr Ala Leu Glu Asn Pro  
1 5 10 15  
Gln Ser Tyr Val His Ser Asn Ile Ala Gly Leu Val Asn Leu Leu Glu  
20 25 30  
Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala Ile Val Trp Ala Ser Ser  
35 40 45  
Ser Ser Val Tyr Gly Leu Asn Glu Lys Val Pro Phe Ser Glu Ser Asp  
50 55 60  
Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala Ala Thr Lys Lys Ala Gly  
65 70 75 80  
Glu Glu Ile Thr His Thr Tyr Asn His Ile Tyr Gly Leu Ala Ile Thr  
85 90 95  
Gly Leu Arg Phe Thr Val Tyr Gly Pro Trp Gly Arg Pro Asp Met  
100 105 110  
Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu Gln Gly Lys Pro Ile Thr  
115 120 125  
Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu Ala Arg Asp Phe Thr Tyr  
130 135 140  
Ile Asp Asp Ile Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly  
145 150 155 160  
Lys Ser Thr Gly Ser Gly  
165

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

aagtcacatt ctctctcTtt tttttagtgt gtgcaaagtc atcttctctt ttaatatatta 60  
cctaaaattc caaacaaaag agaacgttat gaaaccaaag agcaaagttg cagaatctac 120  
agctgcatca tgttttctcg tcatgagctt gttatgcagc tgcattattg gtgaccaaatt 180  
ggagactaat aatgaaggct tgtcttacag ttactacgag aaaacttgtc ccaaagtcga 240

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(2) INFORMATION FOR SEQ ID NO:1365:

(A) LENGTH: 368 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1569733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ser<br>1   | His        | Leu        | Leu        | Ser<br>5   | Leu        | Phe        | Phe        | Ser        | Val<br>10  | Cys        | Lys        | Val        | Ile        | Phe<br>15  | Ser        |
| Phe        | Asn        | Ile        | Tyr<br>20  | Leu        | Lys        | Phe        | Gln        | Thr<br>25  | Lys        | Glu        | Asn        | Val        | Met<br>30  | Lys        | Pro        |
| Lys        | Ser        | Lys<br>35  | Val        | Ala        | Glu        | Ser        | Thr<br>40  | Ala        | Ala        | Ser        | Cys        | Phe<br>45  | Leu        | Val        | Met        |
| Ser        | Leu        | Leu        | Cys        | Ser        | Cys        | Ile<br>55  | Ile        | Gly        | Asp        | Gln        | Met<br>60  | Glu        | Thr        | Asn        | Asn        |
| Glu<br>65  | Gly        | Leu        | Ser        | Tyr<br>70  | Ser        | Tyr        | Tyr        | Glu        | Lys        | Thr<br>75  | Cys        | Pro        | Lys        | Val        | Glu<br>80  |
| Glu        | Ile        | Val        | Arg<br>85  | Ser        | Ser        | Leu        | Ser        | Ser        | Met<br>90  | Phe        | Ile        | Leu        | Asp<br>95  | Pro        | Thr        |
| Ser        | Pro        | Ala        | Ala<br>100 | Leu        | Leu        | Arg        | Leu        | Met<br>105 | Phe        | His        | Asp        | Cys        | Gln<br>110 | Val        | Gln        |
| Gly        | Cys        | Asp<br>115 | Ala        | Ser        | Ile        | Leu        | Leu<br>120 | Glu        | Pro        | Ile        | Arg        | Asp<br>125 | Gln        | Gln        | Phe        |
| Thr<br>130 | Glu        | Leu        | Asp        | Ser        | Ala        | Lys<br>135 | Asn        | Phe        | Gly        | Ile        | Arg<br>140 | Lys        | Arg        | Asp        | Leu        |
| Val<br>145 | Gly        | Ser        | Ile        | Lys<br>150 | Thr        | Ser        | Leu        | Glu        | Leu        | Glu<br>155 | Cys        | Pro        | Lys        | Gln        | Val<br>160 |
| Ser        | Cys        | Ser        | Asp<br>165 | Val        | Ile        | Ile        | Leu        | Ala        | Ala<br>170 | Arg        | Asp        | Ala        | Val        | Ala<br>175 | Leu        |
| Thr        | Gly        | Gly<br>180 | Pro        | Leu        | Ile        | Ser        | Val        | Pro<br>185 | Leu        | Gly        | Arg        | Lys        | Asp<br>190 | Ser        | Leu        |
| Ser        | Thr<br>195 | Pro        | Ser        | Lys        | His        | Val        | Ala<br>200 | Asp        | Ser        | Glu        | Leu        | Pro<br>205 | Pro        | Ser        | Thr        |
| Ala<br>210 | Asp        | Val        | Asp        | Thr        | Thr        | Leu        | Ser<br>215 | Leu        | Phe        | Ala        | Asn<br>220 | Lys        | Gly        | Met        | Thr        |
| Ile<br>225 | Glu        | Glu        | Ser        | Val        | Ala<br>230 | Ile        | Met        | Gly        | Ala        | His<br>235 | Thr        | Ile        | Gly        | Val        | Thr<br>240 |
| His        | Cys        | Asn        | Asn<br>245 | Val        | Leu        | Ser        | Arg        | Phe        | Asp<br>250 | Asn        | Ala        | Asn        | Ala        | Thr<br>255 | Ser        |
| Glu        | Asn        | Met        | Asp        | Pro        | Arg        | Phe        | Gln        | Thr        | Phe        | Leu        | Arg        | Val        | Ala        | Cys        | Pro        |

|                                                                 |                             |     |
|-----------------------------------------------------------------|-----------------------------|-----|
| 260                                                             | 265                         | 270 |
| Glu Phe Ser Pro Thr Ser Gln Ala                                 | Glu Ala Thr Phe Val Pro Asn |     |
| 275                                                             | 280                         | 285 |
| Asp Gln Thr Ser Val Ile Phe Asp Thr Ala Tyr Tyr Asp Asp Ala Ile |                             |     |
| 290                                                             | 295                         | 300 |
| Ala Gly Arg Gly Asn Leu Arg Ile Asp Ser Glu Ile Gly Ala Asp Pro |                             |     |
| 305                                                             | 310                         | 315 |
| Arg Thr Arg Pro Phe Val Glu Ala Phe Ala Ala Asp Gln Asp Arg Phe |                             |     |
| 325                                                             | 330                         | 335 |
| Phe Asn Ala Phe Ser Ser Ala Phe Val Lys Leu Ser Ser Tyr Lys Val |                             |     |
| 340                                                             | 345                         | 350 |
| Leu Thr Gly Asn Glu Gly Val Ile Arg Ser Val Cys Asp Lys Val Asp |                             |     |
| 355                                                             | 360                         | 365 |

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1569734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Lys Pro Lys Ser Lys Val Ala Glu Ser Thr Ala Ala Ser Cys Phe |     |
| 1                                                               | 15  |
| Leu Val Met Ser Leu Leu Cys Ser Cys Ile Ile Gly Asp Gln Met Glu |     |
| 20                                                              | 30  |
| Thr Asn Asn Glu Gly Leu Ser Tyr Ser Tyr Tyr Glu Lys Thr Cys Pro |     |
| 35                                                              | 45  |
| Lys Val Glu Glu Ile Val Arg Ser Ser Leu Ser Ser Met Phe Ile Leu |     |
| 50                                                              | 60  |
| Asp Pro Thr Ser Pro Ala Leu Leu Arg Leu Met Phe His Asp Cys     |     |
| 65                                                              | 80  |
| Gln Val Gln Gly Cys Asp Ala Ser Ile Leu Leu Glu Pro Ile Arg Asp |     |
| 85                                                              | 95  |
| Gln Gln Phe Thr Glu Leu Asp Ser Ala Lys Asn Phe Gly Ile Arg Lys |     |
| 100                                                             | 110 |
| Arg Asp Leu Val Gly Ser Ile Lys Thr Ser Leu Glu Leu Glu Cys Pro |     |
| 115                                                             | 125 |
| Lys Gln Val Ser Cys Ser Asp Val Ile Ile Leu Ala Ala Arg Asp Ala |     |
| 130                                                             | 140 |
| Val Ala Leu Thr Gly Gly Pro Leu Ile Ser Val Pro Leu Gly Arg Lys |     |
| 145                                                             | 160 |
| Asp Ser Leu Ser Thr Pro Ser Lys His Val Ala Asp Ser Glu Leu Pro |     |
| 165                                                             | 175 |
| Pro Ser Thr Ala Asp Val Asp Thr Thr Leu Ser Leu Phe Ala Asn Lys |     |
| 180                                                             | 190 |
| Gly Met Thr Ile Glu Glu Ser Val Ala Ile Met Gly Ala His Thr Ile |     |
| 195                                                             | 205 |
| Gly Val Thr His Cys Asn Asn Val Leu Ser Arg Phe Asp Asn Ala Asn |     |
| 210                                                             | 220 |
| Ala Thr Ser Glu Asn Met Asp Pro Arg Phe Gln Thr Phe Leu Arg Val |     |
| 225                                                             | 240 |
| Ala Cys Pro Glu Phe Ser Pro Thr Ser Gln Ala Ala Glu Ala Thr Phe |     |
| 245                                                             | 255 |
| Val Pro Asn Asp Gln Thr Ser Val Ile Phe Asp Thr Ala Tyr Asp     |     |
| 260                                                             | 270 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ala | Ile | Ala | Gly | Arg | Gly | Asn | Leu | Arg | Ile | Asp | Ser | Glu | Ile | Gly |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Asp | Pro | Arg | Thr | Arg | Pro | Phe | Val | Glu | Ala | Phe | Ala | Ala | Asp | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Arg | Phe | Phe | Asn | Ala | Phe | Ser | Ser | Ala | Phe | Val | Lys | Leu | Ser | Ser |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Tyr | Lys | Val | Leu | Thr | Gly | Asn | Glu | Gly | Val | Ile | Arg | Ser | Val | Cys | Asp |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |

Lys Val Asp

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1569735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Leu | Cys | Ser | Cys | Ile | Ile | Gly | Asp | Gln | Met | Glu | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Glu | Gly | Leu | Ser | Tyr | Ser | Tyr | Tyr | Glu | Lys | Thr | Cys | Pro | Lys | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Ile | Val | Arg | Ser | Ser | Leu | Ser | Ser | Met | Phe | Ile | Leu | Asp | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ser | Pro | Ala | Ala | Leu | Leu | Arg | Leu | Met | Phe | His | Asp | Cys | Gln | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gly | Cys | Asp | Ala | Ser | Ile | Leu | Leu | Glu | Pro | Ile | Arg | Asp | Gln | Gln |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Thr | Glu | Leu | Asp | Ser | Ala | Lys | Asn | Phe | Gly | Ile | Arg | Lys | Arg | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Val | Gly | Ser | Ile | Lys | Thr | Ser | Leu | Glu | Leu | Glu | Cys | Pro | Lys | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ser | Cys | Ser | Asp | Val | Ile | Ile | Leu | Ala | Ala | Arg | Asp | Ala | Val | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Thr | Gly | Gly | Pro | Leu | Ile | Ser | Val | Pro | Leu | Gly | Arg | Lys | Asp | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Thr | Pro | Ser | Lys | His | Val | Ala | Asp | Ser | Glu | Leu | Pro | Pro | Ser |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Ala | Asp | Val | Asp | Thr | Thr | Leu | Ser | Leu | Phe | Ala | Asn | Lys | Gly | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Ile | Glu | Glu | Ser | Val | Ala | Ile | Met | Gly | Ala | His | Thr | Ile | Gly | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | His | Cys | Asn | Asn | Val | Leu | Ser | Arg | Phe | Asp | Asn | Ala | Asn | Ala | Thr |
|     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ser | Glu | Asn | Met | Asp | Pro | Arg | Phe | Gln | Thr | Phe | Leu | Arg | Val | Ala | Cys |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Glu | Phe | Ser | Pro | Thr | Ser | Gln | Ala | Ala | Glu | Ala | Thr | Phe | Val | Pro |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Asn | Asp | Gln | Thr | Ser | Val | Ile | Phe | Asp | Thr | Ala | Tyr | Tyr | Asp | Asp | Ala |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ile | Ala | Gly | Arg | Gly | Asn | Leu | Arg | Ile | Asp | Ser | Glu | Ile | Gly | Ala | Asp |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |     |
| Pro | Arg | Thr | Arg | Pro | Phe | Val | Glu | Ala | Phe | Ala | Ala | Asp | Gln | Asp | Arg |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Phe | Phe | Asn | Ala | Phe | Ser | Ser | Ala | Phe | Val | Lys | Leu | Ser | Ser | Tyr | Lys |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Leu | Thr | Gly | Asn | Glu | Gly | Val | Ile | Arg | Ser | Val | Cys | Asp | Lys | Val |

305  
Asp

310

315

320

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1672
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

|             |            |             |            |             |            |      |
|-------------|------------|-------------|------------|-------------|------------|------|
| tacgaagcag  | aagacagaac | ccaaaaacgg  | acaaagctcc | cctattctct  | cgaaaattca | 60   |
| ttacttctaa  | agatggatgt | tgtagggtggc | tgatgactct | tcttcacctag | catgaccttt | 120  |
| attgatacag  | agatgtgtat | gagaagaaac  | aacatcaatt | taacaacagt  | catagattct | 180  |
| aacgaagcca  | ttggtatgga | acatgaatta  | gattctgcta | gacatcaata  | ttcttcagtg | 240  |
| ctcactgcaa  | ttccattctt | ctcgcctaca  | ttgtttattc | ctctctcttt  | gaaaatcact | 300  |
| atacgtgacg  | ggtttcacga | aagtctttaa  | taacatttcc | atacacaaaa  | cacaaatagt | 360  |
| ttagagattt  | gttcttaggg | agattttagct | atctctctgt | tcaaaagatt  | ggtctaaaga | 420  |
| tgcaagcttt  | tgtcttaagt | gggaagaaaa  | ggattgtgaa | tcacggcatg  | tgtttttcca | 480  |
| aaggaaatct  | tgatctcggg | tcacgcttgt  | ctgagaattt | tatggatgat  | cctttgatcc | 540  |
| cgggattgcc  | tgatgatgtc | gctaagcagt  | gtctagcgct | tgttcgcgct  | gctaggttcc | 600  |
| catccatggg  | aagtgtatgc | aagaaatgga  | ggtttgttgt | ccagagcaaa  | gagtttatta | 660  |
| ctgtgagaag  | actcgcctgg | atgcttgagg  | agtggcttta | tgtcttaacg  | atgaatgctg | 720  |
| gtgggaaaga  | taaccgatgg | gaggtgatgg  | actgtttggg | acagaagcta  | tcattctctc | 780  |
| caccgatgcc  | tggctcctga | aaaacagggt  | ttaaggttgt | tgtggttgat  | gggaaacttc | 840  |
| ttgtcattgc  | tgtgtgttgt | atgatcaacg  | gttcgcttgt | tgcattctgt  | gatgtttatc | 900  |
| agtatgatac  | atgcctcaat | agctggagta  | gactagcaga | cctggaggta  | gctcggtagt | 960  |
| atttcgcttg  | tgtctgagtg | aacgggcatg  | tttatgttgt | gggagggtcat | ggggtagatg | 1020 |
| gtgagagtct  | gtcaagtgca | gaggtgTATG  | aTCTgatcct | gagacgtgta  | catggacttt | 1080 |
| catagagtct  | ttaaggcgtc | cgagggtggg  | ttgtttcGct | agcgccttca  | acgggaagct | 1140 |
| atatgtgatg  | ggtgggagat | ccaacttcac  | tattggaaac | tcaaaaacttc | ttgatgtgta | 1200 |
| caacactcaa  | tgtggctcct | ggcatggtag  | caaaaacggg | ttaacgatgg  | tcacagctca | 1260 |
| tgttgaagta  | gggaaaaagc | tgttctgtat  | cgactggaag | aaccaccgga  | agatgtcggg | 1320 |
| gttcaatgcg  | gaagacgaaa | cctggggaag  | gggtgctctt | ccgctatcag  | gaagctcgag | 1380 |
| ggccgggttt  | cagtttggtg | agctgagtg   | gaagcttttg | ctattctcgt  | ctcaggaaga | 1440 |
| aaccgggtcaa | tgtactttac | tgtatgaccc  | ggatgcttca | ccaggcacac  | agtggaaaac | 1500 |
| gtctgagatc  | aaactctctg | gttcttgctg  | atgcagtgtc | acaatcacag  | cctgattgat | 1560 |
| accattgtgt  | tgtttacatt | tctttttatg  | atccaaatcc | aaagagagca  | ttgtcgtctc | 1620 |
| ttttaagttg  | atgataacac | tgatttaata  | aagtggagag | tgttttgttt  | gg         |      |

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ala | Phe | Ala | Leu | Ser | Gly | Lys | Lys | Arg | Ile | Val | Asn | His | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Cys | Phe | Ser | Lys | Gly | Asn | Leu | Asp | Leu | Gly | Ser | Arg | Leu | Ser | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Phe | Met | Asp | Asp | Pro | Leu | Ile | Pro | Gly | Leu | Pro | Asp | Asp | Val | Ala |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 187 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..187  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569747  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asp | Pro | Leu | Ile | Pro | Gly | Leu | Pro | Asp | Asp | Val | Ala | Lys | Gln |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Cys | Leu | Ala | Leu | Val | Pro | Arg | Ala | Arg | Phe | Pro | Ser | Met | Gly | Ser | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Cys | Lys | Lys | Trp | Arg | Phe | Val | Val | Gln | Ser | Lys | Glu | Phe | Ile | Thr | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Leu | Ala | Gly | Met | Leu | Glu | Glu | Trp | Leu | Tyr | Val | Leu | Thr | Met |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ala | Gly | Gly | Lys | Asp | Asn | Arg | Trp | Glu | Val | Met | Asp | Cys | Leu | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Lys | Leu | Ser | Ser | Leu | Pro | Pro | Met | Pro | Gly | Pro | Ala | Lys | Thr | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Lys | Val | Val | Val | Val | Asp | Gly | Lys | Leu | Leu | Val | Ile | Ala | Gly | Cys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Cys | Met | Ile | Asn | Gly | Ser | Leu | Val | Ala | Ser | Ala | Asp | Val | Tyr | Gln | Tyr |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asp | Thr | Cys | Leu | Asn | Ser | Trp | Ser | Arg | Leu | Ala | Asp | Leu | Glu | Val | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Tyr | Asp | Phe | Ala | Cys | Ala | Glu | Val | Asn | Gly | His | Val | Tyr | Val | Val |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Gly | His | Gly | Val | Asp | Gly | Glu | Ser | Leu | Ser | Ser | Ala | Glu | Val | Tyr |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Asp | Leu | Ile | Leu | Arg | Arg | Val | His | Gly | Leu | Ser |     |     |     |     |     |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1412 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1412  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1569748  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| actcaatcgt  | catttcctcg | gtatctcctc  | ctcgaaagaa  | gaatgcctgg  | aattagaggt  | 60  |
| ccttcggaat  | actcgcagga | accacctcgt  | cacccttctc  | tcaaggtcaa  | cgccaaggaa  | 120 |
| cctttcaacg  | ccgagcctcc | ccgctcggcc  | ttagttctcat | cttatgtcac  | tcccgtcgac  | 180 |
| ctttttctaca | agcgaaatca | tgggtcccatc | cccattgttg  | atcaccttca  | aagctactcc  | 240 |
| gtcaccctta  | ctggattgat | ccagaacccg  | agaaagctct  | ttatcaaaga  | catcagggtcc | 300 |
| ctcccaaagt  | acaatgttac | tgctactcct  | cttgtgcggg  | taacagaagg  | actgccatga  | 360 |
| gcaaagttag  | gaatgttaga | ggtgttggat  | gggatgtttc  | tgctattggc  | aacgctgtct  | 420 |
| ggggtggggc  | gaaactggcc | gatgttcttg  | agcttggtgg  | gataccaaag  | ctgactgctt  | 480 |
| ctaccaattt  | aggagccaga | catgttgagt  | tcgtagtggt  | tgatcgctgt  | aaggaggaaa  | 540 |
| atggggggccc | ttataaggcg | tcaatcactc  | taagtcaagc  | cacaaatcct  | gaagcggatg  | 600 |
| ttctaccctt  | tatgagatga | atggagagac  | cctgaacagg  | gatcacggat  | ttccgttaag  | 660 |
| ggtggttgtc  | cctggtgtga | ttggtgctcg  | tAtcagwcaa  | atggcttgat  | tccatcaatg  | 720 |
| tcatcgctga  | agaaagccag | ggattcttca  | tgcaaaaaga  | ttacaaaatg  | tttccaccct  | 780 |
| ctgtcaattg  | ggataatatc | aactggtcct  | ctaggagacc  | gcaaattggat | ttccctgttc  | 840 |



agagtgaat ctgctctgtg gaggatgtgc aaatggtgaa gcctggaaag gtaagtatca 900  
aaggatatgc ggtttcagga ggtggacgcg ggatagaaa agtggacata tccctggatg 960  
gaggcaaaaa ctgggtggaa gcttctagaa cgcaggaacc aggaaagcag tacatctcag 1020  
aacacagctc cagtgcacaa tgggcatggg tgttggttga agccaccatt gatgtttcac 1080  
agactacaga ggtcatcgcc aaagcgggtg attcggcggc gaatgttcaa ccggaataatg 1140  
tgagatcggt gtggaacctg agaggagttc tcaaCacttc gtggcaccgt gtccttctcc 1200  
ggcttggcca ctctaacttg tagaccaagt taccactatg cgtctggtct ctctttatct 1260  
tttctttaag aactaaaaca tccttgaata tgcttgtcct tgtggatctg tgagagcaaa 1320  
atactgttta tagttaaata aaatgggaaa acccatctgt tgtcatgtgg tggattataa 1380  
attatttatt tatatgatag aactgttatt cg

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1569749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

Met Gln Lys Asp Tyr Lys Met Phe Pro Pro Ser Val Asn Trp Asp Asn  
1 5 10 15  
Ile Asn Trp Ser Ser Arg Arg Pro Gln Met Asp Phe Pro Val Gln Ser  
20 25 30  
Ala Ile Cys Ser Val Glu Asp Val Gln Met Val Lys Pro Gly Lys Val  
35 40 45  
Ser Ile Lys Gly Tyr Ala Val Ser Gly Gly Gly Arg Gly Ile Glu Arg  
50 55 60  
Val Asp Ile Ser Leu Asp Gly Gly Lys Asn Trp Val Glu Ala Ser Arg  
65 70 75 80  
Thr Gln Glu Pro Gly Lys Gln Tyr Ile Ser Glu His Ser Ser Ser Asp  
85 90 95  
Lys Trp Ala Trp Val Leu Phe Glu Ala Thr Ile Asp Val Ser Gln Thr  
100 105 110  
Thr Glu Val Ile Ala Lys Ala Val Asp Ser Ala Ala Asn Val Gln Pro  
115 120 125  
Glu Asn Val Glu Ser Val Trp Asn Leu Arg Gly Val Leu Asn Thr Ser  
130 135 140  
Trp His Arg Val Leu Leu Arg Leu Gly His Ser Asn Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1569750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Met Phe Pro Pro Ser Val Asn Trp Asp Asn Ile Asn Trp Ser Ser Arg  
1 5 10 15  
Arg Pro Gln Met Asp Phe Pro Val Gln Ser Ala Ile Cys Ser Val Glu  
20 25 30  
Asp Val Gln Met Val Lys Pro Gly Lys Val Ser Ile Lys Gly Tyr Ala  
35 40 45  
Val Ser Gly Gly Gly Arg Gly Ile Glu Arg Val Asp Ile Ser Leu Asp

50 55 60  
Gly Gly Lys Asn Trp Val Glu Ala Ser Arg Thr Gln Glu Pro Gly Lys  
65 70 75 80  
Gln Tyr Ile Ser Glu His Ser Ser Ser Asp Lys Trp Ala Trp Val Leu  
85 90 95  
Phe Glu Ala Thr Ile Asp Val Ser Gln Thr Thr Glu Val Ile Ala Lys  
100 105 110  
Ala Val Asp Ser Ala Ala Asn Val Gln Pro Glu Asn Val Glu Ser Val  
115 120 125  
Trp Asn Leu Arg Gly Val Leu Asn Thr Ser Trp His Arg Val Leu Leu  
130 135 140  
Arg Leu Gly His Ser Asn Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

Met Asp Phe Pro Val Gln Ser Ala Ile Cys Ser Val Glu Asp Val Gln  
1 5 10 15  
Met Val Lys Pro Gly Lys Val Ser Ile Lys Gly Tyr Ala Val Ser Gly  
20 25 30  
Gly Gly Arg Gly Ile Glu Arg Val Asp Ile Ser Leu Asp Gly Gly Lys  
35 40 45  
Asn Trp Val Glu Ala Ser Arg Thr Gln Glu Pro Gly Lys Gln Tyr Ile  
50 55 60  
Ser Glu His Ser Ser Ser Asp Lys Trp Ala Trp Val Leu Phe Glu Ala  
65 70 75 80  
Thr Ile Asp Val Ser Gln Thr Thr Glu Val Ile Ala Lys Ala Val Asp  
85 90 95  
Ser Ala Ala Asn Val Gln Pro Glu Asn Val Glu Ser Val Trp Asn Leu  
100 105 110  
Arg Gly Val Leu Asn Thr Ser Trp His Arg Val Leu Leu Arg Leu Gly  
115 120 125  
His Ser Asn Leu  
130

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

aatctataat cattttgtga ctcttgaggc actctcttct ctttgtctct gtgactcaca 60  
ttcatccaat ccaggaggca tgcgcacatc tgaggataaa ccggaaatca tcagtagagt 120  
agttcatcag gagggtgacg tggaaaAtcg tcgatagaag tcagaaggat aaggmccgagg 180  
aaaaagaaga aggraaagggt ggattcctcg ataagggtgaa agatttcatt catgacattg 240  
gtgagaaact cgagggaacc attggctttg ggaagccaac tgctgatgtc tctgcgattc 300  
atatccctaa gatcaatctt gagagggcag atattgttgt ggatgtgctt gtcaagaacc 360

cgaatccagt tcctatccct ctcatcgatg tcaactacct ggctcgagagc gatgggagga 420  
aactggtttc tgggtttgatc ccggatgctg gaacactcaa ggctcatgga gaagaaactg 480  
tgaagatacc attgacgttg atNcTatgat gacatcaaga gcacttacia cgatatcaac 540  
cccgggatga tcatacctta cagaatcaag gttgatctga ttgtggatgt gccagtattg 600  
ggaagactga cattgccgct ggagaaatgt ggagagatcc caattccaaa gaaacctgat 660  
gttgatatcg agaagattaa gttccagaag ttctcttttg aggaaaccgt ggcgattctc 720  
catgtgaggc ttcagaacat gaatgatttc gacttggggc tcaatgactt ggactgtgaa 780  
gtttggctgt gtgatgtaag cattgggaaa gcagagatcg cggactcgat caagcttgac 840  
aaaaacggaa gcggtattgat taatgtgccg atgacattcc gaccaaagga ctttggttct 900  
gcgcttttggg atatgattcg tggtaaagga acagggtaca caatcaaagg taatattgat 960  
gttgatacac catttggagc tatgaagctt cctattatca aggaaggtgg agagaccctg 1020  
ctgaagaagg aagatgatga tgacgacgat gagtaataag gaaacaaagt gctgcagaga 1080  
cagaatgggtc atagttacta aatctccgat cttgaaatgt ctatttaaaa ttaaaaaaaaa 1140  
aaagaaagac ttgttttgtg tgctttttga taactgatgg atcagacttt tgaatagagc 1200  
cgtcttttta ttgacttct t

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1569761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

Met Ile Ile Pro Tyr Arg Ile Lys Val Asp Leu Ile Val Asp Val Pro  
1 5 10 15  
Val Leu Gly Arg Leu Thr Leu Pro Leu Glu Lys Cys Gly Glu Ile Pro  
20 25 30  
Ile Pro Lys Lys Pro Asp Val Asp Ile Glu Lys Ile Lys Phe Gln Lys  
35 40 45  
Phe Ser Leu Glu Glu Thr Val Ala Ile Leu His Val Arg Leu Gln Asn  
50 55 60  
Met Asn Asp Phe Asp Leu Gly Leu Asn Asp Leu Asp Cys Glu Val Trp  
65 70 75 80  
Leu Cys Asp Val Ser Ile Gly Lys Ala Glu Ile Ala Asp Ser Ile Lys  
85 90 95  
Leu Asp Lys Asn Gly Ser Gly Leu Ile Asn Val Pro Met Thr Phe Arg  
100 105 110  
Pro Lys Asp Phe Gly Ser Ala Leu Trp Asp Met Ile Arg Gly Lys Gly  
115 120 125  
Thr Gly Tyr Thr Ile Lys Gly Asn Ile Asp Val Asp Thr Pro Phe Gly  
130 135 140  
Ala Met Lys Leu Pro Ile Ile Lys Glu Gly Gly Glu Thr Arg Leu Lys  
145 150 155 160  
Lys Glu Asp Asp Asp Asp Asp Asp Glu  
165

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1569762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

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Met Asn Asp Phe Asp Leu Gly Leu Asn Asp Leu Asp Cys Glu Val Trp  
1 5 10 15  
Leu Cys Asp Val Ser Ile Gly Lys Ala Glu Ile Ala Asp Ser Ile Lys  
20 25 30  
Leu Asp Lys Asn Gly Ser Gly Leu Ile Asn Val Pro Met Thr Phe Arg  
35 40 45  
Pro Lys Asp Phe Gly Ser Ala Leu Trp Asp Met Ile Arg Gly Lys Gly  
50 55 60  
Thr Gly Tyr Thr Ile Lys Gly Asn Ile Asp Val Asp Thr Pro Phe Gly  
65 70 75 80  
Ala Met Lys Leu Pro Ile Ile Lys Glu Gly Glu Thr Arg Leu Lys  
85 90 95  
Lys Glu Asp Asp Asp Asp Asp Asp Glu  
100 105

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aactctcttc tcttctctag tcttgtcttc tattatgcaa aaggtcttct tggccatgga  | 60   |
| tacttgtgct ctagtaatcc atcagtctct gtctcgcatc aaactttctc ctcccaaadc  | 120  |
| ttcttcttct tcttcttctt ctgctttctc ccctgaatoc ttaccgatca gacggatcga  | 180  |
| gctgtgtttc cgaggagcta tatgtgccgc cgtacaaaga aactacgaag aaacgcctc   | 240  |
| ctccgtggaa gaggcagagg aagatgatga gtcacatca tcgtacggag aagtgaacaa   | 300  |
| gatcattgga agccgaacgg cgBgggaagg agccatggag taccttatcg agtgggaagga | 360  |
| cggccattct ccgtcgtggg ttccatcgag ctacatcgca gcagacgtaG tgtcggagta  | 420  |
| cgagacaccc tgggtggacgg cagctagaaa agccgacgag caggccctgt cacagctcct | 480  |
| ggaggaccga gacgtcgatg ccgtggacga aagcggccgg acggctctgc ttttcgtggc  | 540  |
| aggtctgggg tcggacaagt gcgtaaggct tctggcggag gctggagccg atctcgacca  | 600  |
| ccgagacatg aggggaggct tgacggcgct gcacatggcg gctgggttacg tgaggccgga | 660  |
| ggtggtggag gcgctggtgg agctgggagc tgatattgaa gtggaagacg agagagggtt  | 720  |
| aacggcggtg gaactagcga gggagattct gaagacgacg ccgaagggga atccgatgca  | 780  |
| gttcgggagg agaattgggt tagagaaagt gatcaatgct ctggaaggac aagtgttcga  | 840  |
| gtacgccgag gtggatgaga tcgtagagaa acgagggaaa ggcaaagacg ttgaatatct  | 900  |
| ggtcagatgg aaggacggtg gagattgca gtgggtgaaa ggtgtacacg tggcggaaga   | 960  |
| tgtggctaag gactacgagg atgggctgga gtacgctgta gcggagagtg tgatcgggaa  | 1020 |
| gaggggtggga gacgatggga agaccatcga gtatcttctc aaatggactg atatgtctga | 1080 |
| tgccacttgg gagcctcagg acaatgtcga ctctactctt gttctactct accaacaaca  | 1140 |
| acaaccaata aatgaatgat tgattttgat gattacattc ttctcaattt gcttctttct  | 1200 |
| catatgtgtt ggttcacatcg accggttcgg ttggtacgta ccggtacatt ttcattttct | 1260 |
| tttaagatgt gatcttgatg gtttttggcc ttttggggac actatttgat tttatatcca  | 1320 |
| tgctttgaat tttgcttccc tttttgggga gattc                             |      |

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

| Parameter   | Value | Unit | Reference |
|-------------|-------|------|-----------|
| $\alpha$    | 0.001 |      | [1]       |
| $\beta$     | 0.001 |      | [1]       |
| $\gamma$    | 0.001 |      | [1]       |
| $\delta$    | 0.001 |      | [1]       |
| $\epsilon$  | 0.001 |      | [1]       |
| $\zeta$     | 0.001 |      | [1]       |
| $\eta$      | 0.001 |      | [1]       |
| $\theta$    | 0.001 |      | [1]       |
| $\iota$     | 0.001 |      | [1]       |
| $\kappa$    | 0.001 |      | [1]       |
| $\lambda$   | 0.001 |      | [1]       |
| $\mu$       | 0.001 |      | [1]       |
| $\nu$       | 0.001 |      | [1]       |
| $\xi$       | 0.001 |      | [1]       |
| $\omicron$  | 0.001 |      | [1]       |
| $\pi$       | 0.001 |      | [1]       |
| $\rho$      | 0.001 |      | [1]       |
| $\sigma$    | 0.001 |      | [1]       |
| $\tau$      | 0.001 |      | [1]       |
| $\upsilon$  | 0.001 |      | [1]       |
| $\phi$      | 0.001 |      | [1]       |
| $\chi$      | 0.001 |      | [1]       |
| $\psi$      | 0.001 |      | [1]       |
| $\omega$    | 0.001 |      | [1]       |
| $\varphi$   | 0.001 |      | [1]       |
| $\vartheta$ | 0.001 |      | [1]       |
| $\varpi$    | 0.001 |      | [1]       |
| $\varsigma$ | 0.001 |      | [1]       |
| $\eta$      | 0.001 |      | [1]       |
| $\theta$    | 0.001 |      | [1]       |
| $\iota$     | 0.001 |      | [1]       |
| $\kappa$    | 0.001 |      | [1]       |
| $\lambda$   | 0.001 |      | [1]       |
| $\mu$       | 0.001 |      | [1]       |
| $\nu$       | 0.001 |      | [1]       |
| $\xi$       | 0.001 |      | [1]       |
| $\omicron$  | 0.001 |      | [1]       |
| $\pi$       | 0.001 |      | [1]       |
| $\rho$      | 0.001 |      | [1]       |
| $\sigma$    | 0.001 |      | [1]       |
| $\tau$      | 0.001 |      | [1]       |
| $\upsilon$  | 0.001 |      | [1]       |
| $\phi$      | 0.001 |      | [1]       |
| $\chi$      | 0.001 |      | [1]       |
| $\psi$      | 0.001 |      | [1]       |
| $\omega$    | 0.001 |      | [1]       |
| $\varphi$   | 0.001 |      | [1]       |
| $\vartheta$ | 0.001 |      | [1]       |
| $\varpi$    | 0.001 |      | [1]       |
| $\varsigma$ | 0.001 |      | [1]       |
| $\eta$      | 0.001 |      | [1]       |
| $\theta$    | 0.001 |      | [1]       |
| $\iota$     | 0.001 |      | [1]       |
| $\kappa$    | 0.001 |      | [1]       |
| $\lambda$   | 0.001 |      | [1]       |
| $\mu$       | 0.001 |      | [1]       |
| $\nu$       | 0.001 |      | [1]       |
| $\xi$       | 0.001 |      | [1]       |
| $\omicron$  | 0.001 |      | [1]       |
| $\pi$       | 0.001 |      | [1]       |
| $\rho$      | 0.001 |      | [1]       |
| $\sigma$    | 0.001 |      | [1]       |
| $\tau$      | 0.001 |      | [1]       |
| $\upsilon$  | 0.001 |      | [1]       |
| $\phi$      | 0.001 |      | [1]       |
| $\chi$      | 0.001 |      | [1]       |
| $\psi$      | 0.001 |      | [1]       |
| $\omega$    | 0.001 |      | [1]       |
| $\varphi$   | 0.001 |      | [1]       |
| $\vartheta$ | 0.001 |      | [1]       |
| $\varpi$    | 0.001 |      | [1]       |
| $\varsigma$ | 0.001 |      | [1]       |
| $\eta$      | 0.001 |      | [1]       |
| $\theta$    | 0.001 |      | [1]       |
| $\iota$     | 0.001 |      | [1]       |
| $\kappa$    | 0.001 |      | [1]       |
| $\lambda$   | 0.001 |      | [1]       |
| $\mu$       | 0.001 |      | [1]       |
| $\nu$       | 0.001 |      | [1]       |
| $\xi$       | 0.001 |      | [1]       |
| $\omicron$  | 0.001 |      | [1]       |
| $\pi$       | 0.001 |      | [1]       |
| $\rho$      | 0.001 |      | [1]       |
| $\sigma$    | 0.001 |      | [1]       |
| $\tau$      | 0.001 |      | [1]       |
| $\upsilon$  | 0.001 |      | [1]       |
| $\phi$      | 0.001 |      | [1]       |
| $\chi$      | 0.001 |      | [1]       |
| $\psi$      | 0.001 |      | [1]       |
| $\omega$    | 0.001 |      | [1]       |
| $\varphi$   | 0.001 |      | [1]       |
| $\vartheta$ | 0.001 |      | [1]       |
| $\varpi$    | 0.001 |      | [1]       |
| $\varsigma$ | 0.001 |      | [1]       |
| $\eta$      | 0.001 |      | [1]       |
| $\theta$    | 0.001 |      | [1]       |
| $\iota$     | 0.001 |      | [1]       |
| $\kappa$    | 0.001 |      | [1]       |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1569777

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1 | Gln | Lys | Val | Phe<br>5 | Leu | Ala | Met | Asp | Thr<br>10 | Cys | Ala | Leu | Val | Ile<br>15 | His |
| Gln      | Ser | Leu | Ser | Arg      | Ile | Lys | Leu | Ser | Pro       | Pro | Lys | Ser | Ser | Ser       | Ser |
|          |     |     | 20  |          |     |     |     | 25  |           |     |     |     | 30  |           |     |
| Ser      | Ser | Ser | Ser | Ala      | Phe | Ser | Pro | Glu | Ser       | Leu | Pro | Ile | Arg | Arg       | Ile |
|          |     | 35  |     |          |     |     | 40  |     |           |     |     | 45  |     |           |     |
| Glu      | Leu | Cys | Phe | Arg      | Gly | Ala | Ile | Cys | Ala       | Ala | Val | Gln | Arg | Asn       | Tyr |
|          | 50  |     |     |          |     | 55  |     |     |           |     | 60  |     |     |           |     |
| Glu      | Glu | Thr | Thr | Ser      | Ser | Val | Glu | Glu | Ala       | Glu | Glu | Asp | Asp | Glu       | Ser |
| 65       |     |     |     |          | 70  |     |     |     |           | 75  |     |     |     |           | 80  |
| Ser      | Ser | Ser | Tyr | Gly      | Glu | Val | Asn | Lys | Ile       | Ile | Gly | Ser | Arg | Thr       | Ala |
|          |     |     | 85  |          |     |     |     |     | 90        |     |     |     |     | 95        |     |
| Xaa      | Glu | Gly | Ala | Met      | Glu | Tyr | Leu | Ile | Glu       | Trp | Lys | Asp | Gly | His       | Ser |
|          |     |     | 100 |          |     |     |     | 105 |           |     |     |     | 110 |           |     |
| Pro      | Ser | Trp | Val | Pro      | Ser | Ser | Tyr | Ile | Ala       | Ala | Asp | Val | Val | Ser       | Glu |
|          |     | 115 |     |          |     |     | 120 |     |           |     |     | 125 |     |           |     |
| Tyr      | Glu | Thr | Pro | Trp      | Trp | Thr | Ala | Ala | Arg       | Lys | Ala | Asp | Glu | Gln       | Ala |
|          | 130 |     |     |          |     | 135 |     |     |           |     | 140 |     |     |           |     |
| Leu      | Ser | Gln | Leu | Leu      | Glu | Asp | Arg | Asp | Val       | Asp | Ala | Val | Asp | Glu       | Ser |
| 145      |     |     |     |          | 150 |     |     |     |           | 155 |     |     |     |           | 160 |
| Gly      | Arg | Thr | Ala | Leu      | Leu | Phe | Val | Ala | Gly       | Leu | Gly | Ser | Asp | Lys       | Cys |
|          |     |     | 165 |          |     |     |     |     | 170       |     |     |     |     | 175       |     |
| Val      | Arg | Leu | Leu | Ala      | Glu | Ala | Gly | Ala | Asp       | Leu | Asp | His | Arg | Asp       | Met |
|          |     |     | 180 |          |     |     |     | 185 |           |     |     |     | 190 |           |     |
| Arg      | Gly | Gly | Leu | Thr      | Ala | Leu | His | Met | Ala       | Ala | Gly | Tyr | Val | Arg       | Pro |
|          |     | 195 |     |          |     |     | 200 |     |           |     |     | 205 |     |           |     |
| Glu      | Val | Val | Glu | Ala      | Leu | Val | Glu | Leu | Gly       | Ala | Asp | Ile | Glu | Val       | Glu |
|          | 210 |     |     |          |     | 215 |     |     |           |     | 220 |     |     |           |     |
| Asp      | Glu | Arg | Gly | Leu      | Thr | Ala | Leu | Glu | Leu       | Ala | Arg | Glu | Ile | Leu       | Lys |
| 225      |     |     |     |          | 230 |     |     |     |           | 235 |     |     |     |           | 240 |
| Thr      | Thr | Pro | Lys | Gly      | Asn | Pro | Met | Gln | Phe       | Gly | Arg | Arg | Ile | Gly       | Leu |
|          |     |     | 245 |          |     |     |     |     | 250       |     |     |     |     | 255       |     |
| Glu      | Lys | Val | Ile | Asn      | Val | Leu | Glu | Gly | Gln       | Val | Phe | Glu | Tyr | Ala       | Glu |
|          |     |     | 260 |          |     |     |     | 265 |           |     |     |     | 270 |           |     |
| Val      | Asp | Glu | Ile | Val      | Glu | Lys | Arg | Gly | Lys       | Gly | Lys | Asp | Val | Glu       | Tyr |
|          | 275 |     |     |          |     |     | 280 |     |           |     |     | 285 |     |           |     |
| Leu      | Val | Arg | Trp | Lys      | Asp | Gly | Gly | Asp | Cys       | Glu | Trp | Val | Lys | Gly       | Val |
|          | 290 |     |     |          |     | 295 |     |     |           | 300 |     |     |     |           |     |
| His      | Val | Ala | Glu | Asp      | Val | Ala | Lys | Asp | Tyr       | Glu | Asp | Gly | Leu | Glu       | Tyr |
| 305      |     |     |     |          | 310 |     |     |     |           | 315 |     |     |     |           | 320 |
| Ala      | Val | Ala | Glu | Ser      | Val | Ile | Gly | Lys | Arg       | Val | Gly | Asp | Asp | Gly       | Lys |
|          |     |     | 325 |          |     |     |     |     | 330       |     |     |     |     | 335       |     |
| Thr      | Ile | Glu | Tyr | Leu      | Val | Lys | Trp | Thr | Asp       | Met | Ser | Asp | Ala | Thr       | Trp |
|          |     | 340 |     |          |     |     |     | 345 |           |     |     |     | 350 |           |     |
| Glu      | Pro | Gln | Asp | Asn      | Val | Asp | Ser | Thr | Leu       | Val | Leu | Leu | Tyr | Gln       |     |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1569778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

(2) INFORMATION FOR SEQ ID NO:1383:

(A) LENGTH: 1287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1287  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569787

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acactttctc | tagccatta  | taaacgcttc | atttctatat | aaacatctct | tatcttggtg | 60  |
| aaaatctctc | gcagcttttg | aaaaacatga | cctttctaaa | aatgaaaagc | ctttctttct | 120 |
| tcttcaccat | ctctctctct | ctctcgacct | tcttcaccat | ctccaacgca | cggaagttaa | 180 |

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| atgtcggagg  | cagtggcgcg | tgggttacaa | accacactga  | aaactacgaa  | tcttggctctg | 240  |
| gcaaaaaccg  | tttccttgtt | cacgacactc | tctatttttag | ctatgctaag  | ggagctgact  | 300  |
| cggtgctaga  | ggtgaacaag | gctgattacg | acgcttgtaa  | tacaaagaat  | ccgatcaaaa  | 360  |
| gagtggacga  | tggagattct | gagatctctc | ttgatcgtaa  | tgggtccgttt | tacttcatca  | 420  |
| gtggcaatga  | agataactgt | aagaagggtc | aaaagcttaa  | tgtcgttgctc | atatctgcta  | 480  |
| ggattccatc  | aacggctcag | tctcctcacg | ccgctgcacc  | gggaagctct  | acgccgggat  | 540  |
| caatgactcc  | gccgggagga | gcccactcgc | ctaaatcttc  | ctcccctgtt  | tctccgacga  | 600  |
| cttctcctcc  | gggatcgact | actcgcctg  | gaggagctca  | ctcgcctaaa  | tcttcatcag  | 660  |
| ctgtctctcc  | ggcgacttct | cctccaggat | caatggcgcc  | taaatccggc  | tccccctgtt  | 720  |
| ctccgacgac  | tTcAcGcacc | ggcaccacct | aaatccacgt  | ccccctgttc  | cccctcctct  | 780  |
| gctccgatga  | cttcaccgcc | ggcaccaatg | gcacctaaat  | catcttcaac  | tattcctccg  | 840  |
| tcttctgctc  | cgatgacttc | accacctgga | tcaatggcac  | ctaaatcttc  | gtcccctgtt  | 900  |
| tcaaaactcac | ccaccgtttc | tccatcgttg | gctccgggag  | gctctacttc  | ttcttcaccg  | 960  |
| tcagattctc  | cgtcaggctc | ggcgatgggt | cctTcaggag  | atgggtccatc | agccgctggt  | 1020 |
| gatatctcta  | cgccggctgg | agctccaggg | cagaaaaaat  | cgtcggcgaa  | tggyatgacc  | 1080 |
| gttatgtcka  | ttactacggt | tytaagtttg | gttttgacca  | tctttctgctc | agcttaagaa  | 1140 |
| cacttgtag   | acttgtttca | tgtcggatcc | gatttgttct  | tgtttcgggt  | gagtttccaa  | 1200 |
| ctttgtttta  | aattgwtttt | ggatcccagt | ttgattctgt  | attattcagt  | atagttggat  | 1260 |
| tgttttgtta  | taaataatag | acagttc    |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Phe | Leu | Lys | Met | Lys | Ser | Leu | Ser | Phe | Phe | Phe | Thr | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Leu | Ser | Thr | Leu | Phe | Thr | Ile | Ser | Asn | Ala | Arg | Lys | Phe | Asn |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Val | Gly | Gly | Ser | Gly | Ala | Trp | Val | Thr | Asn | Pro | Pro | Glu | Asn | Tyr | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ser | Trp | Ser | Gly | Lys | Asn | Arg | Phe | Leu | Val | His | Asp | Thr | Leu | Tyr | Phe |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Ser | Tyr | Ala | Lys | Gly | Ala | Asp | Ser | Val | Leu | Glu | Val | Asn | Lys | Ala | Asp |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Tyr | Asp | Ala | Cys | Asn | Thr | Lys | Asn | Pro | Ile | Lys | Arg | Val | Asp | Asp | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Ser | Glu | Ile | Ser | Leu | Asp | Arg | Tyr | Gly | Pro | Phe | Tyr | Phe | Ile | Ser |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gly | Asn | Glu | Asp | Asn | Cys | Lys | Lys | Gly | Gln | Lys | Leu | Asn | Val | Val | Val |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Ile | Ser | Ala | Arg | Ile | Pro | Ser | Thr | Ala | Gln | Ser | Pro | His | Ala | Ala | Ala |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Pro | Gly | Ser | Ser | Thr | Pro | Gly | Ser | Met | Thr | Pro | Pro | Gly | Gly | Ala | His |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |
| Ser | Pro | Lys | Ser | Ser | Pro | Val | Ser | Pro | Thr | Thr | Ser | Pro | Pro | Gly |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Thr | Thr | Pro | Pro | Gly | Gly | Ala | His | Ser | Pro | Lys | Ser | Ser | Ser | Ala |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Val | Ser | Pro | Ala | Thr | Ser | Pro | Pro | Gly | Ser | Met | Ala | Pro | Lys | Ser | Gly |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Ser | Pro | Val | Ser | Pro | Thr | Thr | Ser | Arg | Thr | Gly | Thr | Thr |     |     |     |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 216 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..216  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569789  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

Met Lys Ser Leu Ser Phe Phe Phe Thr Ile Leu Leu Ser Leu Ser Thr  
1 5 10 15  
Leu Phe Thr Ile Ser Asn Ala Arg Lys Phe Asn Val Gly Gly Ser Gly  
20 25 30  
Ala Trp Val Thr Asn Pro Pro Glu Asn Tyr Glu Ser Trp Ser Gly Lys  
35 40 45  
Asn Arg Phe Leu Val His Asp Thr Leu Tyr Phe Ser Tyr Ala Lys Gly  
50 55 60  
Ala Asp Ser Val Leu Glu Val Asn Lys Ala Asp Tyr Asp Ala Cys Asn  
65 70 75 80  
Thr Lys Asn Pro Ile Lys Arg Val Asp Asp Gly Asp Ser Glu Ile Ser  
85 90 95  
Leu Asp Arg Tyr Gly Pro Phe Tyr Phe Ile Ser Gly Asn Glu Asp Asn  
100 105 110  
Cys Lys Lys Gly Gln Lys Leu Asn Val Val Val Ile Ser Ala Arg Ile  
115 120 125  
Pro Ser Thr Ala Gln Ser Pro His Ala Ala Ala Pro Gly Ser Ser Thr  
130 135 140  
Pro Gly Ser Met Thr Pro Pro Gly Gly Ala His Ser Pro Lys Ser Ser  
145 150 155 160  
Ser Pro Val Ser Pro Thr Thr Ser Pro Pro Gly Ser Thr Thr Pro Pro  
165 170 175  
Gly Gly Ala His Ser Pro Lys Ser Ser Ser Ala Val Ser Pro Ala Thr  
180 185 190  
Ser Pro Pro Gly Ser Met Ala Pro Lys Ser Gly Ser Pro Val Ser Pro  
195 200 205  
Thr Thr Ser Arg Thr Gly Thr Thr  
210 215

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569790  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

Met Thr Ser Pro Pro Ala Pro Met Ala Pro Lys Ser Ser Ser Thr Ile  
1 5 10 15  
Pro Pro Ser Ser Ala Pro Met Thr Ser Pro Pro Gly Ser Met Ala Pro  
20 25 30  
Lys Ser Ser Ser Pro Val Ser Asn Ser Pro Thr Val Ser Pro Ser Leu  
35 40 45  
Ala Pro Gly Gly Ser Thr Ser Ser Ser Pro Ser Asp Ser Pro Ser Gly  
50 55 60  
Ser Ala Met Gly Pro Ser Gly Asp Gly Pro Ser Ala Ala Gly Asp Ile  
65 70 75 80  
Ser Thr Pro Ala Gly Ala Pro Gly Gln Lys Lys Ser Ser Ala Asn Xaa

85 90 95  
Met Thr Val Met Xaa Ile Thr Thr Val Xaa Ser Leu Val Leu Thr Ile  
100 105 110  
Phe Leu Ser Ala  
115

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

gattacttgt ttcttttgatt tctccttcca tagaaccgaa ttgttttcag tctgagattt 60  
ctcctgccga gagaacgatt ttaatctatt ttctcgcaga gtagaaaatg gctgatgggtg 120  
aagatattca accccttgct tgtgacaatg gaactggaat ggtaaggct gggttttgctg 180  
gggatgatgc accgagggct gtgtttccaa gtattgttgg ccgtcctcgc cacactggag 240  
tgatggttgg aatgggacag aaggatgc atgttggcga tgaagctcaa tccaagcgtg 300  
gtattcttac ccttaaatac cctattgagc acggtattgt caacaattgg gatgatatgg 360  
aaaaaatctg gcatcatact ttctacaatg agctccgtgt tgctcccgag gagcatccta 420  
ttctgctcac tgaagcgctt cttaacccaa aggctaaccg tgagaagatg actcagatca 480  
tgtttgaaac ctttaacgct ccggctatgt atgtcgccat tcaagctgtc ctgtcgcttt 540  
atgctagtgg tcgtactact ggtattgtgc ttgactctgg agatgggtgtg agtcacacgg 600  
tccctatcta tgaggggttac gctctccgc atgcaatcct acgtcttgat cttgcaggtc 660  
gtgacctcac agatgctctg atgaagatcc tcaactgagcg tggttactct ttcaccacaa 720  
cagctgagcg tgaaattgtc agagacatca aggagaagct ttgctacatt gctcttgact 780  
atgagcagga gcttgagacg gctaaaacca gctcttctgt agagaagaac tatgagttac 840  
ctgatgggca agtgatcacc attggatctg agcgtttccg ttgccctgag gttctttacc 900  
agccatctat gatcgggatg gagaatgctg gtatccatga aaccacctac aactccataa 960  
tgaaatgtga tgttgacatc agaaaggact tgtatggtaa cattgtgctc agtgggtggaa 1020  
caactatgtt ccctggaatt gctgacagaa tgagcaaaga gatcactgct ttggcaccga 1080  
gcagcatGaa gatcaaagtc gttgcacctc ctgagaggaa atactctgtc tggattggag 1140  
gatccatctt ggctccctc agtaccttcc agcagatgtg gatcgcaaag gcagaatatg 1200  
atgagtcagg ccctgcgatt gttcaccgga aatgcttttg agcttgaagt taagtctgct 1260  
tccggagaag ccctgggggt tttccagttt gtcttactg ggtttttatc ttcgttctct 1320  
gctcttcttt gtttttcttc ttcaatatatt tcagattctg gcctaagaca ttttgaagaa 1380  
tttacattat ctgtttgtag tgttaaactg ttgtcttgtt ccttttattt attttggatg 1440  
acacaactgt gtttgagtga ataagaactc ctgatttttc c

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..377
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val Cys Asp Asn Gly Thr  
1 5 10 15  
Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val  
20 25 30  
Phe Pro Ser Ile Val Gly Arg Pro Arg His Thr Gly Val Met Val Gly  
35 40 45  
Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg

50 55 60  
Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Asn Asn  
65 70 75 80  
Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu  
85 90 95  
Arg Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu Ala Pro Leu  
100 105 110  
Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr  
115 120 125  
Phe Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu  
130 135 140  
Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly  
145 150 155 160  
Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala  
165 170 175  
Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ala Leu Met  
180 185 190  
Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg  
195 200 205  
Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile Ala Leu Asp  
210 215 220  
Tyr Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser Val Glu Lys  
225 230 235 240  
Asn Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ser Glu Arg  
245 250 255  
Phe Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile Gly Met Glu  
260 265 270  
Asn Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp  
275 280 285  
Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu Ser Gly Gly  
290 295 300  
Thr Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu Ile Thr  
305 310 315 320  
Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro Pro Glu  
325 330 335  
Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser  
340 345 350  
Thr Phe Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp Glu Ser Gly  
355 360 365  
Pro Ser Ile Val His Arg Lys Cys Phe  
370 375

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1569801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

Met Val Lys Ala Gly Phe Ala Gly Asp Ala Pro Arg Ala Val Phe  
1 5 10 15  
Pro Ser Ile Val Gly Arg Pro Arg His Thr Gly Val Met Val Gly Met  
20 25 30  
Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly  
35 40 45  
Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Asn Asn Trp  
50 55 60

Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg  
65 70 75 80  
Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu Ala Pro Leu Asn  
85 90 95  
Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe  
100 105 110  
Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr  
115 120 125  
Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly Val  
130 135 140  
Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile  
145 150 155 160  
Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ala Leu Met Lys  
165 170 175  
Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu  
180 185 190  
Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile Ala Leu Asp Tyr  
195 200 205  
Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser Val Glu Lys Asn  
210 215 220  
Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ser Glu Arg Phe  
225 230 235 240  
Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile Gly Met Glu Asn  
245 250 255  
Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp Val  
260 265 270  
Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu Ser Gly Gly Thr  
275 280 285  
Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu Ile Thr Ala  
290 295 300  
Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro Pro Glu Arg  
305 310 315 320  
Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr  
325 330 335  
Phe Gln Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp Glu Ser Gly Pro  
340 345 350  
Ser Ile Val His Arg Lys Cys Phe  
355 360

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

Met Val Gly Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln  
1 5 10 15  
Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile  
20 25 30  
Val Asn Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr  
35 40 45  
Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu  
50 55 60  
Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met  
65 70 75 80  
Phe Glu Thr Phe Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 85  |  | 90  |  | 95  |
| Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser |     |  |     |  |     |
|                                                                 | 100 |  | 105 |  | 110 |
| Gly Asp Gly Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu |     |  |     |  |     |
|                                                                 | 115 |  | 120 |  | 125 |
| Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp |     |  |     |  |     |
|                                                                 | 130 |  | 135 |  | 140 |
| Ala Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr |     |  |     |  |     |
|                                                                 | 145 |  | 150 |  | 155 |
| Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile |     |  |     |  |     |
|                                                                 | 165 |  | 170 |  | 175 |
| Ala Leu Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser |     |  |     |  |     |
|                                                                 | 180 |  | 185 |  | 190 |
| Val Glu Lys Asn Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly |     |  |     |  |     |
|                                                                 | 195 |  | 200 |  | 205 |
| Ser Glu Arg Phe Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile |     |  |     |  |     |
|                                                                 | 210 |  | 215 |  | 220 |
| Gly Met Glu Asn Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met |     |  |     |  |     |
|                                                                 | 225 |  | 230 |  | 235 |
| Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu |     |  |     |  |     |
|                                                                 | 245 |  | 250 |  | 255 |
| Ser Gly Gly Thr Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys |     |  |     |  |     |
|                                                                 | 260 |  | 265 |  | 270 |
| Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala |     |  |     |  |     |
|                                                                 | 275 |  | 280 |  | 285 |
| Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala |     |  |     |  |     |
|                                                                 | 290 |  | 295 |  | 300 |
| Ser Leu Ser Thr Phe Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp     |     |  |     |  |     |
|                                                                 | 305 |  | 310 |  | 315 |
| Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe                 |     |  |     |  |     |
|                                                                 | 325 |  | 330 |  |     |

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| cacgaaaaaa aagaaacgat gaggttaaat ggggattcgg gtccgggtca ggatgaaccc | 60   |
| ggttcgagcg ggtttcacgg cggaatcaga cgattcccgt tagcagctca gccggagatt | 120  |
| atgagagctg ctgagaaaga cgatcaatac gcttctttca tccacgaagc ttgccgcgat | 180  |
| gccttccgac accttttcgg tacaagaatc gctcttgctt accagaagga gatgaagcta | 240  |
| cttgacaga tgctttacta tgttcttacg acaggttcag ggcaacaaac tttaggagag  | 300  |
| gaatattgtg acattataca ggttgcaggg ccttatggac tctctcctac accagctaga | 360  |
| cgtgctttgt tcatattgta ccagaccgca gttccatata tcgcagagag aattagcact | 420  |
| cgagctgcta cgcaagcagt cacctttgat gagtctgatg agtttttttg tgatagtcac | 480  |
| atccactcac caagaatgat agatcttcca tcttcatctc aagttgaaac ttcaacttct | 540  |
| gtagtatcta ggtaaacga tagacttaag agatbttggc accgagctWt tcagcgatgg  | 600  |
| cctgtggttc ttctgtttgc ccgcgaagtc ttacaactgg ttttgcgtgc caatctgatg | 660  |
| cttttctact ctgaagggtt ttattatcat atatcgaaac gtgcatccgg ggttcgttat | 720  |
| gttttcatag gaaagcaact gaatcagaga cctagatacc aaattcttgg ggttttccct | 780  |
| ctaattccaat tgtgcatcct tgcgtctgag ggcttgcgtc ggagtaattt gtcactatc | 840  |
| actagctcca ttcagcaggc ttctatagga tcttatcaaa cttcaggagg gagaggttta | 900  |
| cctgttttaa atgaagagg gaatttgata acttcggaag ctgaaaaggg aaactggtct  | 960  |
| acctccgatt caacttcaac ggaggcagta gggaaatgca ctctctgctt aagcaccctg | 1020 |
| cagcacccaa cggccactcc ttgtggtcat gtgttttgtt ggagctgcat tatggaatgg | 1080 |

tgcaacgaga atcaagaatg cccctctttgt cgaacgccca atacccattc aagtttgggt 1140  
tgtttgtatc attctgattt ttaggcacaa tgggatcaac aaggacaggc actgcagaaa 1200  
ggcaaagcag ctaagacagt gacacctaag gacagtgcac ctgctacagg aatggaatct 1260  
gcttcggctt cagacttttt gagtaagatc aacaagttat gagagaagac agaataaata 1320  
tatttctgac atcattctcg atcccatgcc tacctttttc tctatgatat ttagtgcaga 1380  
aaccacagag gtttgttgtt ttacatttca ttaaaaagag ttggagatgt taggtggtt

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..387

(D) OTHER INFORMATION: / Ceres Seq. ID 1569808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

His Glu Lys Lys Thr Met Arg Leu Asn Gly Asp Ser Gly Pro Gly  
1 5 10 15  
Gln Asp Glu Pro Gly Ser Ser Gly Phe His Gly Gly Ile Arg Arg Phe  
20 25 30  
Pro Leu Ala Ala Gln Pro Glu Ile Met Arg Ala Ala Glu Lys Asp Asp  
35 40 45  
Gln Tyr Ala Ser Phe Ile His Glu Ala Cys Arg Asp Ala Phe Arg His  
50 55 60  
Leu Phe Gly Thr Arg Ile Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu  
65 70 75 80  
Leu Gly Gln Met Leu Tyr Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln  
85 90 95  
Thr Leu Gly Glu Glu Tyr Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr  
100 105 110  
Gly Leu Ser Pro Thr Pro Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln  
115 120 125  
Thr Ala Val Pro Tyr Ile Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr  
130 135 140  
Gln Ala Val Thr Phe Asp Glu Ser Asp Glu Phe Phe Gly Asp Ser His  
145 150 155 160  
Ile His Ser Pro Arg Met Ile Asp Leu Pro Ser Ser Ser Gln Val Glu  
165 170 175  
Thr Ser Thr Ser Val Val Ser Arg Leu Asn Asp Arg Leu Lys Arg Xaa  
180 185 190  
Trp His Arg Ala Xaa Gln Arg Trp Pro Val Val Leu Pro Val Ala Arg  
195 200 205  
Glu Val Leu Gln Leu Val Leu Arg Ala Asn Leu Met Leu Phe Tyr Ser  
210 215 220  
Glu Gly Phe Tyr Tyr His Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr  
225 230 235 240  
Val Phe Ile Gly Lys Gln Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu  
245 250 255  
Gly Val Phe Leu Leu Ile Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu  
260 265 270  
Arg Arg Ser Asn Leu Ser Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser  
275 280 285  
Ile Gly Ser Tyr Gln Thr Ser Gly Gly Arg Gly Leu Pro Val Leu Asn  
290 295 300  
Glu Glu Gly Asn Leu Ile Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser  
305 310 315 320  
Thr Ser Asp Ser Thr Ser Thr Glu Ala Val Gly Lys Cys Thr Leu Cys  
325 330 335  
Leu Ser Thr Arg Gln His Pro Thr Ala Thr Pro Cys Gly His Val Phe

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(2) INFORMATION FOR SEQ ID NO:1393:

(A) LENGTH: 381 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1569809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Arg        | Leu        | Asn        | Gly<br>5   | Asp        | Ser        | Gly        | Pro        | Gly<br>10  | Gln        | Asp        | Glu        | Pro        | Gly<br>15  | Ser |
| Ser        | Gly        | Phe        | His<br>20  | Gly        | Gly        | Ile        | Arg        | Arg<br>25  | Phe        | Pro        | Leu        | Ala<br>30  | Ala        | Gln        | Pro |
| Glu        | Ile        | Met<br>35  | Arg        | Ala        | Ala        | Glu        | Lys<br>40  | Asp        | Asp        | Gln        | Tyr        | Ala<br>45  | Ser        | Phe        | Ile |
| His        | Glu<br>50  | Ala        | Cys        | Arg        | Asp        | Ala<br>55  | Phe        | Arg        | His        | Leu<br>60  | Phe        | Gly        | Thr        | Arg        | Ile |
| Ala<br>65  | Leu        | Ala        | Tyr        | Gln        | Lys<br>70  | Glu        | Met        | Lys        | Leu<br>75  | Leu        | Gly        | Gln        | Met        | Leu<br>80  | Tyr |
| Tyr        | Val        | Leu        | Thr        | Thr<br>85  | Gly        | Ser        | Gly        | Gln        | Gln<br>90  | Thr        | Leu        | Gly        | Glu        | Glu<br>95  | Tyr |
| Cys        | Asp        | Ile        | Ile<br>100 | Gln        | Val        | Ala        | Gly        | Pro<br>105 | Tyr        | Gly        | Leu        | Ser        | Pro<br>110 | Thr        | Pro |
| Ala        | Arg        | Arg<br>115 | Ala        | Leu        | Phe        | Ile        | Leu<br>120 | Tyr        | Gln        | Thr        | Ala<br>125 | Val        | Pro        | Tyr        | Ile |
| Ala<br>130 | Glu        | Arg        | Ile        | Ser        | Thr        | Arg<br>135 | Ala        | Ala        | Thr        | Gln        | Ala<br>140 | Val        | Thr        | Phe        | Asp |
| Glu<br>145 | Ser        | Asp        | Glu        | Phe        | Phe<br>150 | Gly        | Asp        | Ser        | His        | Ile<br>155 | His        | Ser        | Pro        | Arg<br>160 | Met |
| Ile        | Asp        | Leu        | Pro        | Ser<br>165 | Ser        | Ser        | Gln        | Val        | Glu<br>170 | Thr        | Ser        | Thr        | Ser        | Val<br>175 | Val |
| Ser        | Arg        | Leu<br>180 | Asn        | Asp        | Arg        | Leu        | Lys<br>185 | Arg        | Xaa        | Trp        | His        | Arg<br>190 | Ala        | Xaa        | Gln |
| Arg        | Trp        | Pro<br>195 | Val        | Val        | Leu        | Pro        | Val<br>200 | Ala        | Arg        | Glu        | Val<br>205 | Leu        | Gln        | Leu        | Val |
| Leu<br>210 | Arg        | Ala        | Asn        | Leu        | Met        | Leu<br>215 | Phe        | Tyr        | Ser        | Glu        | Gly<br>220 | Phe        | Tyr        | Tyr        | His |
| Ile<br>225 | Ser        | Lys        | Arg        | Ala<br>230 | Ser        | Gly        | Val        | Arg        | Tyr        | Val<br>235 | Phe        | Ile        | Gly        | Lys<br>240 | Gln |
| Leu        | Asn        | Gln        | Arg<br>245 | Pro        | Arg        | Tyr        | Gln        | Ile        | Leu<br>250 | Gly        | Val        | Phe        | Leu<br>255 | Leu        | Ile |
| Gln        | Leu        | Cys<br>260 | Ile        | Leu        | Ala        | Ala        | Glu<br>265 | Gly        | Leu        | Arg        | Arg        | Ser<br>270 | Asn        | Leu        | Ser |
| Ser        | Ile<br>275 | Thr        | Ser        | Ser        | Ile        | Gln        | Gln<br>280 | Ala        | Ser        | Ile        | Gly<br>285 | Ser        | Tyr        | Gln        | Thr |
| Ser        | Gly<br>290 | Gly        | Arg        | Gly        | Leu        | Pro<br>295 | Val        | Leu        | Asn        | Glu<br>300 | Glu        | Gly        | Asn        | Leu        | Ile |
| Thr<br>305 | Ser        | Glu        | Ala<br>310 | Glu        | Lys        | Gly        | Asn        | Trp        | Ser<br>315 | Thr        | Ser        | Asp        | Ser        | Thr        | Ser |
| Thr        | Glu        | Ala        | Val<br>325 | Gly        | Lys        | Cys        | Thr        | Leu<br>330 | Cys        | Leu        | Ser        | Thr        | Arg<br>335 | Gln        | His |

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met  
340 345 350  
Glu Trp Cys Asn Glu Asn Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn  
355 360 365  
Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe  
370 375 380

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1569810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile His Glu  
1 5 10 15  
Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile Ala Leu  
20 25 30  
Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr Tyr Val  
35 40 45  
Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr Cys Asp  
50 55 60  
Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro Ala Arg  
65 70 75 80  
Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile Ala Glu  
85 90 95  
Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp Glu Ser  
100 105 110  
Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met Ile Asp  
115 120 125  
Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val Ser Arg  
130 135 140  
Leu Asn Asp Arg Leu Lys Arg Xaa Trp His Arg Ala Xaa Gln Arg Trp  
145 150 155 160  
Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val Leu Arg  
165 170 175  
Ala Asn Leu Met Leu Phe Tyr Ser Glu Gly Phe Tyr Tyr His Ile Ser  
180 185 190  
Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln Leu Asn  
195 200 205  
Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile Gln Leu  
210 215 220  
Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser Ser Ile  
225 230 235 240  
Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr Ser Gly  
245 250 255  
Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile Thr Ser  
260 265 270  
Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser Thr Glu  
275 280 285  
Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His Pro Thr  
290 295 300  
Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met Glu Trp  
305 310 315 320  
Cys Asn Glu Asn Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn Thr His  
325 330 335  
Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe

SEQUENCE 1394



340 345  
(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1824
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

aaggtgacct tcgtcttttg ttgaccatca aaaactacaa cgctctttct ccgtaGgaaa 60  
ggggaagcaa ataaattatc gaagcccact ggtttcggag ctgacgggtc tctattttctc 120  
tcttcataca tatctcaagc agataaagtt gatcggatac tagaatggga ggaggattta 180  
gagttttgca tttggtgagg ccattcttgg cttttctgcc tgagggttcag agtgctgata 240  
ggaaggttcc attcagagag aagggttatct acactgtcat ctctctcttc atctttcttg 300  
tctgcagtca gcttctcttt tatggaatcc attccaccac cgggtgcggat ccattctatt 360  
ggatgcgtgt cattcttgcg tccaaccgtg gaactgtcat ggagctcggg attactccta 420  
ttgttacatc tggactttgt atgcaactct tggctgggtc caagattatt gaggttgaca 480  
acaatgttcg tgaggatcgt gccctcttga atggtgctca gaagcttcta ggtattctga 540  
ttgccattgg tgaggctgtt gcatatgttc tttctggaat gtatgggtccc gttggacagc 600  
ttggtgttgg aaatgccatt ctgatcatcc ttcagctttt ctttgctgga atcattgtta 660  
tctgccttga tgaactcctt cagaagggat atggtctcgg atcaggaatc tcccttttca 720  
ttgccaccaa catttgtaa agcattatct ggaaggcatt tagcccaact accatcaaca 780  
ccgggcgtgg agctgagttt gaagggtgctg ttattgcaact gttccatatg ctgataacca 840  
agtccaacaa ggttgccggt ctccgccaa gctttctacc gcaaaacctt ccaaattgta 900  
ccaacttgct tgccacagtc ttgatcttcc tgattgtgat ctacttccaa ggtttccgtg 960  
tggttttgcc tgtgagatca aagaatgccc gtggacaaca gggttcttac ccaatcaagc 1020  
tgttctacac ctctaacatg cccatcatcc tccaatccgc cctcgtctca aatctttact 1080  
tcattttctca gcttctctac cggaagtcca gcggaattt ctttgtaaac cttttgggac 1140  
aatggaaaga atctgagtac agtggacaat ctattccagt tagtggtctg gcttacctca 1200  
tcacagctcc agcaagtttc tctgacatgg cagctcacc gttccatgca ctgttctaca 1260  
tcgtcttcat gctcactgct tgtgctcttt tctcaaagac atggattgaa gtctctggat 1320  
cttctgctag ggatgtagct aagcagctaa aggaacaaca aatgggtgat ccaggacaca 1380  
gagaatcaaa cttacagaag gaactgaaca gatacatccc aacagcagca gcttttggag 1440  
cagtttgtat cgggtgcact accgtttttg ctgatttcat cggagccatc gggtcgggaa 1500  
ccggaattct gttggcggtc acgatcatat accagtattt cgagacctt gagagggaaa 1560  
aagccagtga actcggcttc ttcgggttct aagttagctt aaagaagggtg taaactttgc 1620  
ctgaggcaaa aaagcagagc agaagaggct ttagcttctg tgcccacctc aaacacagac 1680  
aatttgtggg ggcacttggg ttagactact ttttttgtt gttgttgaaa cgaaattttc 1740  
tcttttagtca tttatgttt tttgttactt tttacaagtt aaaaaactta tgtgatagac 1800  
gcttttctaa tgtatgtttc twgc

(2) INFORMATION FOR SEQ ID NO:1396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

Met Gly Gly Gly Phe Arg Val Leu His Leu Val Arg Pro Phe Leu Ala  
1 5 10 15  
Phe Leu Pro Glu Val Gln Ser Ala Asp Arg Lys Val Pro Phe Arg Glu  
20 25 30  
Lys Val Ile Tyr Thr Val Ile Ser Leu Phe Ile Phe Leu Val Cys Ser

(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:1398:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 397 amino acids

[illegible]

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..397  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Gly | Ile | Thr | Pro | Ile | Val | Thr | Ser | Gly | Leu | Val | Met | Gln |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Ala | Gly | Ser | Lys | Ile | Ile | Glu | Val | Asp | Asn | Asn | Val | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Arg | Ala | Leu | Leu | Asn | Gly | Ala | Gln | Lys | Leu | Leu | Gly | Ile | Leu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ile | Gly | Glu | Ala | Val | Ala | Tyr | Val | Leu | Ser | Gly | Met | Tyr | Gly | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Gly | Gln | Leu | Gly | Val | Gly | Asn | Ala | Ile | Leu | Ile | Ile | Leu | Gln | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Phe | Ala | Gly | Ile | Val | Ile | Cys | Leu | Asp | Glu | Leu | Leu | Gln | Lys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Tyr | Gly | Leu | Gly | Ser | Gly | Ile | Ser | Leu | Phe | Ile | Ala | Thr | Asn | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Glu | Ser | Ile | Ile | Trp | Lys | Ala | Phe | Ser | Pro | Thr | Thr | Ile | Asn | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Gly | Ala | Glu | Phe | Glu | Gly | Ala | Val | Ile | Ala | Leu | Phe | His | Met |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Ile | Thr | Lys | Ser | Asn | Lys | Val | Ala | Ala | Leu | Arg | Gln | Ala | Phe | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Gln | Asn | Leu | Pro | Asn | Val | Thr | Asn | Leu | Leu | Ala | Thr | Val | Leu | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Leu | Ile | Val | Ile | Tyr | Phe | Gln | Gly | Phe | Arg | Val | Val | Leu | Pro | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Lys | Asn | Ala | Arg | Gly | Gln | Gln | Gly | Ser | Tyr | Pro | Ile | Lys | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Tyr | Thr | Ser | Asn | Met | Pro | Ile | Ile | Leu | Gln | Ser | Ala | Leu | Val | Ser |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Asn | Leu | Tyr | Phe | Ile | Ser | Gln | Leu | Leu | Tyr | Arg | Lys | Phe | Ser | Gly | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Phe | Phe | Val | Asn | Leu | Leu | Gly | Gln | Trp | Lys | Glu | Ser | Glu | Tyr | Ser | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Ser | Ile | Pro | Val | Ser | Gly | Leu | Ala | Tyr | Leu | Ile | Thr | Ala | Pro | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Phe | Ser | Asp | Met | Ala | Ala | His | Pro | Phe | His | Ala | Leu | Phe | Tyr | Ile |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Phe | Met | Leu | Thr | Ala | Cys | Ala | Leu | Phe | Ser | Lys | Thr | Trp | Ile | Glu |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Val | Ser | Gly | Ser | Ser | Ala | Arg | Asp | Val | Ala | Lys | Gln | Leu | Lys | Glu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Met | Val | Met | Pro | Gly | His | Arg | Glu | Ser | Asn | Leu | Gln | Lys | Glu | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Arg | Tyr | Ile | Pro | Thr | Ala | Ala | Ala | Phe | Gly | Gly | Val | Cys | Ile | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Leu | Thr | Val | Leu | Ala | Asp | Phe | Met | Gly | Ala | Ile | Gly | Ser | Gly | Thr |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gly | Ile | Leu | Leu | Ala | Val | Thr | Ile | Ile | Tyr | Gln | Tyr | Phe | Glu | Thr | Phe |
|     |     |     | 370 |     |     |     | 375 |     |     |     | 380 |     |     |     |     |
| Glu | Lys | Glu | Lys | Ala | Ser | Glu | Leu | Gly | Phe | Phe | Gly | Phe |     |     |     |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1853  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569834  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

```
attccttgct tcatttttcg tcaccctagc cgctttactc tcttgcgata tctctgaggt 60
aattctggag cagcataaac aatcaattga ttcattcttc ttgataccaa gttgtggaaa 120
ctctaggatt gtttgctgta tatctccaga attgctgttt tgattgaatt taggtcgctt 180
agctcagttg atagagcacc acattttttg ttgtagaaat cgatttgttt gacagtctct 240
aaccatgggt aaagagaatt ttcacatcaa catttgtggtc attggccacg tcgattctgg 300
aaagtcgacc accactggac acttgatcta caagttgggt ggtattgaca agcgtgtcat 360
tgagagggtc gagaaggagg ctgctgagat gaacaagagg tccttcaagt acgcatgggt 420
tttgacaaa cttaaggctg agcgtgagcg tggatcacc attgacattg ctctctggaa 480
gttcgagacc accaagtact actgcactgt cattgatgct cctggccatc gtgatttcat 540
caagaacatg atcactggtg cctcccaggc tgatttgtgt gtccttatca tcgactccac 600
cactgggtgt tttgaggctg gtatctccaa ggatggtcag acccgtgagc acgctctcct 660
tgctttcacc cttggtgtca aacagatgat ctgctgttgt aacaagatgg atgccactac 720
ccccaaagta tccaaggcca ggtacgatga aattatcaag gaggtgtctt cctacttgaa 780
gaagggttgt tacaaccccg acaaaatccc atttgtgcc atctctggat tcgagggtga 840
caacatgatt gagagggtcca ccaacctaga ctggtacaag ggaccaactc ttcttgaggc 900
tcttgaccag atcaacgagc ccaagaggcc atcagacaag ccccttcgtc tcccacttca 960
ggatgtctac aagattgggtg gtattggaac ggtgccagtg ggacgtgttg agactggtat 1020
gatcaagcct ggtatgggtg tgacctttgc tcccacaggg ttgaccactg aggtcaagtc 1080
tggtgagatg caccacgagt ctcttcttga ggcacttcca ggtgacaacg ttgggttcaa 1140
tgtaagaatg gttgctgtca aggatcttaa gagagggtac gtcgcatcca actccaagga 1200
tgacctgccc aagggtgctg ctaacttcac ctcccagggt atcatcaTda accaccctgg 1260
tcagattggt aacggttacg ccccagtcct ggattgccac acctctcaca ttgcagtcaa 1320
gttctctgag atcttgacca agattgacag gcgttctggt aaggagattg agaaggagcc 1380
caagttcttg aagaatgggt atgctggtat ggtgaagatg actccaacca agcccatggt 1440
tgtggagacc ttctctgagt acccaccact tggacgtttc gctgtgaggg acatgaggca 1500
gactgttgca gtcggtgtta tcaagagtgt tgacaagaag gacccaaccg gagccaaggt 1560
taccaaggct gccgtcaaga aggggtcgaa gtgaaccatc ctcaaaactc tatctgcgcg 1620
aggtgaatca aaggacagtg ttagttttat tacaatagtt tggattttgg tcgcggtgtc 1680
gtgttcttgt ttggttttct ccccgtcaga gcgttgttct cgtaattggg ttcttgatcg 1740
gaggtggcgg atctacacac acattcttcc tgttttttgc tttttatttg ttttctcatt 1800
ttgaactgtt taaaatttct gttatatgaa tgaatgtttt ccctgcggtt att
```

(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 449 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..449  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569835  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

```
Met Gly Lys Glu Asn Phe His Ile Asn Ile Val Val Ile Gly His Val
1 5 10 15
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
20 25 30
Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
35 40 45
Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50 55 60
```

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe  
65 70 75 80  
Glu Thr Thr Lys Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg  
85 90 95  
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala  
100 105 110  
Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser  
115 120 125  
Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly  
130 135 140  
Val Lys Gln Met Ile Cys Cys Asn Lys Met Asp Ala Thr Thr Pro  
145 150 155 160  
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser  
165 170 175  
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro  
180 185 190  
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu  
195 200 205  
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn  
210 215 220  
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp  
225 230 235 240  
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu  
245 250 255  
Thr Gly Met Ile Lys Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly  
260 265 270  
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ser Leu Leu  
275 280 285  
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala  
290 295 300  
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp  
305 310 315 320  
Pro Ala Lys Gly Ala Ala Asn Phe Thr Ser Gln Val Ile Ile Xaa Asn  
325 330 335  
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His  
340 345 350  
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp  
355 360 365  
Arg Arg Ser Gly Lys Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn  
370 375 380  
Gly Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val  
385 390 395 400  
Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp  
405 410 415  
Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys  
420 425 430  
Asp Pro Thr Gly Ala Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala  
435 440 445  
Lys

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Thr | Lys | Tyr | Tyr | Cys | Thr | Val | Ile | Asp | Ala | Pro | Gly | His | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Phe | Ile | Lys | Asn | Met | Ile | Thr | Gly | Thr | Ser | Gln | Ala | Asp | Cys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Ile | Ile | Asp | Ser | Thr | Thr | Gly | Gly | Phe | Glu | Ala | Gly | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asp | Gly | Gln | Thr | Arg | Glu | His | Ala | Leu | Leu | Ala | Phe | Thr | Leu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Lys | Gln | Met | Ile | Cys | Cys | Cys | Asn | Lys | Met | Asp | Ala | Thr | Thr | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Lys | Tyr | Ser | Lys | Ala | Arg | Tyr | Asp | Glu | Ile | Ile | Lys | Glu | Val | Ser | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Leu | Lys | Lys | Val | Gly | Tyr | Asn | Pro | Asp | Lys | Ile | Pro | Phe | Val | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ile | Ser | Gly | Phe | Glu | Gly | Asp | Asn | Met | Ile | Glu | Arg | Ser | Thr | Asn | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |
| Asp | Trp | Tyr | Lys | Gly | Pro | Thr | Leu | Leu | Glu | Ala | Leu | Asp | Gln | Ile | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Pro | Lys | Arg | Pro | Ser | Asp | Lys | Pro | Leu | Arg | Leu | Pro | Leu | Gln | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Val | Tyr | Lys | Ile | Gly | Gly | Ile | Gly | Thr | Val | Pro | Val | Gly | Arg | Val | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Thr | Gly | Met | Ile | Lys | Pro | Gly | Met | Val | Val | Thr | Phe | Ala | Pro | Thr | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Leu | Thr | Thr | Glu | Val | Lys | Ser | Val | Glu | Met | His | His | Glu | Ser | Leu | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ala | Leu | Pro | Gly | Asp | Asn | Val | Gly | Phe | Asn | Val | Lys | Asn | Val | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Lys | Asp | Leu | Lys | Arg | Gly | Tyr | Val | Ala | Ser | Asn | Ser | Lys | Asp | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Ala | Lys | Gly | Ala | Ala | Asn | Phe | Thr | Ser | Gln | Val | Ile | Ile | Xaa | Asn |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| His | Pro | Gly | Gln | Ile | Gly | Asn | Gly | Tyr | Ala | Pro | Val | Leu | Asp | Cys | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Thr | Ser | His | Ile | Ala | Val | Lys | Phe | Ser | Glu | Ile | Leu | Thr | Lys | Ile | Asp |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Arg | Arg | Ser | Gly | Lys | Glu | Ile | Glu | Lys | Glu | Pro | Lys | Phe | Leu | Lys | Asn |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Asp | Ala | Gly | Met | Val | Lys | Met | Thr | Pro | Thr | Lys | Pro | Met | Val | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Thr | Phe | Ser | Glu | Tyr | Pro | Pro | Leu | Gly | Arg | Phe | Ala | Val | Arg | Asp |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Met | Arg | Gln | Thr | Val | Ala | Val | Gly | Val | Ile | Lys | Ser | Val | Asp | Lys | Lys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asp | Pro | Thr | Gly | Ala | Lys | Val | Thr | Lys | Ala | Ala | Val | Lys | Lys | Gly | Ala |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1569837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp  
1 5 10 15  
Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr  
20 25 30  
Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile  
35 40 45  
Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro Lys Tyr Ser Lys Ala  
50 55 60  
Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser Tyr Leu Lys Lys Val  
65 70 75 80  
Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu  
85 90 95  
Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly  
100 105 110  
Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn Glu Pro Lys Arg Pro  
115 120 125  
Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly  
130 135 140  
Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Met Ile Lys  
145 150 155 160  
Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly Leu Thr Thr Glu Val  
165 170 175  
Lys Ser Val Glu Met His His Glu Ser Leu Leu Glu Ala Leu Pro Gly  
180 185 190  
Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala Val Lys Asp Leu Lys  
195 200 205  
Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Gly Ala  
210 215 220  
Ala Asn Phe Thr Ser Gln Val Ile Ile Xaa Asn His Pro Gly Gln Ile  
225 230 235 240  
Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala  
245 250 255  
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys  
260 265 270  
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met  
275 280 285  
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu  
290 295 300  
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val  
305 310 315 320  
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala  
325 330 335  
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys  
340 345

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1442

(D) OTHER INFORMATION: / Ceres Seq. ID 1569846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

gcccaatttta aaccgagact gatgattgag aagaaactgt cgaagatgaa gatgagaacc



|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aaatcgattc | cggttaggtc  | ttcgcgcaaa  | tccctcgatt  | cgcttctgga  | tgatgaagct  | 120  |
| aatgaaaaca | cacaatgtga  | tgaaagagat  | gtgccacaca  | agaagcgtcg  | ttgtcttggg  | 180  |
| actagtgaga | ctactgatag  | aggaggatct  | gtagagccgc  | tgctggactt  | ggatgcttgt  | 240  |
| attgtatgtg | aagtttcaga  | cgagcggtga  | tctcgttgtt  | gcgggggtga  | ctgtcttctt  | 300  |
| tcgtttcacg | gcgagtgttt  | gtatgctgat  | ttgggtagta  | ctagtagtag  | tagtagtagt  | 360  |
| agtagtgagg | atgtttcgaa  | tccattttgt  | ccttattgct  | ggctcaagat  | tggtgcaactg | 420  |
| aaatccaaaa | cattgagaga  | aaagaccctt  | gagggcgaaa  | aggcggtctg  | caagtatcta  | 480  |
| gataaagaga | tgaamAgcAg  | ggatgaggat  | ataaccttat  | ctgggtgatga | aattggaaac  | 540  |
| caagagcaga | gtacagacat  | tgtaagtgtat | catgagttac  | aaggagagaa  | ggatggctgt  | 600  |
| tcatcaaaac | cagatgcgga  | tcaagggaaa  | gtgggtactg  | gtaaagtgat  | tgacgaagtt  | 660  |
| ggagcatcag | agaaggtagc  | tacagaaaaa  | tttcaagacg  | ctgaagatga  | tgaaacagct  | 720  |
| aaagatcaag | gtacaagaat  | cctgaataca  | gggtgcaggga | aaaagagaga  | ggtttcttcg  | 780  |
| tttttgtcta | tgcaagaatc  | gttttcagca  | aaagaacagg  | accaggteca  | gcagaatgag  | 840  |
| aagcgaagaa | ggagaggatt  | gaaaattatc  | gatagtgcac  | tctcatcaaa  | gggatcaagt  | 900  |
| aacgaacgaa | atggagaaga  | tgtaactgag  | caggtaactt  | catcggttca  | agtaacctcc  | 960  |
| ccgtcaggga | gaatgaggaa  | ccagcaggca  | acaaccaaa   | tggttaagtc  | aaagacagtg  | 1020 |
| agggacattt | ctttctttta  | gatggatcaa  | agaaggaggc  | tactttggac  | gtacgaagaa  | 1080 |
| gaagagatgc | ttaaagggtgg | agtggagaaa  | tttgcagcag  | aagcaaaca   | gaacatgcc   | 1140 |
| tgaggaaaaa | ttctggaaat  | gggagagaa   | gtgttccacg  | aaacacgtac  | tccagctgat  | 1200 |
| ctcaaggaca | aatggaggag  | catggtcaag  | attatgaaca  | aaaacgaaca  | aggcagcaca  | 1260 |
| ctaacccta  | ctgctatgta  | atcaaatagt  | agtgtgactt  | attgagatga  | agccagactt  | 1320 |
| ggtgaactaa | tgtgggagtt  | gatctgtgta  | atagacaaaa  | gttcctcctt  | tacaagaact  | 1380 |
| gacttctact | ttttgtgtat  | cttcgacatc  | tttagatttt  | cagtatagat  | aatatatggc  | 1440 |
| tc         |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1569847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Phe | Lys | Pro | Arg | Leu | Met | Ile | Glu | Lys | Lys | Leu | Ser | Lys | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Met | Arg | Thr | Lys | Ser | Ile | Pro | Val | Arg | Ser | Ser | Arg | Lys | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Ser | Leu | Leu | Asp | Asp | Glu | Ala | Asn | Glu | Asn | Thr | Gln | Cys | Asp | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asp | Val | Pro | His | Lys | Lys | Arg | Arg | Cys | Leu | Gly | Thr | Ser | Glu | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Asp | Arg | Gly | Gly | Ser | Val | Glu | Pro | Leu | Leu | Asp | Leu | Asp | Ala | Cys |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ile | Val | Cys | Glu | Val | Ser | Asp | Glu | Arg | Val | Ser | Arg | Cys | Cys | Gly | Val |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Asp | Cys | Leu | Leu | Ser | Phe | His | Gly | Glu | Cys | Leu | Tyr | Ala | Asp | Leu | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Thr | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Glu | Asp | Val | Ser | Asn | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Cys | Pro | Tyr | Cys | Trp | Leu | Lys | Ile | Val | Ala | Leu | Lys | Ser | Lys | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Leu | Arg | Glu | Lys | Thr | Leu | Glu | Ala | Glu | Lys | Ala | Val | Cys | Lys | Tyr | Leu |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Asp | Lys | Glu | Met | Xaa | Ser | Arg | Asp | Glu | Asp | Ile | Thr | Leu | Ser | Gly | Asp |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |
| Glu | Ile | Gly | Asn | Gln | Glu | Gln | Ser | Thr | Asp | Ile | Val | Ser | Asp | His | Glu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Gln | Gly | Glu | Lys | Asp | Gly | Cys | Ser | Ser | Lys | Pro | Asp | Ala | Asp | Gln |

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 195 |     | 200 |     | 205 |
| Gly | Lys | Val | Gly | Thr | Gly |
| 210 |     |     | 215 |     | 220 |
| Lys | Val | Ala | Thr | Glu | Lys |
| 225 |     |     | 230 |     | 235 |
| Lys | Asp | Gln | Gly | Thr | Arg |
|     |     |     | 245 |     | 250 |
| Glu | Val | Ser | Ser | Phe | Leu |
|     |     |     | 260 |     | 265 |
| Gln | Asp | Gln | Val | Gln | Gln |
| 275 |     |     | 280 |     | 285 |
| Ile | Ile | Asp | Ser | Asp | Ile |
| 290 |     |     | 295 |     | 300 |
| Gly | Glu | Asp | Val | Thr | Glu |
| 305 |     |     | 310 |     | 315 |
| Pro | Ser | Gly | Arg | Met | Arg |
|     |     |     | 325 |     | 330 |
| Ser | Lys | Thr | Val | Arg | Asp |
|     |     |     | 340 |     | 345 |
| Arg | Leu | Leu | Trp | Thr | Tyr |
|     |     |     | 355 |     | 360 |
| Glu | Lys | Phe | Ala | Ala | Glu |
| 370 |     |     | 375 |     | 380 |
| Leu | Glu | Met | Gly | Glu | Lys |
| 385 |     |     | 390 |     | 395 |
| Leu | Lys | Asp | Lys | Trp | Arg |
|     |     |     | 405 |     | 410 |
| Gln | Gly | Ser | Thr | Leu | Thr |
|     |     |     | 420 |     | 425 |

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Glu | Lys | Lys | Leu | Ser | Lys | Met | Lys | Met | Arg | Thr | Lys | Ser | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Val | Arg | Ser | Ser | Arg | Lys | Ser | Leu | Asp | Ser | Leu | Leu | Asp | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asn | Glu | Asn | Thr | Gln | Cys | Asp | Glu | Arg | Asp | Val | Pro | His | Lys | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Cys | Leu | Gly | Thr | Ser | Glu | Thr | Thr | Asp | Arg | Gly | Gly | Ser | Val |
|     |     |     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |
| Glu | Pro | Leu | Leu | Asp | Leu | Asp | Ala | Cys | Ile | Val | Cys | Glu | Val | Ser | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Arg | Val | Ser | Arg | Cys | Cys | Gly | Val | Asp | Cys | Leu | Leu | Ser | Phe | His |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Glu | Cys | Leu | Tyr | Ala | Asp | Leu | Gly | Ser | Thr | Ser | Ser | Ser | Ser | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Ser | Ser | Glu | Asp | Val | Ser | Asn | Pro | Phe | Cys | Pro | Tyr | Cys | Trp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Ile | Val | Ala | Leu | Lys | Ser | Lys | Thr | Leu | Arg | Glu | Lys | Thr | Leu | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Glu | Lys | Ala | Val | Cys | Lys | Tyr | Leu | Asp | Lys | Glu | Met | Xaa | Ser | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

SEQUENCE: 1569848

```

Asp Glu Asp Ile Thr Leu Ser Gly Asp Glu Ile Gly Asn Gln Glu Gln
 165 170 175
Ser Thr Asp Ile Val Ser Asp His Glu Leu Gln Gly Glu Lys Asp Gly
 180 185 190
Cys Ser Ser Lys Pro Asp Ala Asp Gln Gly Lys Val Gly Thr Gly Lys
 195 200 205
Val Ile Asp Glu Val Gly Ala Ser Glu Lys Val Ala Thr Glu Lys Phe
 210 215 220
Gln Asp Ala Glu Asp Asp Glu Thr Ala Lys Asp Gln Gly Thr Arg Ile
 225 230 235
Leu Asn Thr Gly Ala Gly Lys Lys Arg Glu Val Ser Ser Phe Leu Ser
 245 250 255
Met Gln Glu Ser Phe Ser Ala Lys Glu Gln Asp Gln Val Gln Gln Asn
 260 265 270
Glu Lys Arg Arg Arg Arg Gly Leu Lys Ile Ile Asp Ser Asp Ile Ser
 275 280 285
Ser Lys Gly Ser Ser Asn Glu Arg Asn Gly Glu Asp Val Thr Glu Gln
 290 295 300
Val Thr Ser Ser Val Gln Val Thr Ser Pro Ser Gly Arg Met Arg Asn
 305 310 315
Gln Gln Ala Thr Thr Lys Val Ala Lys Ser Lys Thr Val Arg Asp Ile
 325 330 335
Ser Phe Phe Lys Met Asp Gln Arg Arg Arg Leu Leu Trp Thr Tyr Glu
 340 345 350
Glu Glu Glu Met Leu Lys Val Gly Val Glu Lys Phe Ala Ala Glu Ala
 355 360 365
Asn Lys Asn Met Pro Trp Arg Lys Ile Leu Glu Met Gly Glu Lys Val
 370 375 380
Phe His Glu Thr Arg Thr Pro Ala Asp Leu Lys Asp Lys Trp Arg Ser
 385 390 395
Met Val Lys Ile Met Asn Lys Asn Glu Gln Gly Ser Thr Leu Thr Pro
 405 410 415
Thr Ala Met

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(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1569849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

```

Met Lys Met Arg Thr Lys Ser Ile Pro Val Arg Ser Ser Arg Lys Ser
1 5 10 15
Leu Asp Ser Leu Leu Asp Asp Glu Ala Asn Glu Asn Thr Gln Cys Asp
 20 25 30
Glu Arg Asp Val Pro His Lys Lys Arg Arg Cys Leu Gly Thr Ser Glu
 35 40 45
Thr Thr Asp Arg Gly Gly Ser Val Glu Pro Leu Leu Asp Leu Asp Ala
 50 55 60
Cys Ile Val Cys Glu Val Ser Asp Glu Arg Val Ser Arg Cys Cys Gly
 65 70 75 80
Val Asp Cys Leu Leu Ser Phe His Gly Glu Cys Leu Tyr Ala Asp Leu
 85 90 95
Gly Ser Thr Ser Ser Ser Ser Ser Ser Ser Ser Glu Asp Val Ser Asn
 100 105 110
Pro Phe Cys Pro Tyr Cys Trp Leu Lys Ile Val Ala Leu Lys Ser Lys

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|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Thr Leu Arg Glu Lys Thr Leu Glu Ala Glu Lys Ala Val Cys Lys Tyr |     |     |
| 130                                                             | 135 | 140 |
| Leu Asp Lys Glu Met Xaa Ser Arg Asp Glu Asp Ile Thr Leu Ser Gly |     |     |
| 145                                                             | 150 | 155 |
| Asp Glu Ile Gly Asn Gln Glu Gln Ser Thr Asp Ile Val Ser Asp His |     |     |
|                                                                 | 165 | 170 |
| Glu Leu Gln Gly Glu Lys Asp Gly Cys Ser Ser Lys Pro Asp Ala Asp |     |     |
|                                                                 | 180 | 185 |
| Gln Gly Lys Val Gly Thr Gly Lys Val Ile Asp Glu Val Gly Ala Ser |     |     |
|                                                                 | 195 | 200 |
| Glu Lys Val Ala Thr Glu Lys Phe Gln Asp Ala Glu Asp Asp Glu Thr |     |     |
|                                                                 | 210 | 215 |
| Ala Lys Asp Gln Gly Thr Arg Ile Leu Asn Thr Gly Ala Gly Lys Lys |     |     |
| 225                                                             | 230 | 235 |
| Arg Glu Val Ser Ser Phe Leu Ser Met Gln Glu Ser Phe Ser Ala Lys |     |     |
|                                                                 | 245 | 250 |
| Glu Gln Asp Gln Val Gln Gln Asn Glu Lys Arg Arg Arg Arg Gly Leu |     |     |
|                                                                 | 260 | 265 |
| Lys Ile Ile Asp Ser Asp Ile Ser Ser Lys Gly Ser Ser Asn Glu Arg |     |     |
|                                                                 | 275 | 280 |
| Asn Gly Glu Asp Val Thr Glu Gln Val Thr Ser Ser Val Gln Val Thr |     |     |
|                                                                 | 290 | 295 |
| Ser Pro Ser Gly Arg Met Arg Asn Gln Gln Ala Thr Thr Lys Val Ala |     |     |
| 305                                                             | 310 | 315 |
| Lys Ser Lys Thr Val Arg Asp Ile Ser Phe Phe Lys Met Asp Gln Arg |     |     |
|                                                                 | 325 | 330 |
| Arg Arg Leu Leu Trp Thr Tyr Glu Glu Glu Met Leu Lys Val Gly     |     |     |
|                                                                 | 340 | 345 |
| Val Glu Lys Phe Ala Ala Glu Ala Asn Lys Asn Met Pro Trp Arg Lys |     |     |
|                                                                 | 355 | 360 |
| Ile Leu Glu Met Gly Glu Lys Val Phe His Glu Thr Arg Thr Pro Ala |     |     |
|                                                                 | 370 | 375 |
| Asp Leu Lys Asp Lys Trp Arg Ser Met Val Lys Ile Met Asn Lys Asn |     |     |
| 385                                                             | 390 | 395 |
| Glu Gln Gly Ser Thr Leu Thr Pro Thr Ala Met                     |     |     |
|                                                                 | 405 | 410 |

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..986
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aatctcactc cctccctccc ttaagtcttg ttgaatctgc tgaattgttt tataaagagt | 60  |
| tactttggca aaatggaaaa tccggcgaag agagtgttga tgacatccaa cggcgacgag | 120 |
| gtgtcccgaa acatcgcttt ccatctagcc aaacacgggt gcaagttggt aatgatggga | 180 |
| aatgagggtt ccctaaggag cattgtagag attccattga gggagccttc cctgccgatg | 240 |
| ttatagcact cgacatggaa tctgactctg aagttgcttt tcatgccgct gtccaaaagg | 300 |
| catggaaact ttccggccat ttcgatgctt ttctcaactc ttatacctac caaggaaagg | 360 |
| tgcaggacat tcttcaagtc tctcaagatg agttccacag aatcacaaag atcaatctca | 420 |
| ccgctccatg gtttctctaa aggctgtagc cacaaggatg aaggaccatg gatcaggagg | 480 |
| ctccattgtc ttcatggcca ctatcgccag cggagagagg gcgctttacc ctggcgctga | 540 |
| tgcctacgct tcaacttctg ccgctattca ccagctcggt cgggcatcag ccatgagtct | 600 |
| cgggaagcac aagatacggg tcaacatgat ctctagaggg ctgcatctgg atgatgagta | 660 |
| tacagcttct gtgggaagag accgagcaca gaagctggtc aaggacgctg caccctcgg  | 720 |

ccagtggctc aacccggaga cagacctcta ctccactgtt atctacttga tcagcgtatgg 780  
Ctcacgcttc atgacaggca ccactgtctt ggtggatgga gcgcagtccc ttacgcgacc 840  
ccgtctcaaa tcctacatgt gatcaacgcg tagtattata attctatgtt gtgtgtaaaa 900  
agtgaatatg aatcaagttt gaataacttt ggagggatta ataatccatg gaatcaatga 960  
ttacatactt ttgacaagta tagaag

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

Met Val Ser Leu Lys Ala Val Ala Thr Arg Met Lys Asp His Gly Ser  
1 5 10 15  
Gly Gly Ser Ile Val Phe Met Ala Thr Ile Ala Ser Gly Glu Arg Ala  
20 25 30  
Leu Tyr Pro Gly Ala Asp Ala Tyr Ala Ser Thr Ser Ala Ala Ile His  
35 40 45  
Gln Leu Val Arg Ala Ser Ala Met Ser Leu Gly Lys His Lys Ile Arg  
50 55 60  
Val Asn Met Ile Ser Arg Gly Leu His Leu Asp Asp Glu Tyr Thr Ala  
65 70 75 80  
Ser Val Gly Arg Asp Arg Ala Gln Lys Leu Val Lys Asp Ala Ala Pro  
85 90 95  
Leu Gly Gln Trp Leu Asn Pro Glu Thr Asp Leu Tyr Ser Thr Val Ile  
100 105 110  
Tyr Leu Ile Ser Asp Gly Ser Arg Phe Met Thr Gly Thr Thr Val Leu  
115 120 125  
Val Asp Gly Ala Gln Ser Leu Thr Arg Pro Arg Leu Lys Ser Tyr Met  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

Met Lys Asp His Gly Ser Gly Gly Ser Ile Val Phe Met Ala Thr Ile  
1 5 10 15  
Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp Ala Tyr Ala Ser  
20 25 30  
Thr Ser Ala Ala Ile His Gln Leu Val Arg Ala Ser Ala Met Ser Leu  
35 40 45  
Gly Lys His Lys Ile Arg Val Asn Met Ile Ser Arg Gly Leu His Leu  
50 55 60  
Asp Asp Glu Tyr Thr Ala Ser Val Gly Arg Asp Arg Ala Gln Lys Leu  
65 70 75 80  
Val Lys Asp Ala Ala Pro Leu Gly Gln Trp Leu Asn Pro Glu Thr Asp  
85 90 95

Leu Tyr Ser Thr Val Ile Tyr Leu Ile Ser Asp Gly Ser Arg Phe Met  
100 105 110  
Thr Gly Thr Thr Val Leu Val Asp Gly Ala Gln Ser Leu Thr Arg Pro  
115 120 125  
Arg Leu Lys Ser Tyr Met  
130

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp  
1 5 10 15  
Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Ala Ser  
20 25 30  
Ala Met Ser Leu Gly Lys His Lys Ile Arg Val Asn Met Ile Ser Arg  
35 40 45  
Gly Leu His Leu Asp Asp Glu Tyr Thr Ala Ser Val Gly Arg Asp Arg  
50 55 60  
Ala Gln Lys Leu Val Lys Asp Ala Ala Pro Leu Gly Gln Trp Leu Asn  
65 70 75 80  
Pro Glu Thr Asp Leu Tyr Ser Thr Val Ile Tyr Leu Ile Ser Asp Gly  
85 90 95  
Ser Arg Phe Met Thr Gly Thr Thr Val Leu Val Asp Gly Ala Gln Ser  
100 105 110  
Leu Thr Arg Pro Arg Leu Lys Ser Tyr Met  
115 120

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1573
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ccttctctct | ctctctccct | ctctaactgt | atcttcttct | tcttcttcaa | ccttcagact | 60  |
| tttctagttg | caactctcat | tcaattgttc | aatttctctg | taaaaatcaa | agcttttttg | 120 |
| aatcttttct | cggcgagata | tttcttcacc | ggcgcaagct | tctcttgagc | gtgattcatc | 180 |
| actgggtttg | cattttttcc | tggtgggtat | tcttcaaatt | gttcaaagct | ccgacctttt | 240 |
| cttccttaga | atctgattac | tggaatcttg | aagctggaga | gactcgagtt | tatatggttt | 300 |
| caagcatcgt | tgagtcaatc | attgagttgt | gtagaagaaa | ggtttggttt | tcttctccgt | 360 |
| ttaagtgggt | ttgggtttgg | taggatttgg | tgtaatctgg | gagataaaga | aagatgaata | 420 |
| tgagtgattt | aggttgggat | gatgaagata | aatcggtggt | tagtgctggt | ttagggcatt | 480 |
| tagcttctga | ttttcttcga | gcaaactcta | attcgaatca | gaatctcttt | cttggtatgg | 540 |
| gaactgatga | tactctgaat | aagaagctct | ctagtctcgt | tgattggcca | aactcggaga | 600 |
| atttcagctg | gaactacgct | atthttctgc | aacaaaccat | gtctagatcc | ggacaacaag | 660 |
| tcttaggttg | gggagatggg | tgttgctcag | agcctaata  | ggaagaggaa | tcaaaagttg | 720 |
| ttaggtctta | taattttaac | aacatggggg | cagaggaaga | gacatggcaa | gatatgagga | 780 |
| agagagtgtt | gcagaagctt | cataggttgt | ttggtggatc | tgatgaagac | aattatgctt | 840 |
| tgagcttaga | gaaagttact | gctactgaga | ttttcttctt | agcttccatg | tatttcttct | 900 |

tcaatcacgg tgaaggcggg cctgggaggt gttattcttc agggaaacat gtgtggctct 960  
ctgatgcggt taactctgag tctgactatt gtttcaggtc ttttatggcg aaatctgcgg 1020  
gaatcagaac gatcggtatg gttcctactg atgctgggtg tcttgagctt ggttctgttt 1080  
ggctctttgcc tgaaaacatt ggcttggtta agtctgttca agctttgttc atgaggagag 1140  
ttacgcaacc agtaatggtg acttcaaaca ctaacatgac tggagggatt cacaagcttt 1200  
tcgggcagga tttgagtggg gCtcacgcgt atcctaagaa gctcgaagtg agaagaaact 1260  
tggatgagag attcactcct caaagttggg aaggctataa taacaataaa ggtccaacat 1320  
ttggttacac acctcagagg gatgatgtga aagtgttaga gaatgtgaat atggtttag 1380  
ataataacaa ttacaagacg cagattgagt ttgcgggata atcagttgct gcttcttcga 1440  
atccatctac aaacactcag caagaaaaat cagaatcttg tacagagaaa agaccagtga 1500  
gcttgtagc aggagcagga atagtttctg ttgttgatga gaagagaccg agaaagagag 1560  
ggagaaagcc tgc

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met Asn Met Ser Asp Leu Gly Trp Asp Asp Glu Asp Lys Ser Val Val  
1 5 10 15  
Ser Ala Val Leu Gly His Leu Ala Ser Asp Phe Leu Arg Ala Asn Ser  
20 25 30  
Asn Ser Asn Gln Asn Leu Phe Leu Val Met Gly Thr Asp Asp Thr Leu  
35 40 45  
Asn Lys Lys Leu Ser Ser Leu Val Asp Trp Pro Asn Ser Glu Asn Phe  
50 55 60  
Ser Trp Asn Tyr Ala Ile Phe Trp Gln Gln Thr Met Ser Arg Ser Gly  
65 70 75 80  
Gln Gln Val Leu Gly Trp Gly Asp Gly Cys Cys Arg Glu Pro Asn Glu  
85 90 95  
Glu Glu Glu Ser Lys Val Val Arg Ser Tyr Asn Phe Asn Asn Met Gly  
100 105 110  
Ala Glu Glu Glu Thr Trp Gln Asp Met Arg Lys Arg Val Leu Gln Lys  
115 120 125  
Leu His Arg Leu Phe Gly Gly Ser Asp Glu Asp Asn Tyr Ala Leu Ser  
130 135 140  
Leu Glu Lys Val Thr Ala Thr Glu Ile Phe Phe Leu Ala Ser Met Tyr  
145 150 155 160  
Phe Phe Phe Asn His Gly Glu Gly Gly Pro Gly Arg Cys Tyr Ser Ser  
165 170 175  
Gly Lys His Val Trp Leu Ser Asp Ala Val Asn Ser Glu Ser Asp Tyr  
180 185 190  
Cys Phe Arg Ser Phe Met Ala Lys Ser Ala Gly Ile Arg Thr Ile Val  
195 200 205  
Met Val Pro Thr Asp Ala Gly Val Leu Glu Leu Gly Ser Val Trp Ser  
210 215 220  
Leu Pro Glu Asn Ile Gly Leu Val Lys Ser Val Gln Ala Leu Phe Met  
225 230 235 240  
Arg Arg Val Thr Gln Pro Val Met Val Thr Ser Asn Thr Asn Met Thr  
245 250 255  
Gly Gly Ile His Lys Leu Phe Gly Gln Asp Leu Ser Gly Ala His Ala  
260 265 270  
Tyr Pro Lys Lys Leu Glu Val Arg Arg Asn Leu Asp Glu Arg Phe Thr  
275 280 285  
Pro Gln Ser Trp Glu Gly Tyr Asn Asn Asn Lys Gly Pro Thr Phe Gly

000001-1569872

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asp | Leu | Gly | Trp | Asp | Asp | Glu | Asp | Lys | Ser | Val | Val | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Leu | Gly | His | Leu | Ala | Ser | Asp | Phe | Leu | Arg | Ala | Asn | Ser | Asn | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asn | Gln | Asn | Leu | Phe | Leu | Val | Met | Gly | Thr | Asp | Asp | Thr | Leu | Asn | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Leu | Ser | Ser | Leu | Val | Asp | Trp | Pro | Asn | Ser | Glu | Asn | Phe | Ser | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Tyr | Ala | Ile | Phe | Trp | Gln | Gln | Thr | Met | Ser | Arg | Ser | Gly | Gln | Gln |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Leu | Gly | Trp | Gly | Asp | Gly | Cys | Cys | Arg | Glu | Pro | Asn | Glu | Glu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Ser | Lys | Val | Val | Arg | Ser | Tyr | Asn | Phe | Asn | Asn | Met | Gly | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Glu | Thr | Trp | Gln | Asp | Met | Arg | Lys | Arg | Val | Leu | Gln | Lys | Leu | His |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Leu | Phe | Gly | Gly | Ser | Asp | Glu | Asp | Asn | Tyr | Ala | Leu | Ser | Leu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Thr | Ala | Thr | Glu | Ile | Phe | Phe | Leu | Ala | Ser | Met | Tyr | Phe | Phe |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Asn | His | Gly | Glu | Gly | Gly | Pro | Gly | Arg | Cys | Tyr | Ser | Ser | Gly | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Val | Trp | Leu | Ser | Asp | Ala | Val | Asn | Ser | Glu | Ser | Asp | Tyr | Cys | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Phe | Met | Ala | Lys | Ser | Ala | Gly | Ile | Arg | Thr | Ile | Val | Met | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Thr | Asp | Ala | Gly | Val | Leu | Glu | Leu | Gly | Ser | Val | Trp | Ser | Leu | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Asn | Ile | Gly | Leu | Val | Lys | Ser | Val | Gln | Ala | Leu | Phe | Met | Arg | Arg |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Thr | Gln | Pro | Val | Met | Val | Thr | Ser | Asn | Thr | Asn | Met | Thr | Gly | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | His | Lys | Leu | Phe | Gly | Gln | Asp | Leu | Ser | Gly | Ala | His | Ala | Tyr | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Lys | Leu | Glu | Val | Arg | Arg | Asn | Leu | Asp | Glu | Arg | Phe | Thr | Pro | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Trp | Glu | Gly | Tyr | Asn | Asn | Asn | Lys | Gly | Pro | Thr | Phe | Gly | Tyr | Thr |
| 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Pro | Gln | Arg | Asp | Asp | Val | Lys | Val | Leu | Glu | Asn | Val | Asn | Met | Val | Val |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asp | Asn | Asn | Asn | Tyr | Lys | Thr | Gln | Ile | Glu | Phe | Ala | Gly | Ser | Ser | Val |
|     |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |
| Ala | Ala | Ser | Ser | Asn | Pro | Ser | Thr | Asn | Thr | Gln | Gln | Glu | Lys | Ser | Glu |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Cys | Thr | Glu | Lys | Arg | Pro | Val | Ser | Leu | Leu | Ala | Gly | Ala | Gly | Ile |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Val | Ser | Val | Val | Asp | Glu | Lys | Arg | Pro | Arg | Lys | Arg | Gly | Arg | Lys | Pro |
| 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..345
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Thr | Asp | Asp | Thr | Leu | Asn | Lys | Lys | Leu | Ser | Ser | Leu | Val | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Pro | Asn | Ser | Glu | Asn | Phe | Ser | Trp | Asn | Tyr | Ala | Ile | Phe | Trp | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Thr | Met | Ser | Arg | Ser | Gly | Gln | Gln | Val | Leu | Gly | Trp | Gly | Asp | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Cys | Cys | Arg | Glu | Pro | Asn | Glu | Glu | Glu | Glu | Ser | Lys | Val | Val | Arg | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Asn | Phe | Asn | Asn | Met | Gly | Ala | Glu | Glu | Glu | Thr | Trp | Gln | Asp | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Lys | Arg | Val | Leu | Gln | Lys | Leu | His | Arg | Leu | Phe | Gly | Gly | Ser | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Asn | Tyr | Ala | Leu | Ser | Leu | Glu | Lys | Val | Thr | Ala | Thr | Glu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Phe | Leu | Ala | Ser | Met | Tyr | Phe | Phe | Phe | Asn | His | Gly | Glu | Gly | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gly | Arg | Cys | Tyr | Ser | Ser | Gly | Lys | His | Val | Trp | Leu | Ser | Asp | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asn | Ser | Glu | Ser | Asp | Tyr | Cys | Phe | Arg | Ser | Phe | Met | Ala | Lys | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Gly | Ile | Arg | Thr | Ile | Val | Met | Val | Pro | Thr | Asp | Ala | Gly | Val | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Leu | Gly | Ser | Val | Trp | Ser | Leu | Pro | Glu | Asn | Ile | Gly | Leu | Val | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Gln | Ala | Leu | Phe | Met | Arg | Arg | Val | Thr | Gln | Pro | Val | Met | Val |
|     |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Thr | Ser | Asn | Thr | Asn | Met | Thr | Gly | Gly | Ile | His | Lys | Leu | Phe | Gly | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Asp | Leu | Ser | Gly | Ala | His | Ala | Tyr | Pro | Lys | Lys | Leu | Glu | Val | Arg | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Leu | Asp | Glu | Arg | Phe | Thr | Pro | Gln | Ser | Trp | Glu | Gly | Tyr | Asn | Asn |
|     |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |
| Asn | Lys | Gly | Pro | Thr | Phe | Gly | Tyr | Thr | Pro | Gln | Arg | Asp | Asp | Val | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Leu | Glu | Asn | Val | Asn | Met | Val | Val | Asp | Asn | Asn | Asn | Tyr | Lys | Thr |

SEQUENCE: 1569874

275 280 285  
Gln Ile Glu Phe Ala Gly Ser Ser Val Ala Ala Ser Ser Asn Pro Ser  
290 295 300  
Thr Asn Thr Gln Gln Glu Lys Ser Glu Ser Cys Thr Glu Lys Arg Pro  
305 310 315 320  
Val Ser Leu Leu Ala Gly Ala Gly Ile Val Ser Val Val Asp Glu Lys  
325 330 335  
Arg Pro Arg Lys Arg Gly Arg Lys Pro  
340 345

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

|             |              |             |             |            |            |      |
|-------------|--------------|-------------|-------------|------------|------------|------|
| ggttaaAttt  | gtttcatctg   | atcgaaaagg  | aatcagttta  | ggtctttgcc | tcctctctcc | 60   |
| ggccagctca  | attctcgatc   | aaagggtgacg | tggatatatg  | aagcagatgt | tttggggaac | 120  |
| cagagttctg  | taaatagaaa   | ccttcacgcg  | acgttgaaag  | gtttttgaga | cgaatatagg | 180  |
| aggagaagat  | gggatgtggt   | tcttcttgct  | tccgggtcga  | ggacattgat | gagtacatga | 240  |
| atccaaacag  | ctctgtctat   | aggaactgtc  | cctgcataag  | atgccttgct | cataatttcc | 300  |
| ttaacctgta  | tatttcggtc   | ttcagaagag  | gggaaactcg  | ctctctccca | tcttcggttc | 360  |
| aagctactgc  | atcgataact   | tcctcttctt  | cacacgataa  | ctttttgtct | gaagcattcc | 420  |
| gttctactcc  | aagacctctg   | ccttatgatg  | ctgacccctag | atacttccgc | tcactcgtct | 480  |
| caaggcgga   | gaagggttca   | agtcattctc  | atgaggaagt  | tgaaccttta | agaagcgata | 540  |
| gcgatgcaga  | ttctgaatct   | ttcggggtag  | gagggtgcaa  | atgggcta   | aataagtcca | 600  |
| ccctctctga  | taaagattcc   | aaagaagagt  | actctagtaa  | atccagctct | aggattttga | 660  |
| gatcaaggtc  | caagtcaata   | atggccgact  | ctgaaaacat  | gtatatattg | tctgaagacg | 720  |
| aagatgtctg  | cccaacttgt   | cttgaagaat  | atacatcaga  | gaacccaaag | attgtgacaa | 780  |
| aatgttcaca  | ccatttccac   | cttagttgca  | tttatgagtg  | gatggagaga | agtgaaaact | 840  |
| gtccagctctg | cggaaaagggtg | atggaattca  | acgaaacacc  | gtgatcatcg | accattgatc | 900  |
| cgtgtcctgt  | atctgaactg   | aaaccgggga  | agatgacaag  | gcaatgcaag | gaatataatt | 960  |
| tgtaaatttg  | gctttgttgg   | tttgtgaata  | ttttcattta  | caatggtaaa | tatatgaagc | 1020 |
| agaaaaggag  | aaactgttac   | tctgcaacag  | tttaagttcc  | tgagaaattt | taacttccat | 1080 |
| gaaacaagaa  | gcaatgtttc   | ttctttaagt  | gactttttct  | catgaaatgc | ctctgttggt | 1140 |
| gtattctcta  | gtcagtcac    | aaaactctta  | catcattgtc  | gttatataaa | taaatttttc | 1200 |
| tttttttatg  | tgttc        |             |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Cys Val Ser Ser Cys Phe Arg Val Glu Asp Ile Asp Glu Tyr |  |
| 1 5 10 15                                                       |  |
| Met Asn Pro Asn Ser Ser Val Tyr Arg Asn Cys Pro Cys Ile Arg Cys |  |
| 20 25 30                                                        |  |
| Leu Ala His Asn Phe Leu Asn Leu Tyr Ile Ser Val Phe Arg Arg Gly |  |
| 35 40 45                                                        |  |
| Glu Thr Arg Ser Leu Pro Ser Ser Val Gln Ala Thr Ala Ser Ile Thr |  |

50 55 60  
Ser Ser Ser Ser His Asp Asn Phe Leu Ser Glu Ala Phe Arg Ser Thr  
65 70 75 80  
Pro Arg Pro Leu Pro Tyr Asp Ala Asp Pro Arg Tyr Phe Arg Ser Leu  
85 90 95  
Val Ser Arg Arg Glu Lys Gly Ser Ser His Ser His Glu Glu Val Glu  
100 105 110  
Pro Leu Arg Ser Asp Ser Asp Ala Asp Ser Glu Ser Phe Gly Val Gly  
115 120 125  
Gly Cys Lys Trp Ala Asn Asn Lys Ser Thr Leu Ser Asp Lys Asp Ser  
130 135 140  
Lys Glu Glu Tyr Ser Ser Lys Ser Ser Leu Arg Ile Leu Arg Ser Arg  
145 150 155 160  
Ser Lys Ser Ile Met Ala Asp Ser Glu Asn Met Tyr Ile Leu Ser Glu  
165 170 175  
Asp Glu Asp Val Cys Pro Thr Cys Leu Glu Glu Tyr Thr Ser Glu Asn  
180 185 190  
Pro Lys Ile Val Thr Lys Cys Ser His His Phe His Leu Ser Cys Ile  
195 200 205  
Tyr Glu Trp Met Glu Arg Ser Glu Asn Cys Pro Val Cys Gly Lys Val  
210 215 220  
Met Glu Phe Asn Glu Thr Pro  
225 230

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

Met Asn Pro Asn Ser Ser Val Tyr Arg Asn Cys Pro Cys Ile Arg Cys  
1 5 10 15  
Leu Ala His Asn Phe Leu Asn Leu Tyr Ile Ser Val Phe Arg Arg Gly  
20 25 30  
Glu Thr Arg Ser Leu Pro Ser Ser Val Gln Ala Thr Ala Ser Ile Thr  
35 40 45  
Ser Ser Ser Ser His Asp Asn Phe Leu Ser Glu Ala Phe Arg Ser Thr  
50 55 60  
Pro Arg Pro Leu Pro Tyr Asp Ala Asp Pro Arg Tyr Phe Arg Ser Leu  
65 70 75 80  
Val Ser Arg Arg Glu Lys Gly Ser Ser His Ser His Glu Glu Val Glu  
85 90 95  
Pro Leu Arg Ser Asp Ser Asp Ala Asp Ser Glu Ser Phe Gly Val Gly  
100 105 110  
Gly Cys Lys Trp Ala Asn Asn Lys Ser Thr Leu Ser Asp Lys Asp Ser  
115 120 125  
Lys Glu Glu Tyr Ser Ser Lys Ser Ser Leu Arg Ile Leu Arg Ser Arg  
130 135 140  
Ser Lys Ser Ile Met Ala Asp Ser Glu Asn Met Tyr Ile Leu Ser Glu  
145 150 155 160  
Asp Glu Asp Val Cys Pro Thr Cys Leu Glu Glu Tyr Thr Ser Glu Asn  
165 170 175  
Pro Lys Ile Val Thr Lys Cys Ser His His Phe His Leu Ser Cys Ile  
180 185 190  
Tyr Glu Trp Met Glu Arg Ser Glu Asn Cys Pro Val Cys Gly Lys Val  
195 200 205

Met Glu Phe Asn Glu Thr Pro  
210 215

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaacacatga  | cccctaaatc  | gagaggcttc  | gtaggagaa   | ggagaagcag  | aagagtgttg  | 60   |
| gttctcgatt  | gtcgatctca  | acaatggcgt  | agtctcccca  | aaatgcgtca  | acctcgagct  | 120  |
| tctctgccg   | cgtatgttaa  | ggatggctctg | atcattgtga  | ttggagggtg  | caggtccaag  | 180  |
| aatatcgaga  | cttggggaga  | gatttatgat  | ctaaagacca  | atacttgggg  | gcgaataactg | 240  |
| ctccaatcac  | atgatcccac  | agttcaaaat  | gcttacttga  | atcgctttaa  | acctaacttg  | 300  |
| cagacgaatg  | cttgctatgt  | agagattgac  | aaggtgtcgt  | gcctgatatt  | tttatccgat  | 360  |
| gggaagctat  | tttggcgtga  | aacaaagcaa  | ggttttgaga  | gggtgtagtgt | tatatggga   | 420  |
| gatgatgagc  | aagtgtcctc  | ttatcaactt  | gtttcggtgg  | caaacgccgc  | cggaggagga  | 480  |
| agagtgcacg  | tttgggtgga  | gtcggggtta  | aaagttctgg  | atctcttaag  | tggcactgag  | 540  |
| acttgggaat  | gttacacaaa  | tagtcggtgt  | gcagagattt  | cgtttgagag  | aagagggttta | 600  |
| agagagcttt  | ggggattcgt  | tgaatggtct  | agagagggtgt | ttaccgttga  | tggatatgac  | 660  |
| gatacttacg  | atttcttttt  | aaattctgct  | attgtgacct  | attgatcagt  | gggactttat  | 720  |
| cttacttgta  | ctgtgggaat  | tttgagtatg  | attttaatag  | ataaataaat  | gtgatttgct  | 780  |
| aacaacatta  | caacatagat  | ctaagcattc  | aaggttgTtg  | tggtgcctga  | tggcttttga  | 840  |
| tgaaggggag  | gtttttctact | ttgtatcaga  | cttttgcttg  | ctagtgaaag  | agagaataat  | 900  |
| gggcacaaca  | tttttgttac  | tccatgggaa  | agataatgta  | gagtgggtctc | aaggaaaaaa  | 960  |
| tgggtgtggag | agtggtcaag  | ggacttggat  | tgccaaacat  | tgtgtttcag  | tttgggtggtg | 1020 |
| tacaatgttg  | gatcacccct  | atggctgtaa  | agtgcagatt  | tcgcagagct  | ttccaaggga  | 1080 |
| atcatagaat  | cgtcaacgga  | gttgtgtttc  | gaaccaaagg  | atgtatatatt | cgttccactt  | 1140 |
| tcttcttgca  | ctctgctaca  | gtaacacatg  | gatttgtatg  | ctctcatggg  | agtgtaaaaa  | 1200 |
| ctcctagtga  | ttgggtgttt  | tatttgtcct  | ttggaatgct  | taaagaatga  | tat         |      |

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | His | Met | Thr | Pro | Lys | Ser | Arg | Gly | Phe | Val | Arg | Arg | Arg | Arg | Ser |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Val | Leu | Val | Leu | Asp | Cys | Arg | Ser | Gln | Gln | Trp | Arg | Ser | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Lys | Met | Arg | Gln | Pro | Arg | Ala | Ser | Pro | Ala | Ala | Tyr | Val | Lys | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Ile | Ile | Val | Ile | Gly | Gly | Cys | Arg | Ser | Lys | Asn | Ile | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Gly | Glu | Ile | Tyr | Asp | Leu | Lys | Thr | Asn | Thr | Trp | Gly | Arg | Ile | Leu |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gln | Ser | His | Asp | Pro | Thr | Val | Gln | Asn | Ala | Tyr | Leu | Asn | Arg | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Pro | Asn | Leu | Gln | Thr | Asn | Ala | Cys | Tyr | Val | Glu | Ile | Asp | Lys | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Ser Cys Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr  
115 120 125  
Lys Gln Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln  
130 135 140  
Val Ser Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly  
145 150 155 160  
Arg Val Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu  
165 170 175  
Ser Gly Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu  
180 185 190  
Ile Ser Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu  
195 200 205  
Trp Ser Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp  
210 215 220  
Phe Phe Leu Asn Ser Ala Ile Val Thr Tyr  
225 230

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1569934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser Arg Arg  
1 5 10 15  
Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu Pro Lys  
20 25 30  
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu  
35 40 45  
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly  
50 55 60  
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln  
65 70 75 80  
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro  
85 90 95  
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys  
100 105 110  
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln  
115 120 125  
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser  
130 135 140  
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val  
145 150 155 160  
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly  
165 170 175  
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser  
180 185 190  
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser  
195 200 205  
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe  
210 215 220  
Leu Asn Ser Ala Ile Val Thr Tyr  
225 230

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids

00000000-00000000

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..200  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569935  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu  
1 5 10 15  
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly  
20 25 30  
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln  
35 40 45  
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro  
50 55 60  
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys  
65 70 75 80  
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln  
85 90 95  
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser  
100 105 110  
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val  
115 120 125  
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly  
130 135 140  
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser  
145 150 155 160  
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser  
165 170 175  
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe  
180 185 190  
Leu Asn Ser Ala Ile Val Thr Tyr  
195 200

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 715 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..715  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

aatggattat ctaggaatcg acttgagctg cgcaatcgGa tctctcCgta acggtgagtt 60  
TccgGcgaaa gattgtctTc tTcctctcat tTcaaAgcta ctcggtTact tcctcgtcgc 120  
tgcttcaatg accgttaagc ttccctcagat aatgaaaatc gtggacaaca agagtgtaaa 180  
aggcctaagt gttgtagcat ttgagcttga agtgattggt Tacacaatct cacttgctta 240  
ctgtcttaac aaagaccttc ctttttcagc ttttggtgaa ttagcttttc ttttgatcca 300  
agctttaatc ttggtggcct gtatctacta tttctcaca cctctctctg taacaacttg 360  
ggtcaaagca attctttatt ttgctatagc accaactgtg tttgctgaat ccctcagatt 420  
tggaagaact tcagaaacaa aagcactgga caacttagtt tcttgacttg tctcatgaac 480  
tttggtgag ctttggcgag agttttcacc agcattcaag agaaggctcc acttagcatg 540  
cttttggtgta ttgttctttc tatcttcacc aatTggaatc attatgagtc agatTctttt 600  
gtatagaagc aaagGaaacg aagataagct agtgaaaAgt aaaaAgattT catgatatat 660  
tgtaaaagtg attcaaacga tgttgactt cattgaataa agtaaagctt ttttc

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..154
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569943
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

Met Asp Tyr Leu Gly Ile Asp Leu Ser Cys Ala Ile Gly Ser Leu Arg  
1 5 10 15  
Asn Gly Glu Phe Pro Ala Lys Asp Cys Leu Leu Pro Leu Ile Ser Lys  
20 25 30  
Leu Leu Gly Tyr Phe Leu Val Ala Ala Ser Met Thr Val Lys Leu Pro  
35 40 45  
Gln Ile Met Lys Ile Val Asp Asn Lys Ser Val Lys Gly Leu Ser Val  
50 55 60  
Val Ala Phe Glu Leu Glu Val Ile Gly Tyr Thr Ile Ser Leu Ala Tyr  
65 70 75 80  
Cys Leu Asn Lys Asp Leu Pro Phe Ser Ala Phe Gly Glu Leu Ala Phe  
85 90 95  
Leu Leu Ile Gln Ala Leu Ile Leu Val Ala Cys Ile Tyr Tyr Phe Ser  
100 105 110  
Gln Pro Leu Ser Val Thr Thr Trp Val Lys Ala Ile Leu Tyr Phe Ala  
115 120 125  
Ile Ala Pro Thr Val Phe Ala Glu Ser Leu Arg Phe Gly Arg Thr Ser  
130 135 140  
Glu Thr Lys Ala Leu Asp Asn Leu Val Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:1424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..112
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1569945
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

Met Thr Val Lys Leu Pro Gln Ile Met Lys Ile Val Asp Asn Lys Ser  
1 5 10 15  
Val Lys Gly Leu Ser Val Val Ala Phe Glu Leu Glu Val Ile Gly Tyr  
20 25 30  
Thr Ile Ser Leu Ala Tyr Cys Leu Asn Lys Asp Leu Pro Phe Ser Ala  
35 40 45  
Phe Gly Glu Leu Ala Phe Leu Leu Ile Gln Ala Leu Ile Leu Val Ala  
50 55 60  
Cys Ile Tyr Tyr Phe Ser Gln Pro Leu Ser Val Thr Thr Trp Val Lys  
65 70 75 80  
Ala Ile Leu Tyr Phe Ala Ile Ala Pro Thr Val Phe Ala Glu Ser Leu  
85 90 95  
Arg Phe Gly Arg Thr Ser Glu Thr Lys Ala Leu Asp Asn Leu Val Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1425:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 496 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..496  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| atgacgaaag  | ctctctggct | tctgttgctc  | tctcagtcctg | gttagatctt | cgtcttctca | 60  |
| cgtatcatat  | ggatagtgac | attgtttcca  | gcgtagatcg  | atctcagaca | gcaatgcctg | 120 |
| atgcttttagc | attcaagagt | atcaatgac   | ctatcaagaa  | ccagatcaat | agttgtgctg | 180 |
| caatctgtgt  | taagcaagat | gatccatgcc  | atttcttgcg  | tgtcctgtat | gagtccttga | 240 |
| taacaggagg  | gttagctggg | gttggtggg   | aagctgctct  | gtatccaatt | gatacaatca | 300 |
| aaactcgagt  | acaggtagca | cgggatggg   | gaaagataat  | atggaaggga | ctatactctg | 360 |
| gtcttggtgc  | aaatcttgct | gggtgtcttac | ctgcttcggc  | tctatttttt | gggttatatg | 420 |
| aaccaacca   | acagaagctg | Gcactaagat  | tttctggtaa  | aaccttagc  | agcttctgtt | 480 |
| tggttggttc  | atatac     |             |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 164 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..164  
(D) OTHER INFORMATION: / Ceres Seq. ID 1569947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Glu | Ser | Ser | Leu | Ala | Ser | Val | Ala | Leu | Ser | Val | Trp | Leu | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Leu | Leu | Thr | Tyr | His | Met | Asp | Ser | Asp | Ile | Val | Ser | Ser | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Ser | Gln | Thr | Ala | Met | Pro | Asp | Ala | Leu | Ala | Phe | Lys | Ser | Ile | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | Pro | Ile | Lys | Asn | Gln | Ile | Asn | Ser | Cys | Ala | Ala | Ile | Cys | Val | Lys |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Gln | Asp | Asp | Pro | Cys | His | Phe | Leu | Arg | Val | Leu | Tyr | Glu | Ser | Leu | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Thr | Gly | Gly | Leu | Ala | Gly | Val | Val | Val | Glu | Ala | Ala | Leu | Tyr | Pro | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Thr | Ile | Lys | Thr | Arg | Val | Gln | Val | Ala | Arg | Asp | Gly | Gly | Lys | Ile |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Trp | Lys | Gly | Leu | Tyr | Ser | Gly | Leu | Gly | Ala | Asn | Leu | Val | Gly | Val |
|     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |     |
| Leu | Pro | Ala | Ser | Ala | Leu | Phe | Gly | Val | Tyr | Glu | Pro | Thr | Lys | Gln |     |
|     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| Lys | Leu | Ala | Leu | Arg | Phe | Ser | Gly | Lys | Thr | Phe | Ser | Ser | Phe | Cys | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Val | Gly | Ser | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide



(D) OTHER INFORMATION: / Ceres Seq. ID 1569948

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Asp | Ile | Val | Ser | Ser | Val | Asp | Arg | Ser | Gln | Thr | Ala | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Asp | Ala | Leu | Ala | Phe | Lys | Ser | Ile | Asn | Asp | Pro | Ile | Lys | Asn | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asn | Ser | Cys | Ala | Ala | Ile | Cys | Val | Lys | Gln | Asp | Asp | Pro | Cys | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Arg | Val | Leu | Tyr | Glu | Ser | Leu | Ile | Thr | Gly | Gly | Leu | Ala | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Val | Val | Glu | Ala | Ala | Leu | Tyr | Pro | Ile | Asp | Thr | Ile | Lys | Thr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Gln | Val | Ala | Arg | Asp | Gly | Gly | Lys | Ile | Ile | Trp | Lys | Gly | Leu | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Leu | Gly | Ala | Asn | Leu | Val | Gly | Val | Leu | Pro | Ala | Ser | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Phe | Gly | Val | Tyr | Glu | Pro | Thr | Lys | Gln | Lys | Leu | Ala | Leu | Arg | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Lys | Thr | Phe | Ser | Ser | Phe | Cys | Leu | Val | Gly | Ser | Tyr |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1569949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asp | Ala | Leu | Ala | Phe | Lys | Ser | Ile | Asn | Asp | Pro | Ile | Lys | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ile | Asn | Ser | Cys | Ala | Ala | Ile | Cys | Val | Lys | Gln | Asp | Asp | Pro | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Phe | Leu | Arg | Val | Leu | Tyr | Glu | Ser | Leu | Ile | Thr | Gly | Gly | Leu | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Val | Val | Val | Glu | Ala | Ala | Leu | Tyr | Pro | Ile | Asp | Thr | Ile | Lys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Val | Gln | Val | Ala | Arg | Asp | Gly | Gly | Lys | Ile | Ile | Trp | Lys | Gly | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Ser | Gly | Leu | Gly | Ala | Asn | Leu | Val | Gly | Val | Leu | Pro | Ala | Ser | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Phe | Phe | Gly | Val | Tyr | Glu | Pro | Thr | Lys | Gln | Lys | Leu | Ala | Leu | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Gly | Lys | Thr | Phe | Ser | Ser | Phe | Cys | Leu | Val | Gly | Ser | Tyr |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1368 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1368

(D) OTHER INFORMATION: / Ceres Seq. ID 1569950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

aactgataaa gtgataacgg agttgggttg aacgtgaaaC gcttataaaa ataaaccggt 60  
ttaatttcac cggtttacct tccgccgtag atatcagccg caatgtacat tctcgacacc 120  
ggagctcgat tctccgcgct cagattctca ccggtattca atcctcctcc aacatctctc 180  
cgtagacgat acttcacgt aagagctaata cttccattcc caaagcatca agctaagtat 240  
cataaagagc ttgaggctgc cattgatgct gttgatcgag cttgtcgtct ctgtgttgat 300  
gtcaaaagat ctcttttttc ttctaaagag aagattgttg agaagaatga tcaaactcca 360  
gttacaattg cagatttttg agttcaagct ttagtcagct tggagctttc gaaattgttt 420  
ccttcaatac cattagtggc tgaggaagac tctcattttg tgcgtgctaa taaccttgta 480  
agctctgtgg taagtgaagt caaatcaaaa gcaagcattg gagacaatca cttgtctgat 540  
gctgatgtac ttgaagcaat tgatagaggt ggcaaagatg cttacacgtt ttgcaacaaa 600  
ccagctactt attgggtttt ggatccaatt gatggcacca ggggatttct taaaggagat 660  
gaggctttat atgtggttag attggccctt gttgtagata atgaaattgt gctaggagtc 720  
atgggttgct caaactggcc aggagattct tcagatggat ctactggaac cctaattgctc 780  
tcgcatatag gctgtggaac gtggaccaag aagttacaaa atgtctctgg caatgtagcc 840  
ggtgattgga taaggtgttt cgttgatgct tgtgttttaa tgaacaaagc aagattttgt 900  
atacaagaaa gccaaacctg ggaatcactt cctctctctg gtttcttcga cgcaagtact 960  
gtttcagagg acttaaaaca taaagagatt cttcttttgc ccacatgttg tggaagtttg 1020  
tgcaagtatc tgatggtagc ttctggcaga gcatcagttt ttcttctccg agccaaaact 1080  
cagagaacaa taaagtcgtg ggatcatgct gttgggatca tatgtgtaca tgaagctgga 1140  
ggaaaggtaa cagattggga aggagatgaa ataaatttg aggaagatca atcagaaagg 1200  
aggctcattt ttccggcggg cgggtgttga gtaagcaacg gaagtttaca taatcagatt 1260  
cttgagatga tctcttctgc ttcaccaact ctttgattta tgacactact actctctata 1320  
cacttgttaa tgtttaccgt tactatttat ttatcataat ccttttct

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1569951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

Met Tyr Ile Leu Asp Thr Gly Ala Arg Phe Ser Ala Val Arg Phe Ser  
1 5 10 15  
Pro Val Phe Asn Pro Pro Pro Thr Ser Leu Arg Arg Arg Tyr Phe Ile  
20 25 30  
Val Arg Ala Asn Leu Pro Phe Pro Lys His Gln Ala Lys Tyr His Lys  
35 40 45  
Glu Leu Glu Val Ala Ile Asp Ala Val Asp Arg Ala Cys Arg Leu Cys  
50 55 60  
Val Asp Val Lys Arg Ser Leu Phe Ser Ser Lys Glu Lys Ile Val Glu  
65 70 75 80  
Lys Asn Asp Gln Thr Pro Val Thr Ile Ala Asp Phe Gly Val Gln Ala  
85 90 95  
Leu Val Ser Leu Glu Leu Ser Lys Leu Phe Pro Ser Ile Pro Leu Val  
100 105 110  
Ala Glu Glu Asp Ser His Phe Val Arg Ala Asn Asn Leu Val Ser Ser  
115 120 125  
Val Val Ser Glu Val Lys Ser Lys Ala Ser Ile Gly Asp Asn His Leu  
130 135 140  
Ser Asp Ala Asp Val Leu Glu Ala Ile Asp Arg Gly Gly Lys Asp Ala  
145 150 155 160  
Tyr Thr Phe Cys Asn Lys Pro Ala Thr Tyr Trp Val Leu Asp Pro Ile  
165 170 175  
Asp Gly Thr Arg Gly Phe Leu Lys Gly Asp Glu Ala Leu Tyr Val Val  
180 185 190  
Gly Leu Ala Leu Val Val Asp Asn Glu Ile Val Leu Gly Val Met Gly  
195 200 205

Cys Pro Asn Trp Pro Gly Asp Ser Ser Asp Gly Ser Thr Gly Thr Leu  
210 215 220  
Met Leu Ser His Ile Gly Cys Gly Thr Trp Thr Lys Lys Leu Gln Asn  
225 230 235 240  
Val Ser Gly Asn Val Ala Gly Asp Trp Ile Arg Cys Phe Val Asp Ala  
245 250 255  
Cys Val Leu Met Asn Lys Ala Arg Phe Cys Ile Gln Glu Ser Gln Thr  
260 265 270  
Trp Glu Ser Leu Pro Leu Ser Gly Phe Phe Asp Ala Ser Thr Val Ser  
275 280 285  
Glu Asp Leu Lys His Lys Glu Ile Leu Leu Leu Pro Thr Cys Cys Gly  
290 295 300  
Ser Leu Cys Lys Tyr Leu Met Val Ala Ser Gly Arg Ala Ser Val Phe  
305 310 315 320  
Leu Leu Arg Ala Lys Thr Gln Arg Thr Ile Lys Ser Trp Asp His Ala  
325 330 335  
Val Gly Ile Ile Cys Val His Glu Ala Gly Gly Lys Val Thr Asp Trp  
340 345 350  
Glu Gly Asp Glu Ile Asn Leu Glu Glu Asp Gln Ser Glu Arg Arg Leu  
355 360 365  
Ile Phe Pro Ala Gly Gly Val Val Val Ser Asn Gly Ser Leu His Asn  
370 375 380  
Gln Ile Leu Glu Met Ile Ser Ser Ala Ser Pro Thr Leu  
385 390 395

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| acgtctgacg  | gaagtcggtt  | cacttccacc | tgtgccgttg | ggatgttctg | tcgtcacagt | 60  |
| cggtaacag   | atgtatgtaa  | ttggtggact | cctagacata | agacgtttac | aggtaatgac | 120 |
| tctcatcgat  | tgcagaactc  | acaaatttcg | ctcgcttcg  | agtatgaaaa | gaggtcgttg | 180 |
| caaagcagcc  | gcgaggttg   | tcgacggaaa | gatttacgta | atcggagggt | tcaggatgag | 240 |
| aaaaccggat  | gctgaatgga  | ttgaagtgtt | tgatctaaag | acacagattt | gggaatcttt | 300 |
| gcctgggtccg | taccctaaaa  | ctagttcgtg | ttgcgagttg | gacgcttatg | tggtgatgga | 360 |
| agagaagtta  | tacatgttgg  | gttctaaatt | ttgtttggtt | tacgaaccaa | aaagaaacgg | 420 |
| tgaatggGac  | gcatccgtcg  | gagcaacccc | attaaaagat | ttgtgggaca | agacttgttg | 480 |
| tgtggtagat  | gatatgttgt  | atacgactga | tcctcggcgt | actcttggac | atccaatagt | 540 |
| cgtgtatcat  | ccaaaggaca  | agacttggag | acctgtgaaa | ggtgaatcct | tggggagttt | 600 |
| gcctagttat  | ttcttttcta  | agtctgaaaa | tggcgaattt | tggtggaaag | ttggtgattt | 660 |
| tgggcagaaa  | caagagctat  | gttactggtg | attgcattgg | agaaaaagtt | atttgggtcg | 720 |
| taatgatcga  | gttggaaaaa  | cgtgaaggag | gtgagatttg | ggggaagggt | gaatcactcg | 780 |
| actgtgtgtt  | tggatacata  | gacatttgtt | cggttgggct | ttgtcgatct | ctgaccattt | 840 |
| gatgatacat  | gggatgggtat | cttgcaggta | cgttgatgtg | aatgagtatg | acttttttgt | 900 |
| tgttcatgcc  | ttttcttttag | cctcaagact | tacttgtctt | tttcatgatc | tttattactc | 960 |
| accttaacct  | ttgtgc      |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1569973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

Arg Leu Thr Glu Val Gly Ser Leu Pro Pro Val Pro Trp Gly Cys Ser  
1 5 10 15  
Val Val Thr Val Gly Gln Glu Met Tyr Val Ile Gly Gly Leu Leu Asp  
20 25 30  
Ile Arg Arg Leu Gln Val Met Thr Leu Ile Asp Cys Arg Thr His Lys  
35 40 45  
Phe Arg Ser Leu Pro Ser Met Lys Arg Gly Arg Cys Lys Ala Ala Ala  
50 55 60  
Gly Val Val Asp Gly Lys Ile Tyr Val Ile Gly Gly Phe Arg Met Arg  
65 70 75 80  
Lys Pro Asp Ala Glu Trp Ile Glu Val Phe Asp Leu Lys Thr Gln Ile  
85 90 95  
Trp Glu Ser Leu Pro Gly Pro Tyr Pro Lys Thr Ser Ser Cys Cys Glu  
100 105 110  
Leu Asp Ala Tyr Val Val Met Glu Lys Leu Tyr Met Leu Gly Ser  
115 120 125  
Lys Phe Cys Leu Val Tyr Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala  
130 135 140  
Ser Val Gly Ala Thr Pro Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys  
145 150 155 160  
Val Val Asp Asp Met Leu Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly  
165 170 175  
His Pro Ile Val Val Tyr His Pro Lys Asp Lys Thr Trp Arg Pro Val  
180 185 190  
Lys Gly Glu Ser Leu Gly Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser  
195 200 205  
Glu Asn Gly Glu Phe Trp Trp Lys Val Gly Asp Phe Gly Gln Lys Gln  
210 215 220  
Glu Leu Cys Tyr Trp  
225

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1569974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met Tyr Val Ile Gly Leu Leu Asp Ile Arg Arg Leu Gln Val Met  
1 5 10 15  
Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser Met  
20 25 30  
Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys Ile  
35 40 45  
Tyr Val Ile Gly Gly Phe Arg Met Arg Lys Pro Asp Ala Glu Trp Ile  
50 55 60  
Glu Val Phe Asp Leu Lys Thr Gln Ile Trp Glu Ser Leu Pro Gly Pro  
65 70 75 80  
Tyr Pro Lys Thr Ser Ser Cys Cys Glu Leu Asp Ala Tyr Val Val Met  
85 90 95  
Glu Glu Lys Leu Tyr Met Leu Gly Ser Lys Phe Cys Leu Val Tyr Glu  
100 105 110  
Pro Lys Arg Asn Gly Glu Trp Asp Ala Ser Val Gly Ala Thr Pro Leu

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Lys Asp Leu Trp Asp Lys Thr Cys Cys Val Val Asp Asp Met Leu Tyr |     |     |
| 130                                                             | 135 | 140 |
| Thr Thr Asp Pro Arg Arg Thr Leu Gly His Pro Ile Val Val Tyr His |     |     |
| 145                                                             | 150 | 155 |
| Pro Lys Asp Lys Thr Trp Arg Pro Val Lys Gly Glu Ser Leu Gly Ser |     |     |
| 165                                                             | 170 | 175 |
| Leu Pro Ser Tyr Phe Phe Ser Lys Ser Glu Asn Gly Glu Phe Trp Trp |     |     |
| 180                                                             | 185 | 190 |
| Lys Val Gly Asp Phe Gly Gln Lys Gln Glu Leu Cys Tyr Trp         |     |     |
| 195                                                             | 200 | 205 |

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1569975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser |     |     |
| 1                                                               | 5   | 10  |
| Met Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys |     |     |
| 20                                                              | 25  | 30  |
| Ile Tyr Val Ile Gly Gly Phe Arg Met Arg Lys Pro Asp Ala Glu Trp |     |     |
| 35                                                              | 40  | 45  |
| Ile Glu Val Phe Asp Leu Lys Thr Gln Ile Trp Glu Ser Leu Pro Gly |     |     |
| 50                                                              | 55  | 60  |
| Pro Tyr Pro Lys Thr Ser Ser Cys Cys Glu Leu Asp Ala Tyr Val Val |     |     |
| 65                                                              | 70  | 75  |
| Met Glu Glu Lys Leu Tyr Met Leu Gly Ser Lys Phe Cys Leu Val Tyr |     |     |
| 85                                                              | 90  | 95  |
| Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala Ser Val Gly Ala Thr Pro |     |     |
| 100                                                             | 105 | 110 |
| Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys Val Val Asp Asp Met Leu |     |     |
| 115                                                             | 120 | 125 |
| Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly His Pro Ile Val Val Tyr |     |     |
| 130                                                             | 135 | 140 |
| His Pro Lys Asp Lys Thr Trp Arg Pro Val Lys Gly Glu Ser Leu Gly |     |     |
| 145                                                             | 150 | 155 |
| Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser Glu Asn Gly Glu Phe Trp |     |     |
| 165                                                             | 170 | 175 |
| Trp Lys Val Gly Asp Phe Gly Gln Lys Gln Glu Leu Cys Tyr Trp     |     |     |
| 180                                                             | 185 | 190 |

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1663

(D) OTHER INFORMATION: / Ceres Seq. ID 1569986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aagcaaaaat gctacaaatt aaaaagtgtc tccaacatgt gcatattcac acacaagttg | 60  |
| gtgtcaacgc tcagacaaga aaggcgtgtg ttcattgttg aatcttccca tttcctcatc | 120 |

caaattccga cataactatc ctagccgccg tttgtttctcc acattacaaa accctcagca 180  
gcttcaaaac tcttccgatc tctccctcac gctcgcaatt ctctcgtctc cattttaata 240  
gtttttcttc tcggaatcac aaatcttcgg cttcttgttc cttggcgtgt gtgtgtgttg 300  
ttgaatggct cttgttcagc ggattccaat ttctctctcc agtattcgga attggcaaca 360  
agcgaggacc aatttgactc ctatttggtg tttacattac aatactgcat cttcttcttc 420  
ttcacccctt acagagaagc actctgtgga gagataccaa agggatcaat ggctgtacaa 480  
agcggttgaa ccaacgccac catcgactcc atctccatcg ccatttgaag atgaagtctt 540  
tgtaggggaa aacgacattg catcgagct gcctgagctg aagaagcttt tggcagtgct 600  
gaaagagaag agagttaaag gatgcaaagg tgggtgattgt ggaccaggag atgtgtatct 660  
tgtagggaca gggccaggag atcctgagct tttgactctt aaagctgtca gagttattca 720  
aagtgccgat cttttgcttt acgacaggct tgtctccaat gatgtcttgg agttggttg 780  
tctgatgct agacttcttt atgtcggcaa aactgctggt tatcatagca gaactcagga 840  
agagattcat gaactactcc taaattttgc tgaagctggt gccactgttg tcaggcttaa 900  
aggtggagat cctctggtct ttggacgggg cggcgaagaa atggactttc tgcaacagca 960  
agggattcga gttcaagtta taccagggat aactgcgggc tcggggatag cagcagagtt 1020  
ggggattcca ctaacacatc gaggtgttgc aactagtgtg aggtttctca ctggtcattc 1080  
aaggaaagga gggacagacc ctctgtttgt tgcagagaat gcagctgacc cggatacaac 1140  
acttgctggt tatatgggtt tgggaacttt accttctctt gcacaaaaac taatggacca 1200  
tggtctccct tctgatacac cagctgttgc ggttgaacgt ggaaccactc ctctacagcg 1260  
tacagttttt gctgagctta aagattttgc aactgagatt cagtcagctg gattggtgtc 1320  
accaacactc atcatcatag ggaaagtcgt tgagctctca cttttatggc cacattgcac 1380  
gaaagaatcc tcctgccttg tagagaccog gtagatatct cactcttatt ttacgggcgt 1440  
gtggcttcca tcgacattac ggtgaagtta taggagctat ggagctatga aggttgagac 1500  
ttgagagatg taataaacia aaaggaaagc tgatagtctt ttatgacgtg tccttcaatt 1560  
gttttgggac aatggtaatg gcaatgttaa tgtaataaac aagttAtcaa tcagtgccac 1620  
tgtgactaat ttttccacca caagatgatg tctttaaaac ttt

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1569987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

Met Ala Leu Val Gln Arg Ile Pro Ile Ser Ser Ser Ile Arg Asn  
1 5 10 15  
Trp Gln Gln Ala Arg Thr Asn Leu Thr Pro Ile Cys Cys Leu His Tyr  
20 25 30  
Asn Thr Ala Ser Ser Ser Ser Pro Phe Thr Glu Lys His Ser Val  
35 40 45  
Glu Arg Tyr Gln Arg Asp Gln Trp Leu Tyr Lys Ala Val Glu Pro Thr  
50 55 60  
Pro Pro Ser Thr Pro Ser Ser Pro Phe Glu Asp Glu Val Phe Val  
65 70 75 80  
Arg Glu Asn Asp Ile Ala Ser Gln Leu Pro Glu Leu Lys Lys Leu Leu  
85 90 95  
Ala Val Leu Lys Glu Lys Arg Val Lys Gly Cys Lys Gly Gly Asp Cys  
100 105 110  
Gly Pro Gly Asp Val Tyr Leu Val Gly Thr Gly Pro Gly Asp Pro Glu  
115 120 125  
Leu Leu Thr Leu Lys Ala Val Arg Val Ile Gln Ser Ala Asp Leu Leu  
130 135 140  
Leu Tyr Asp Arg Leu Val Ser Asn Asp Val Leu Glu Leu Val Ala Pro  
145 150 155 160  
Asp Ala Arg Leu Leu Tyr Val Gly Lys Thr Ala Gly Tyr His Ser Arg  
165 170 175  
Thr Gln Glu Glu Ile His Glu Leu Leu Leu Asn Phe Ala Glu Ala Gly

180 185 190  
Ala Thr Val Val Arg Leu Lys Gly Gly Asp Pro Leu Val Phe Gly Arg  
195 200 205  
Gly Gly Glu Glu Met Asp Phe Leu Gln Gln Gln Gly Ile Arg Val Gln  
210 215 220  
Val Ile Pro Gly Ile Thr Ala Ala Ser Gly Ile Ala Ala Glu Leu Gly  
225 230 235 240  
Ile Pro Leu Thr His Arg Gly Val Ala Thr Ser Val Arg Phe Leu Thr  
245 250 255  
Gly His Ser Arg Lys Gly Gly Thr Asp Pro Leu Phe Val Ala Glu Asn  
260 265 270  
Ala Ala Asp Pro Asp Thr Thr Leu Val Val Tyr Met Gly Leu Gly Thr  
275 280 285  
Leu Pro Ser Leu Ala Gln Lys Leu Met Asp His Gly Leu Pro Ser Asp  
290 295 300  
Thr Pro Ala Val Ala Val Glu Arg Gly Thr Thr Pro Leu Gln Arg Thr  
305 310 315 320  
Val Phe Ala Glu Leu Lys Asp Phe Ala Thr Glu Ile Gln Ser Ala Gly  
325 330 335  
Leu Val Ser Pro Thr Leu Ile Ile Ile Gly Lys Val Val Glu Leu Ser  
340 345 350  
Pro Leu Trp Pro His Cys Thr Lys Glu Ser Ser Cys Leu Val Glu Thr  
355 360 365  
Arg

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acgaatcaaaa | attcaatttaa | aaaaaacctt  | tcgattttctc | tcattccaatc | gaatcgaaaa  | 60   |
| tcttggttatc | tctttctctc  | taactctact  | gcactcagaa  | tctctctgta  | tagaaaaacc  | 120  |
| ctaagttagt  | tgtgatgttg  | cgagcttttag | cacggcctct  | cgaacggtgt  | ttgggaagca  | 180  |
| gagctagtgg  | tgatggttta  | ctctggcaat  | cggaattgag  | acctcacgct  | ggcggtgatt  | 240  |
| attcgatcgc  | ggtggttcaa  | gccaatcca   | ggcttgaaga  | tcagagtcag  | gttttcacat  | 300  |
| cttcttctgc  | tacttacgtc  | ggtgtatacg  | atggtcattg  | tggaacctgaa | gcttctagat  | 360  |
| tcgttaacag  | acatctcttt  | cottatatgc  | acaaatttgc  | aagagaacat  | ggcggattat  | 420  |
| ctgtagatgt  | tatcaaaaaag | gcattcaaa   | aaacagaaga  | agagttttgt  | ggtatggtta  | 480  |
| aacgatccCt  | tcccatgaaa  | ccgcaaattg  | ctactgtagg  | atcttgctgt  | cttggttggtg | 540  |
| caatctctaa  | tgacacactg  | tatgttgcca  | atcttgggga  | ctcgagagcc  | gttcttgga   | 600  |
| gcgttggttc  | aggggttgat  | agtaataaag  | gtgcgtagc   | tgaacggtta  | tctactgatc  | 660  |
| ataatgttgc  | tgttgaagaa  | gtgagaaagg  | agggttaaggc | acttaacctt  | gatgactcac  | 720  |
| aaatcgctct  | atacacacgt  | ggagtttggc  | ggattaaagg  | cattattcag  | gtatcgagat  | 780  |
| caattgggga  | tgtatacttg  | aaaaaacccg  | agtattacag  | ggacccgatt  | ttccagcgac  | 840  |
| atggaaatcc  | cattcctttg  | aggagacccg  | cgatgacagc  | cgaacctcc   | attatagtaa  | 900  |
| ggaagcttaa  | gccacaggac  | ttgtttctga  | tatttgcatt  | agatggtctc  | tggaacatc   | 960  |
| ttagtgatga  | aacagccgta  | gaaatcgccc  | tcaaacaccc  | aagaactggt  | attgcacgaa  | 1020 |
| gacttgtaag  | agctgctctg  | gaagaagcgg  | caaagaagag  | agaatgaga   | tatggagata  | 1080 |
| taaagaaaa   | agccaaagga  | attcgacgac  | atttccatga  | cgacataagc  | gttattgtag  | 1140 |
| tttatctaga  | tcaaaacaaa  | accagttcat  | cgaatagtaa  | attggtgaag  | caaggaggta  | 1200 |
| tcaccgctcc  | accggatact  | tactcattac  | actctgatga  | agcagagcaa  | cgacggttac  | 1260 |
| tcaatgtgtt  | atactgactg  | tttgattatg  | gtaaaatggc  | tgcttgggaa  | agatccgaat  | 1320 |
| aggagaaaa   | cttggtttaca | tatttgttta  | tttgtttttc  | tacgaagaac  | tgtttttttt  | 1380 |
| ttttttttca  | atattggagt  | tggatttgt   |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1570001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Ala | Leu | Ala | Arg | Pro | Leu | Glu | Arg | Cys | Leu | Gly | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Gly | Asp | Gly | Leu | Leu | Trp | Gln | Ser | Glu | Leu | Arg | Pro | His | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Asp | Tyr | Ser | Ile | Ala | Val | Val | Gln | Ala | Asn | Ser | Arg | Leu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Ser | Gln | Val | Phe | Thr | Ser | Ser | Ser | Ala | Thr | Tyr | Val | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Asp | Gly | His | Gly | Gly | Pro | Glu | Ala | Ser | Arg | Phe | Val | Asn | Arg | His |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Phe | Pro | Tyr | Met | His | Lys | Phe | Ala | Arg | Glu | His | Gly | Gly | Leu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Asp | Val | Ile | Lys | Lys | Ala | Phe | Lys | Glu | Thr | Glu | Glu | Glu | Phe | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Met | Val | Lys | Arg | Ser | Leu | Pro | Met | Lys | Pro | Gln | Met | Ala | Thr | Val |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Cys | Cys | Leu | Val | Gly | Ala | Ile | Ser | Asn | Asp | Thr | Leu | Tyr | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Asn | Leu | Gly | Asp | Ser | Arg | Ala | Val | Leu | Gly | Ser | Val | Val | Ser | Gly |
|     | 145 |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Asp | Ser | Asn | Lys | Gly | Ala | Val | Ala | Glu | Arg | Leu | Ser | Thr | Asp | His |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Val | Ala | Val | Glu | Glu | Val | Arg | Lys | Glu | Val | Lys | Ala | Leu | Asn | Pro |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Asp | Ser | Gln | Ile | Val | Leu | Tyr | Thr | Arg | Gly | Val | Trp | Arg | Ile | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gly | Ile | Ile | Gln | Val | Ser | Arg | Ser | Ile | Gly | Asp | Val | Tyr | Leu | Lys | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Glu | Tyr | Tyr | Arg | Asp | Pro | Ile | Phe | Gln | Arg | His | Gly | Asn | Pro | Ile |
|     | 225 |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Leu | Arg | Arg | Pro | Ala | Met | Thr | Ala | Glu | Pro | Ser | Ile | Ile | Val | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Leu | Lys | Pro | Gln | Asp | Leu | Phe | Leu | Ile | Phe | Ala | Ser | Asp | Gly | Leu |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |     |
| Trp | Glu | His | Leu | Ser | Asp | Glu | Thr | Ala | Val | Glu | Ile | Val | Leu | Lys | His |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Pro | Arg | Thr | Gly | Ile | Ala | Arg | Arg | Leu | Val | Arg | Ala | Ala | Leu | Glu | Glu |
|     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ala | Ala | Lys | Lys | Arg | Glu | Met | Arg | Tyr | Gly | Asp | Ile | Lys | Lys | Ile | Ala |
|     | 305 |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Lys | Gly | Ile | Arg | Arg | His | Phe | His | Asp | Asp | Ile | Ser | Val | Ile | Val | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Tyr | Leu | Asp | Gln | Asn | Lys | Thr | Ser | Ser | Ser | Asn | Ser | Lys | Leu | Val | Lys |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Gln | Gly | Gly | Ile | Thr | Ala | Pro | Pro | Asp | Ile | Tyr | Ser | Leu | His | Ser | Asp |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Glu | Ala | Glu | Gln | Arg | Arg | Leu | Leu | Asn | Val | Leu | Tyr |     |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1439:



(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 296 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..296  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570002  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Lys | Phe | Ala | Arg | Glu | His | Gly | Gly | Leu | Ser | Val | Asp | Val | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Lys | Ala | Phe | Lys | Glu | Thr | Glu | Glu | Glu | Phe | Cys | Gly | Met | Val | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Arg | Ser | Leu | Pro | Met | Lys | Pro | Gln | Met | Ala | Thr | Val | Gly | Ser | Cys | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Gly | Ala | Ile | Ser | Asn | Asp | Thr | Leu | Tyr | Val | Ala | Asn | Leu | Gly |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Arg | Ala | Val | Leu | Gly | Ser | Val | Val | Ser | Gly | Val | Asp | Ser | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Gly | Ala | Val | Ala | Glu | Arg | Leu | Ser | Thr | Asp | His | Asn | Val | Ala | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Glu | Val | Arg | Lys | Glu | Val | Lys | Ala | Leu | Asn | Pro | Asp | Asp | Ser | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Val | Leu | Tyr | Thr | Arg | Gly | Val | Trp | Arg | Ile | Lys | Gly | Ile | Ile | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ser | Arg | Ser | Ile | Gly | Asp | Val | Tyr | Leu | Lys | Lys | Pro | Glu | Tyr | Tyr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Asp | Pro | Ile | Phe | Gln | Arg | His | Gly | Asn | Pro | Ile | Pro | Leu | Arg | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Ala | Met | Thr | Ala | Glu | Pro | Ser | Ile | Ile | Val | Arg | Lys | Leu | Lys | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asp | Leu | Phe | Leu | Ile | Phe | Ala | Ser | Asp | Gly | Leu | Trp | Glu | His | Leu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Asp | Glu | Thr | Ala | Val | Glu | Ile | Val | Leu | Lys | His | Pro | Arg | Thr | Gly |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Ala | Arg | Arg | Leu | Val | Arg | Ala | Ala | Leu | Glu | Glu | Ala | Ala | Lys | Lys |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Glu | Met | Arg | Tyr | Gly | Asp | Ile | Lys | Lys | Ile | Ala | Lys | Gly | Ile | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | His | Phe | His | Asp | Asp | Ile | Ser | Val | Ile | Val | Val | Tyr | Leu | Asp | Gln |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Lys | Thr | Ser | Ser | Ser | Asn | Ser | Lys | Leu | Val | Lys | Gln | Gly | Gly | Ile |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Ala | Pro | Pro | Asp | Ile | Tyr | Ser | Leu | His | Ser | Asp | Glu | Ala | Glu | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Arg | Arg | Leu | Leu | Asn | Val | Leu | Tyr |     |     |     |     |     |     |     |     |
|     |     | 290 |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 267 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..267  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570003  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly  
1 5 10 15  
Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val Ala  
20 25 30  
Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly Val  
35 40 45  
Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His Asn  
50 55 60  
Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp  
65 70 75 80  
Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys Gly  
85 90 95  
Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys Pro  
100 105 110  
Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile Pro  
115 120 125  
Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg Lys  
130 135 140  
Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu Trp  
145 150 155 160  
Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His Pro  
165 170 175  
Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu Ala  
180 185 190  
Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala Lys  
195 200 205  
Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val Tyr  
210 215 220  
Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys Gln  
225 230 235 240  
Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp Glu  
245 250 255  
Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr  
260 265

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1649
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aattttctct | gaaaaccctt  | aaatctccgg | atttcgattc | ccgaggctcg  | aaaaaacctt | 60  |
| aaatctcttc | tccgttcact  | catccaaccg | aagatgcgtg | agattcttca  | catccagggt | 120 |
| ggtcaatgcg | gtaaccagat  | cggcgccaag | ttctgggaag | tggtttgccg  | cgagcacggc | 180 |
| atcgatccaa | ccggaaggta  | caccggagac | tcagatctgc | aacttgagcg  | catcaacggt | 240 |
| tactacaatg | aagcgagttg  | cggtagattc | gttctcgtg  | cagtgtcat   | ggatttggag | 300 |
| cctgggacta | tggatagtct  | cagatctgga | ccgtacggtc | agaccttctg  | acctgataac | 360 |
| ttcgtctttg | gccaatccgg  | tgtctgtaac | aactgggcca | agggacacta  | cacggaagga | 420 |
| gctgaactaa | tcgattccgt  | tctcgatggt | gttcgtaagg | aagctgGaga  | actgtgactg | 480 |
| tctccaagg  | ttccagggtt  | gtcactcgtt | gggaggagga | actggatctg  | gtatgggaac | 540 |
| attgttgatc | tctaagatcc  | gtgaagagta | cccagatcgc | atgatgctta  | ccttctcggg | 600 |
| gttcccttca | ccaaagggtt  | ctgatactgt | ggttgagcct | tacaacgcta  | ctctgtctgt | 660 |
| ccatcagctt | gttgagaatg  | ctgatgagtg | catggttctt | gataatgagg  | ccttgtacga | 720 |
| tatttgcttc | aggactctca  | aactcactac | ccccagcttt | ggtgatttga  | accacttgat | 780 |
| ttctgctact | atgtctgggtg | tgacttgctg | tctgagggtc | cctgggtcaac | tcaactctga | 840 |
| cctccgaaag | cttgctgtga  | atctcatccc | attcccccg  | cttcacttct  | tcatggtg   | 900 |

```
ttttgtctct ctcacctcaa gaggtttctca gcagtagcgt tccctcacag tccctgagct 960
caccagcaaa atgtgggact ccaagaacat gatgtgtgct gcagacccaa ggcacggacg 1020
ctacctcaca gcctctgcca tgttccgtgg caagatgagc acaaaggaag ttgacgagca 1080
gatgctgaat gtgcagaaca agaactcgtc ctactttgtg gagtggatcc ccaacaacgt 1140
gaaatcgaca gtctgtgaca tccacactac tggctctgaag atggcatcaa ctttcattgg 1200
aaactcaaca tcaatccaag agatgttcag gcgagtgaat gagcagttca cagctatgtt 1260
caggagaaaag gctttcttgc attggtacac aggtgagggg atggacgaga tggaaattcac 1320
agaagcggag agcaacatga acgatcttgt gtcagagtac cagcaatacc aagatgcaac 1380
tgcggatgaa gaaggtgact acgaggatga ggaagaaggt gaatatcaac aggaggaaga 1440
gtactgagaa taatttagtt ataactgctt taaaaacaaa aacaatttag tcgtttgcta 1500
cttttctttt ttttaaaagg aacacctcaa ctaccagttg tagttttttt ctctgcttgt 1560
atttgacata tctggttgat gtttctgtac ttttgttctt aatcttgtca ttgcctgtga 1620
tgtttctatt aatattttoc agttgtact
```

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1570005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

```
Met Leu Phe Val Arg Lys Leu Glu Asn Cys Asp Cys Leu Gln Gly Phe
1 5 10 15
Gln Val Cys His Ser Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr
 20 25 30
Leu Leu Ile Ser Lys Ile Arg Glu Tyr Pro Asp Arg Met Met Leu
 35 40 45
Thr Phe Ser Val Phe Pro Ser Pro Lys Val Ser Asp Thr Val Val Glu
 50 55 60
Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu Val Glu Asn Ala Asp
65 70 75 80
Glu Cys Met Val Leu Asp Asn Glu Ala Leu Tyr Asp Ile Cys Phe Arg
 85 90 95
Thr Leu Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn His Leu Ile
 100 105 110
Ser Ala Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe Pro Gly Gln
 115 120 125
Leu Asn Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile Pro Phe Pro
 130 135 140
Arg Leu His Phe Phe Met Val Gly Phe Ala Pro Leu Thr Ser Arg Gly
145 150 155 160
Ser Gln Gln Tyr Arg Ser Leu Thr Val Pro Glu Leu Thr Gln Gln Met
 165 170 175
Trp Asp Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg His Gly Arg
 180 185 190
Tyr Leu Thr Ala Ser Ala Met Phe Arg Gly Lys Met Ser Thr Lys Glu
 195 200 205
Val Asp Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser Ser Tyr Phe
210 215 220
Val Glu Trp Ile Pro Asn Asn Val Lys Ser Thr Val Cys Asp Ile Pro
225 230 235 240
Pro Thr Gly Leu Lys Met Ala Ser Thr Phe Ile Gly Asn Ser Thr Ser
 245 250 255
Ile Gln Glu Met Phe Arg Arg Val Ser Glu Gln Phe Thr Ala Met Phe
 260 265 270
Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu
275 280 285
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Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu Val Ser Glu  
290 295 300  
Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Glu Gly Asp Tyr Glu  
305 310 315 320  
Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Glu Tyr  
325 330

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1570006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp Arg  
1 5 10 15  
Met Met Leu Thr Phe Ser Val Phe Pro Ser Pro Lys Val Ser Asp Thr  
20 25 30  
Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu Val Glu  
35 40 45  
Asn Ala Asp Glu Cys Met Val Leu Asp Asn Glu Ala Leu Tyr Asp Ile  
50 55 60  
Cys Phe Arg Thr Leu Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn  
65 70 75 80  
His Leu Ile Ser Ala Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe  
85 90 95  
Pro Gly Gln Leu Asn Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile  
100 105 110  
Pro Phe Pro Arg Leu His Phe Phe Met Val Gly Phe Ala Pro Leu Thr  
115 120 125  
Ser Arg Gly Ser Gln Gln Tyr Arg Ser Leu Thr Val Pro Glu Leu Thr  
130 135 140  
Gln Gln Met Trp Asp Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg  
145 150 155 160  
His Gly Arg Tyr Leu Thr Ala Ser Ala Met Phe Arg Gly Lys Met Ser  
165 170 175  
Thr Lys Glu Val Asp Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser  
180 185 190  
Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Ser Thr Val Cys  
195 200 205  
Asp Ile Pro Pro Thr Gly Leu Lys Met Ala Ser Thr Phe Ile Gly Asn  
210 215 220  
Ser Thr Ser Ile Gln Glu Met Phe Arg Arg Val Ser Glu Gln Phe Thr  
225 230 235 240  
Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly  
245 250 255  
Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu  
260 265 270  
Val Ser Glu Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Glu Gly  
275 280 285  
Asp Tyr Glu Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Tyr  
290 295 300

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..288  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570007  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

Met Met Leu Thr Phe Ser Val Phe Pro Ser Pro Lys Val Ser Asp Thr  
1 5 10 15  
Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu Val Glu  
20 25 30  
Asn Ala Asp Glu Cys Met Val Leu Asp Asn Glu Ala Leu Tyr Asp Ile  
35 40 45  
Cys Phe Arg Thr Leu Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn  
50 55 60  
His Leu Ile Ser Ala Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe  
65 70 75 80  
Pro Gly Gln Leu Asn Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile  
85 90 95  
Pro Phe Pro Arg Leu His Phe Phe Met Val Gly Phe Ala Pro Leu Thr  
100 105 110  
Ser Arg Gly Ser Gln Gln Tyr Arg Ser Leu Thr Val Pro Glu Leu Thr  
115 120 125  
Gln Gln Met Trp Asp Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg  
130 135 140  
His Gly Arg Tyr Leu Thr Ala Ser Ala Met Phe Arg Gly Lys Met Ser  
145 150 155 160  
Thr Lys Glu Val Asp Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser  
165 170 175  
Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Ser Thr Val Cys  
180 185 190  
Asp Ile Pro Pro Thr Gly Leu Lys Met Ala Ser Thr Phe Ile Gly Asn  
195 200 205  
Ser Thr Ser Ile Gln Glu Met Phe Arg Arg Val Ser Glu Gln Phe Thr  
210 215 220  
Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly  
225 230 235 240  
Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu  
245 250 255  
Val Ser Glu Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Glu Gly  
260 265 270  
Asp Tyr Glu Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Glu Tyr  
275 280 285

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 503 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..503  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570008  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

attttttttt gaaacagaMH atctCagaaa gatcaatcta gagagaccaa aaagagatcg 60  
gaagagatgg cttctacctc cgcatgtca ttggtcacac cacttaacca gaccgcgttcg 120

tctcttttcc tcaagccatt acctctgaaa ccattccaagg ctttggttgc aactggaggc 180  
agagcacaga ggcttcaagt taaggccctc aagatggaca aggttttgac cggtatctcc 240  
gcggctgctc ttactgcttc gatggtgatt ccggagatag ctgaagctgc tggttctgga 300  
atctctcctt cctcaagaa tttcttgctc agcattgctt ctggtggcct cgtcctcaact 360  
gtcatcattg gtgtcgtcgt cggcgtctcc aactttgacc ctgtcaagag aacctaagac 420  
ctatatatct ttcttacatc attattgtaa tctgttctcc ttctgtgtat tcgtttcaat 480  
gttgcagcaa tgaacttttg gat

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1570009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

Ile Xaa Phe Arg Asn Arg Xaa Ser Gln Lys Asp Gln Ser Arg Glu Thr  
1 5 10 15  
Lys Lys Arg Ser Glu Glu Met Ala Ser Thr Ser Ala Met Ser Leu Val  
20 25 30  
Thr Pro Leu Asn Gln Thr Arg Ser Ser Pro Phe Leu Lys Pro Leu Pro  
35 40 45  
Leu Lys Pro Ser Lys Ala Leu Val Ala Thr Gly Gly Arg Ala Gln Arg  
50 55 60  
Leu Gln Val Lys Ala Leu Lys Met Asp Lys Ala Leu Thr Gly Ile Ser  
65 70 75 80  
Ala Ala Ala Leu Thr Ala Ser Met Val Ile Pro Glu Ile Ala Glu Ala  
85 90 95  
Ala Gly Ser Gly Ile Ser Pro Ser Leu Lys Asn Phe Leu Leu Ser Ile  
100 105 110  
Ala Ser Gly Gly Leu Val Leu Thr Val Ile Ile Gly Val Val Val Gly  
115 120 125  
Val Ser Asn Phe Asp Pro Val Lys Arg Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1570010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Met Ala Ser Thr Ser Ala Met Ser Leu Val Thr Pro Leu Asn Gln Thr  
1 5 10 15  
Arg Ser Ser Pro Phe Leu Lys Pro Leu Pro Leu Lys Pro Ser Lys Ala  
20 25 30  
Leu Val Ala Thr Gly Gly Arg Ala Gln Arg Leu Gln Val Lys Ala Leu  
35 40 45  
Lys Met Asp Lys Ala Leu Thr Gly Ile Ser Ala Ala Leu Thr Ala  
50 55 60  
Ser Met Val Ile Pro Glu Ile Ala Glu Ala Ala Gly Ser Gly Ile Ser  
65 70 75 80  
Pro Ser Leu Lys Asn Phe Leu Leu Ser Ile Ala Ser Gly Gly Leu Val  
85 90 95

Leu Thr Val Ile Ile Gly Val Val Val Gly Val Ser Asn Phe Asp Pro  
100 105 110  
Val Lys Arg Thr  
115

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

Met Ser Leu Val Thr Pro Leu Asn Gln Thr Arg Ser Ser Pro Phe Leu  
1 5 10 15  
Lys Pro Leu Pro Leu Lys Pro Ser Lys Ala Leu Val Ala Thr Gly Gly  
20 25 30  
Arg Ala Gln Arg Leu Gln Val Lys Ala Leu Lys Met Asp Lys Ala Leu  
35 40 45  
Thr Gly Ile Ser Ala Ala Ala Leu Thr Ala Ser Met Val Ile Pro Glu  
50 55 60  
Ile Ala Glu Ala Ala Gly Ser Gly Ile Ser Pro Ser Leu Lys Asn Phe  
65 70 75 80  
Leu Leu Ser Ile Ala Ser Gly Gly Leu Val Leu Thr Val Ile Ile Gly  
85 90 95  
Val Val Val Gly Val Ser Asn Phe Asp Pro Val Lys Arg Thr  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..691
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

aaccttattc ttatgattaa aattgttcgg tcttgattat ctctgtgttt ttgggaactg 60  
agaagcatcc actcgacaat ggagactgcg atttgtggga gattagctct cgcaccatcc 120  
tctctcttca attctaaatc aggggacaaa catttagtct caaaaggacc atgtgtgaat 180  
cgtagcattc tcatgacctt gtctacatct gctgcattgg gtaaaggagg tgggtgtcta 240  
gacaaaccaa ttatagagaa aaccactcct ggtcgtgaat ccgagtttga tttaaggaaa 300  
tcaaagaaga tagctccacc ttacaggggtg atactacaca atgacaactt caacaagagg 360  
gaatatgtgg ttcaggtgtt gatgaaggta ataccccatg actgtagaca acgcggttaa 420  
cattatgcaa gaagctcata tcaacggttt ggcagttgtg attgtttgtg ctcaggctga 480  
tgcagagcaa cactgtatgc agctgcgcgg taacggcctt ctcagttctg ttgaacctga 540  
tggtggaggc tgctgaaact aattaaactc agtatagatt ttcccacctt ccaggactct 600  
ctatttagtc aaaaacatGt tgttgtttta atgtatataa tatcagaaat ttggtacaag 660  
actgttacta tatgcaatga accttgcccc c

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1570037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

Met Glu Thr Ala Ile Cys Gly Arg Leu Ala Leu Ala Pro Ser Ser Leu  
1 5 10 15  
Phe Asn Ser Lys Ser Gly Asp Lys His Leu Val Ser Lys Gly Pro Cys  
20 25 30  
Val Asn Arg Ser Ile Leu Met Thr Leu Ser Thr Ser Ala Ala Leu Gly  
35 40 45  
Lys Gly Gly Gly Val Leu Asp Lys Pro Ile Ile Glu Lys Thr Thr Pro  
50 55 60  
Gly Arg Glu Ser Glu Phe Asp Leu Arg Lys Ser Lys Lys Ile Ala Pro  
65 70 75 80  
Pro Tyr Arg Val Ile Leu His Asn Asp Asn Phe Asn Lys Arg Glu Tyr  
85 90 95  
Val Val Gln Val Leu Met Lys Val Ile Pro His Asp Cys Arg Gln Arg  
100 105 110  
Gly

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1570038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

Met Thr Leu Ser Thr Ser Ala Ala Leu Gly Lys Gly Gly Gly Val Leu  
1 5 10 15  
Asp Lys Pro Ile Ile Glu Lys Thr Thr Pro Gly Arg Glu Ser Glu Phe  
20 25 30  
Asp Leu Arg Lys Ser Lys Lys Ile Ala Pro Pro Tyr Arg Val Ile Leu  
35 40 45  
His Asn Asp Asn Phe Asn Lys Arg Glu Tyr Val Val Gln Val Leu Met  
50 55 60  
Lys Val Ile Pro His Asp Cys Arg Gln Arg Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 664 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..664

(D) OTHER INFORMATION: / Ceres Seq. ID 1570039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aacggccgat ttattaaaaa aaaactccga caaatgattc gccggccgat ctacgacttc | 60  |
| gccgccgttt ttgccactt aactttctcg ttatcgacat cctcgcgttt tctgttctat  | 120 |
| tcttcactcg aacatgaagc tcgaaaaccg attgtctcga accctaaatc cccaatcggg | 180 |
| tctccgactc gggttcaaaa gctcatagCt tcgcaatcgg atcctctcct cgccaaggag | 240 |
| attttcgatt atgcttctca acagcccaat ttccgccatt ctgatcttc tcatctaata  | 300 |
| ctcattctca aactcggccg tggtagatat ttcaatotta tcgacgacgt tctcgccaaa | 360 |



cacagatcaa gtggttatcc attaacctga gaaattttca cttatctgat caaagtctac 420  
gcagaagcaa agttaccgga gaaagtctta agtacgtttt acaaaatgct ggagttcaat 480  
ttcacgccgc agccaaaaca tctgaatcgg attctagatg ttctcgtaag ccatagaggt 540  
tatctccaga aagcttttga gcttttcaag agttcacggc ttcattggagt aatgcctaac 600  
acgagaagtt acaatttatt gatgcaagct ttttgtttga atgatgattt gagtattgca 660  
tacc

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..129

- (D) OTHER INFORMATION: / Ceres Seq. ID 1570040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

Asn Gly Arg Phe Ile Lys Lys Lys Leu Arg Gln Met Ile Arg Arg Pro  
1 5 10 15  
Ile Tyr Asp Phe Ala Ala Val Phe Arg His Leu Thr Ser Pro Leu Ser  
20 25 30  
Thr Ser Ser Arg Phe Leu Phe Tyr Ser Ser Ser Glu His Glu Ala Arg  
35 40 45  
Lys Pro Ile Val Ser Asn Pro Lys Ser Pro Ile Gly Ser Pro Thr Arg  
50 55 60  
Val Gln Lys Leu Ile Ala Ser Gln Ser Asp Pro Leu Leu Ala Lys Glu  
65 70 75 80  
Ile Phe Asp Tyr Ala Ser Gln Gln Pro Asn Phe Arg His Ser Arg Ser  
85 90 95  
Ser His Leu Ile Leu Ile Leu Lys Leu Gly Arg Gly Arg Tyr Phe Asn  
100 105 110  
Leu Ile Asp Asp Val Leu Ala Lys His Arg Ser Ser Gly Tyr Pro Leu  
115 120 125  
Thr

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..118

- (D) OTHER INFORMATION: / Ceres Seq. ID 1570041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

Met Ile Arg Arg Pro Ile Tyr Asp Phe Ala Ala Val Phe Arg His Leu  
1 5 10 15  
Thr Ser Pro Leu Ser Thr Ser Ser Arg Phe Leu Phe Tyr Ser Ser Ser  
20 25 30  
Glu His Glu Ala Arg Lys Pro Ile Val Ser Asn Pro Lys Ser Pro Ile  
35 40 45  
Gly Ser Pro Thr Arg Val Gln Lys Leu Ile Ala Ser Gln Ser Asp Pro  
50 55 60  
Leu Leu Ala Lys Glu Ile Phe Asp Tyr Ala Ser Gln Gln Pro Asn Phe  
65 70 75 80  
Arg His Ser Arg Ser Ser His Leu Ile Leu Ile Leu Lys Leu Gly Arg  
85 90 95  
Gly Arg Tyr Phe Asn Leu Ile Asp Asp Val Leu Ala Lys His Arg Ser

100 105 110  
Ser Gly Tyr Pro Leu Thr  
115

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

Met Leu Glu Phe Asn Phe Thr Pro Gln Pro Lys His Leu Asn Arg Ile  
1 5 10 15  
Leu Asp Val Leu Val Ser His Arg Gly Tyr Leu Gln Lys Ala Phe Glu  
20 25 30  
Leu Phe Lys Ser Ser Arg Leu His Gly Val Met Pro Asn Thr Arg Ser  
35 40 45  
Tyr Asn Leu Leu Met Gln Ala Phe Cys Leu Asn Asp Asp Leu Ser Ile  
50 55 60  
Ala Tyr  
65

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

acatctccca agatcatttg tgcgttgatt ccatacgatc tccaagtctt gtcgttgacag 60  
aatctctaag aagctaacga aaatggctct tcaaaacgat attgatctgc ttaaccctcc 120  
tgctgagctc gagaagagga agcacaagct caagcgtctt gttcaatcac ccaattcggt 180  
tttcatggat gtcaagtgtc aaggctgctt taacattaacg actgtgttca gccactctca 240  
gaccgttggtg atgtgtggaa actgccagac tttgctctgc acaccacag gagggaaggc 300  
aaagctcact gaaggatgct ctttcaggaa aaagtgaagac tgaagaagaa gatatgactc 360  
cattccattc actcaccac aaattttctt ttcgtttatt atgaattttt gttgatattt 420  
gagctagtag taacccttct ttgtcgatta tcctttggtt taatcagcga agCtcgttcc 480  
tcttttatga atggttatgt attttcttg

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

Met Val Leu Gln Asn Asp Ile Asp Leu Leu Asn Pro Pro Ala Glu Leu  
1 5 10 15  
Glu Lys Arg Lys His Lys Leu Lys Arg Leu Val Gln Ser Pro Asn Ser

20 25 30  
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Asn Ile Thr Thr Val  
35 40 45  
Phe Ser His Ser Gln Thr Val Val Met Cys Gly Asn Cys Gln Thr Leu  
50 55 60  
Leu Cys Thr Pro Thr Gly Gly Lys Ala Lys Leu Thr Glu Gly Cys Ser  
65 70 75 80  
Phe Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

Met Asp Val Lys Cys Gln Gly Cys Phe Asn Ile Thr Thr Val Phe Ser  
1 5 10 15  
His Ser Gln Thr Val Val Met Cys Gly Asn Cys Gln Thr Leu Leu Cys  
20 25 30  
Thr Pro Thr Gly Gly Lys Ala Lys Leu Thr Glu Gly Cys Ser Phe Arg  
35 40 45  
Lys Lys  
50

(2) INFORMATION FOR SEQ ID NO:1459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

aaaattttctc tgccggtgtt gacttcaaac tctctttgat tagatcggcg ccaacttcta 60  
aacgcaaattg ggaatcacga gaaacttgat cctgggtttg gcttggttag cctttgtctc 120  
cattgctaaa gctctgcctc atgaaccaga acttggtctg gctcgtgtcg tcttccagac 180  
tagttatgga gatatcgaat ttgggttcta tcccactgtg gcacccaaga cagtggatca 240  
catcttcaag cttgttcggt taggaggata caacactaat catttcttca gggttgataa 300  
agggtttgtt gctcaagttg cggatgtggc gagtggacga tcagctccaa tgaatgagga 360  
gcaaaggaaa gaagctgaga agaaaattgt gggagagtgc agtgatgtta agcatgtcag 420  
aggtactcTt tccatgggaa gatatgacga tccaaacagt gcacaatctt cattttcgat 480  
gcttcttggc aatgctcttc atcttgatcg ccagtatgct gtgtttggta aagttactaa 540  
aggagatgaa acattgagta agctagaaga agttcccact cgccgcgagg ggatttttgt 600  
tatgccgacg gagcggatca cgattttgtc gacatactat tacgacacta aaatggagag 660  
ctgtgaagaa gagagatctg tcctgaaaag aaggcttcaa gcatcttttg tggagggtcga 720  
aagacagaga atgaagtgtc tcccgatgaat gaagttaaca cataagaaac tgttcaacaa 780  
aagccttaaa acgccaggga acacaaaggt aaatgtatgt ctagtaaaaa aactcagaat 840  
gctagacagt ttttgagtgg tttatcagtg tgagagattg tagttaacag tgtaaacagt 900  
ttgagacatt gaatcatgga ttgtttcctc c

(2) INFORMATION FOR SEQ ID NO:1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..226  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570070  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ile | Thr | Arg | Asn | Leu | Ile | Leu | Gly | Leu | Ala | Cys | Leu | Ala | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ser | Ile | Ala | Lys | Ala | Leu | Pro | His | Glu | Pro | Glu | Leu | Gly | Ser | Ala |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Arg | Val | Val | Phe | Gln | Thr | Ser | Tyr | Gly | Asp | Ile | Glu | Phe | Gly | Phe | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Thr | Val | Ala | Pro | Lys | Thr | Val | Asp | His | Ile | Phe | Lys | Leu | Val | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Gly | Gly | Tyr | Asn | Thr | Asn | His | Phe | Phe | Arg | Val | Asp | Lys | Gly | Phe |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Val | Ala | Gln | Val | Ala | Asp | Val | Ala | Ser | Gly | Arg | Ser | Ala | Pro | Met | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Gln | Arg | Lys | Glu | Ala | Glu | Lys | Lys | Ile | Val | Gly | Glu | Phe | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Val | Lys | His | Val | Arg | Gly | Thr | Leu | Ser | Met | Gly | Arg | Tyr | Asp | Asp |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Asn | Ser | Ala | Gln | Ser | Ser | Phe | Ser | Met | Leu | Leu | Gly | Asn | Ala | Pro |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| His | Leu | Asp | Arg | Gln | Tyr | Ala | Val | Phe | Gly | Lys | Val | Thr | Lys | Gly | Asp |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Glu | Thr | Leu | Ser | Lys | Leu | Glu | Glu | Val | Pro | Thr | Arg | Arg | Glu | Gly | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Val | Met | Pro | Thr | Glu | Arg | Ile | Thr | Ile | Leu | Ser | Thr | Tyr | Tyr | Tyr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Thr | Lys | Met | Glu | Ser | Cys | Glu | Glu | Glu | Arg | Ser | Val | Leu | Lys | Arg |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Arg | Leu | Gln | Ala | Ser | Phe | Val | Glu | Val | Glu | Arg | Gln | Arg | Met | Lys | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 132 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: peptide

    (B) LOCATION: 1..132

    (D) OTHER INFORMATION: / Ceres Seq. ID 1570071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Glu | Glu | Gln | Arg | Lys | Glu | Ala | Glu | Lys | Lys | Ile | Val | Gly | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Ser | Asp | Val | Lys | His | Val | Arg | Gly | Thr | Leu | Ser | Met | Gly | Arg | Tyr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Asp | Pro | Asn | Ser | Ala | Gln | Ser | Phe | Ser | Met | Leu | Gly | Asn |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Pro | His | Leu | Asp | Arg | Gln | Tyr | Ala | Val | Phe | Gly | Lys | Val | Thr | Lys |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Asp | Glu | Thr | Leu | Ser | Lys | Leu | Glu | Glu | Val | Pro | Thr | Arg | Arg | Glu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Gly | Ile | Phe | Val | Met | Pro | Thr | Glu | Arg | Ile | Thr | Ile | Leu | Ser | Thr | Tyr |

85 90 95  
Tyr Tyr Asp Thr Lys Met Glu Ser Cys Glu Glu Glu Arg Ser Val Leu  
100 105 110  
Lys Arg Arg Leu Gln Ala Ser Phe Val Glu Val Glu Arg Gln Arg Met  
115 120 125  
Lys Cys Phe Pro  
130

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

aatagccaca aaGacttttt tctttcatcc tctaaaaaaaa aatcttttcta gtgagtaacg 60  
aaaaaaaaatgt gtccggtgga gaacaaatgg tttaaagggtg gtcaaaaagg agctggctct 120  
ggggctagaa gctcacatgc catgaccgct gttgggaaca aagtttactg ttttggtggt 180  
gagcttaagc caacgatcca tattgataac gatctttacg ttttcgatct tgggactcaa 240  
gaatgggtcga tagctcctgc gaccggagag gtccttttcc cctgttttgg tgtctcgatg 300  
gtaacgatcg gttcaacgat ctatgtctac ggtggccgtg acgataaacg gagatacaac 360  
ggtcttcatt cgtatgatac tgagaccaat gagtggaaat tgttatctcc ggttgaggaa 420  
gggcttcctg gtctagtagta tcattcaatg gctgggtgat atcggaaggt ttatgtgttt 480  
cgtgggtgtga ctgctaaagg acgtgtgaat acgcttcatg cgtacgatgt tgttgatcag 540  
aaatggggtt agtatccggc ggctggggaa gcttgtaaag gcagaggagc acctgggctt 600  
gtgggtgttg aagggagaat ttgggttttg tttgggtttg atggtaatga attgggtgat 660  
attcattggt ttgacttggc tagtgaacag tggaaggctg tggagactac cggggatgta 720  
ccggcggcga gaagcgtgtt tccggcgtt tcttacggga agtacattgt tatttatggt 780  
ggggaggaag agccgcatga gcttatgcac atgggagctg ggaagatgtc tggagagggt 840  
tatcagcttg atacagagac gttagtgtgg gagaggattg tgtgtgggaa tgaagaggag 900  
aagccgagcc aacgcgggtg gtgcgcgttt acgaaagcgg ttaaggatgg tgaggaaggt 960  
ttgttggttc atgggtggaa ttctccgacc aatgagcggc ttgatgattt ggtgttttgg 1020  
ggtttctctc atcttaatgt caattaatga ctagttgctt tgtgtctttc gtgtttatga 1080  
actgtttagt gtgttgttgt ttaaggagt ttaagtgtg atgatatga actgctaagt 1140  
gtctgagttt aaggagctat gtgtgtgtaa actttgctac ctattccaaa tattttatta 1200  
agtttggtgt tttggttaatt taataaaaaa cttgttagtc tgattctc

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

Met Cys Pro Val Glu Asn Lys Trp Leu Lys Val Gly Gln Lys Gly Ala  
1 5 10 15  
Gly Pro Gly Ala Arg Ser Ser His Ala Met Thr Val Val Gly Asn Lys  
20 25 30  
Val Tyr Cys Phe Gly Gly Glu Leu Lys Pro Thr Ile His Ile Asp Asn  
35 40 45  
Asp Leu Tyr Val Phe Asp Leu Gly Thr Gln Glu Trp Ser Ile Ala Pro  
50 55 60  
Ala Thr Gly Glu Ala Pro Phe Pro Cys Phe Gly Val Ser Met Val Thr

```

65 70 75 80
Ile Gly Ser Thr Ile Tyr Val Tyr Gly Gly Arg Asp Asp Lys Arg Arg
 85 90 95
Tyr Asn Gly Leu His Ser Tyr Asp Thr Glu Thr Asn Glu Trp Lys Leu
 100 105 110
Leu Ser Pro Val Glu Glu Gly Leu Pro Gly Arg Ser Tyr His Ser Met
 115 120 125
Ala Gly Asp Asp Arg Lys Val Tyr Val Phe Arg Gly Val Thr Ala Lys
 130 135 140
Gly Arg Val Asn Thr Leu His Ala Tyr Asp Val Val Asp Gln Lys Trp
145 150 155 160
Val Glu Tyr Pro Ala Ala Gly Glu Ala Cys Lys Gly Arg Gly Ala Pro
 165 170 175
Gly Leu Val Val Val Glu Gly Arg Ile Trp Val Leu Phe Gly Phe Asp
 180 185 190
Gly Asn Glu Leu Gly Asp Ile His Cys Phe Asp Leu Ala Ser Glu Gln
 195 200 205
Trp Lys Ala Val Glu Thr Thr Gly Asp Val Pro Ala Ala Arg Ser Val
 210 215 220
Phe Pro Ala Val Ser Tyr Gly Lys Tyr Ile Val Ile Tyr Gly Gly Glu
225 230 235 240
Glu Glu Pro His Glu Leu Met His Met Gly Ala Gly Lys Met Ser Gly
 245 250 255
Glu Val Tyr Gln Leu Asp Thr Glu Thr Leu Val Trp Glu Arg Ile Val
 260 265 270
Cys Gly Asn Glu Glu Glu Lys Pro Ser Gln Arg Gly Trp Cys Ala Phe
 275 280 285
Thr Lys Ala Val Lys Asp Gly Glu Glu Gly Leu Leu Val His Gly Gly
 290 295 300
Asn Ser Pro Thr Asn Glu Arg Leu Asp Asp Leu Val Phe Trp Gly Phe
305 310 315 320
Ser His Leu Asn Val Asn
 325

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(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1570074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

```

Met Thr Val Val Gly Asn Lys Val Tyr Cys Phe Gly Gly Glu Leu Lys
1 5 10 15
Pro Thr Ile His Ile Asp Asn Asp Leu Tyr Val Phe Asp Leu Gly Thr
 20 25 30
Gln Glu Trp Ser Ile Ala Pro Ala Thr Gly Glu Ala Pro Phe Pro Cys
 35 40 45
Phe Gly Val Ser Met Val Thr Ile Gly Ser Thr Ile Tyr Val Tyr Gly
 50 55 60
Gly Arg Asp Asp Lys Arg Arg Tyr Asn Gly Leu His Ser Tyr Asp Thr
65 70 75 80
Glu Thr Asn Glu Trp Lys Leu Leu Ser Pro Val Glu Glu Gly Leu Pro
 85 90 95
Gly Arg Ser Tyr His Ser Met Ala Gly Asp Asp Arg Lys Val Tyr Val
 100 105 110
Phe Arg Gly Val Thr Ala Lys Gly Arg Val Asn Thr Leu His Ala Tyr
 115 120 125

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Val | Asp | Gln | Lys | Trp | Val | Glu | Tyr | Pro | Ala | Ala | Gly | Glu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Lys | Gly | Arg | Gly | Ala | Pro | Gly | Leu | Val | Val | Val | Glu | Gly | Arg | Ile |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Val | Leu | Phe | Gly | Phe | Asp | Gly | Asn | Glu | Leu | Gly | Asp | Ile | His | Cys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Asp | Leu | Ala | Ser | Glu | Gln | Trp | Lys | Ala | Val | Glu | Thr | Thr | Gly | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Pro | Ala | Ala | Arg | Ser | Val | Phe | Pro | Ala | Val | Ser | Tyr | Gly | Lys | Tyr |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Val | Ile | Tyr | Gly | Gly | Glu | Glu | Pro | His | Glu | Leu | Met | His | Met |     |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Gly | Ala | Gly | Lys | Met | Ser | Gly | Glu | Val | Tyr | Gln | Leu | Asp | Thr | Glu | Thr |
|     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Leu | Val | Trp | Glu | Arg | Ile | Val | Cys | Gly | Asn | Glu | Glu | Glu | Lys | Pro | Ser |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Gln | Arg | Gly | Trp | Cys | Ala | Phe | Thr | Lys | Ala | Val | Lys | Asp | Gly | Glu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Leu | Leu | Val | His | Gly | Gly | Asn | Ser | Pro | Thr | Asn | Glu | Arg | Leu | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Leu | Val | Phe | Trp | Gly | Phe | Ser | His | Leu | Asn | Val | Asn |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1570075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Ile | Gly | Ser | Thr | Ile | Tyr | Val | Tyr | Gly | Gly | Arg | Asp | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Arg | Arg | Tyr | Asn | Gly | Leu | His | Ser | Tyr | Asp | Thr | Glu | Thr | Asn | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Lys | Leu | Ser | Pro | Val | Glu | Gly | Leu | Pro | Gly | Arg | Ser | Tyr |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| His | Ser | Met | Ala | Gly | Asp | Asp | Arg | Lys | Val | Tyr | Val | Phe | Arg | Gly | Val |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ala | Lys | Gly | Arg | Val | Asn | Thr | Leu | His | Ala | Tyr | Asp | Val | Val | Asp |
|     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Lys | Trp | Val | Glu | Tyr | Pro | Ala | Ala | Gly | Glu | Ala | Cys | Lys | Gly | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ala | Pro | Gly | Leu | Val | Val | Val | Glu | Gly | Arg | Ile | Trp | Val | Leu | Phe |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gly | Phe | Asp | Gly | Asn | Glu | Leu | Gly | Asp | Ile | His | Cys | Phe | Asp | Leu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Glu | Gln | Trp | Lys | Ala | Val | Glu | Thr | Thr | Gly | Asp | Val | Pro | Ala | Ala |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Ser | Val | Phe | Pro | Ala | Val | Ser | Tyr | Gly | Lys | Tyr | Ile | Val | Ile | Tyr |
|     |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Gly | Glu | Glu | Glu | Pro | His | Glu | Leu | Met | His | Met | Gly | Ala | Gly | Lys |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Met | Ser | Gly | Glu | Val | Tyr | Gln | Leu | Asp | Thr | Glu | Thr | Leu | Val | Trp | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Arg | Ile | Val | Cys | Gly | Asn | Glu | Glu | Glu | Lys | Pro | Ser | Gln | Arg | Gly | Trp |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Cys | Ala | Phe | Thr | Lys | Ala | Val | Lys | Asp | Gly | Glu | Glu | Gly | Leu | Leu | Val |

210 215 220  
His Gly Gly Asn Ser Pro Thr Asn Glu Arg Leu Asp Asp Leu Val Phe  
225 230 235 240  
Trp Gly Phe Ser His Leu Asn Val Asn  
245

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

ctcttttcgac ttcagtgaggc ggcatttcag agattcaaac tcagagaaaa tgggtggcgac 60  
aggcttattc gtgggggctaa acaaaggaca cggttggtacc aaacgcgagc aacctcctcg 120  
ccctaacaac agaaaaggga aaacaagcaa aaggactatt tttatcagga atctcatcaa 180  
ggaagttgcg ggtcaagctc cctatgagaa gaggatcact gataaaaaata gtcctttttgc 240  
tcgtdttaat tttcagttgt taggtacttc tggttc

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

Ser Phe Asp Phe Ser Gly Gly Ala Phe Arg Asp Ser Asn Ser Glu Lys  
1 5 10 15  
Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val  
20 25 30  
Thr Lys Arg Glu Gln Pro Pro Arg Asn Asn Arg Lys Gly Lys Thr  
35 40 45  
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly  
50 55 60  
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Asp Lys Asn Ser Pro Phe Ala  
65 70 75 80  
Arg Xaa Asn Phe Gln Leu Leu Gly Thr Ser Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val  
1 5 10 15  
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr



20 25 30  
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly  
35 40 45  
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Asp Lys Asn Ser Pro Phe Ala  
50 55 60  
Arg Xaa Asn Phe Gln Leu Leu Gly Thr Ser Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..941
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

gacaaaaccaa aaaaaaagcc taaaaagccg accttttttc tttctttctc tcctctacct 60  
ctcagcttct gctggatctc tccagcagac acgatcttgt tcggagagat tcgtagggga 120  
ccgatctatc aaggcttcaa gggcaaacag aaatggacca cgacaagaca ggatgccaaa 180  
gcccacctga aggtcccaag ctatgtacta acaactgcgg tttctttgaa gcgctgccac 240  
aatgaacatg tgttctaagt gtcacaagga tatgttggtc caacagtagc agggcgctaa 300  
gtttgcattc gcagtgctcg gaacatcgtc atccagcaac atcataaagg aaacctttac 360  
cgctgcgttg gtcgatattg aaaccaaadc cggttgagccg atgactgttt ctgtacagcc 420  
atcctctgtc caagtcgttg cagaggtagt agcaccagaa gaagstgcga aaccaaaggg 480  
accaagccga tgtactactt gcaataagcg gggtggcctg actggattca aatgtcgctg 540  
tgaggagcctc ttctgcggaa AAcacaccgc tatgcagaca tacatgactg ctccttcaat 600  
taccatgctG ctgcgcaaga ggcgatagct aaggcaaacc cggttggtgaa agcagagaag 660  
cttgacaaaa tctgaaaatc taagttaaact tctctggttt catcaggtgg cctgggtttt 720  
ccttctcctg tctgtgtctg gttcaagtat tctcatgtta aaaagggttt atataaggtc 780  
gaatgaaagc gtgcttgatc tttagcgtct tccatctctc tgcaatatatt gtggtgtgga 840  
actttctatt atctgtgttt gcaagcagag aaacgtgctc ttaaaaaaaaa tgctttgtgt 900  
gtttatcttt ctactatttt tgagcactgt gttattgttt c

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

Asp Lys Pro Lys Lys Lys Pro Lys Lys Pro Thr Phe Phe Leu Ser Phe  
1 5 10 15  
Ser Pro Leu Pro Leu Ser Phe Cys Trp Ile Ser Pro Ala Asp Thr Ile  
20 25 30  
Leu Phe Gly Glu Ile Arg Arg Gly Pro Ile Tyr Gln Gly Phe Lys Gly  
35 40 45  
Lys Gln Lys Trp Thr Thr Thr Arg Gln Asp Ala Lys Ala His Leu Lys  
50 55 60  
Val Pro Ser Tyr Val Leu Thr Thr Ala Val Ser Leu Lys Arg Cys His  
65 70 75 80  
Asn Glu His Val Phe  
85

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570109  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:  
Thr Asn Gln Lys Lys Ser Leu Lys Ser Arg Pro Phe Phe Phe Leu Ser  
1 5 10 15  
Leu Leu Tyr Leu Ser Ala Ser Ala Gly Ser Leu Gln Gln Thr Arg Ser  
20 25 30  
Cys Ser Glu Arg Phe Val Gly Asp Arg Ser Ile Lys Ala Ser Arg Ala  
35 40 45  
Asn Arg Asn Gly Pro Arg Gln Asp Arg Met Pro Lys Pro Thr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..75  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570110  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:  
Met Thr Val Ser Val Gln Pro Ser Ser Val Gln Val Val Ala Glu Val  
1 5 10 15  
Val Ala Pro Glu Glu Xaa Ala Lys Pro Lys Gly Pro Ser Arg Cys Thr  
20 25 30  
Thr Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys Gly  
35 40 45  
Ser Leu Phe Cys Gly Lys His Thr Ala Met Gln Thr Tyr Met Thr Ala  
50 55 60  
Pro Ser Ile Thr Met Leu Leu Arg Lys Arg Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..601  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570111  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:  
aagacaaagc gcagaaaatg gtgggagcga ctgtagttag taaatggact cccctatgtg 60  
tgGCTtcgcc gccggagaga aactcggcaa gtctcaatcc acactgttct ccagccaggg 120  
ttaatttttag aacagcgttg gccgcatttc gtctcagtt ccgtcttttc tctcgcaatt 180  
ccgcgtctcg ccgccgtctt cgcgcttcca gtcgcgcga atcggcgggc agacgcggat 240  
gctcaaggaa agtatccata cacaggttcg ctogattgtg cgatgaaaac cttaaaagaa 300  
ggaggacctc tgaaatttta ctcaggtttc ccagtttaact gtgtcaggat tgccctcac 360  
gtcatgatga catggatctt cctaaaccag attacgaaat ttcaaaagaa gattggtatg 420  
tgaggaacga agacagcagc aaaaaataa gatgagaaga acgaaaacac aattggaatt 480  
gtgttcattt actttttaat catatacata acctgcotta aaagcatatt attgtagctg 540

tttgaacttt aattttttgt ttcggtcggt gattggtccg gtgaatttta aattttcttc 600  
c

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

Asp Lys Ala Gln Lys Met Val Gly Ala Thr Val Val Ser Lys Trp Thr  
1 5 10 15  
Pro Leu Cys Val Ala Ser Pro Pro Glu Arg Asn Ser Ala Ser Leu Asn  
20 25 30  
Pro His Cys Ser Pro Ala Arg Val Asn Phe Arg Thr Ala Leu Ala Ala  
35 40 45  
Phe Arg Pro Gln Phe Arg Leu Phe Ser Arg Asn Ser Ala Ser Arg Arg  
50 55 60  
Arg Leu Arg Ala Ser Ser Ser Ala Glu Ser Ala Ala Arg Arg Gly Cys  
65 70 75 80  
Ser Arg Lys Val Ser Ile His Arg Phe Ala Arg Leu Cys Asp Glu Asn  
85 90 95  
Leu Lys Arg Arg Arg Thr Ser Glu Ile Leu Leu Arg Phe Pro Ser Leu  
100 105 110  
Leu Cys Gln Asp Cys Pro Ser Arg His Asp Asp Met Asp Leu Pro Lys  
115 120 125  
Pro Asp Tyr Glu Ile Ser Lys Glu Asp Trp Tyr Val Arg Asn Glu Asp  
130 135 140  
Ser Ser Lys Lys Ile Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

Met Val Gly Ala Thr Val Val Ser Lys Trp Thr Pro Leu Cys Val Ala  
1 5 10 15  
Ser Pro Pro Glu Arg Asn Ser Ala Ser Leu Asn Pro His Cys Ser Pro  
20 25 30  
Ala Arg Val Asn Phe Arg Thr Ala Leu Ala Ala Phe Arg Pro Gln Phe  
35 40 45  
Arg Leu Phe Ser Arg Asn Ser Ala Ser Arg Arg Arg Leu Arg Ala Ser  
50 55 60  
Ser Ser Ala Glu Ser Ala Ala Arg Arg Gly Cys Ser Arg Lys Val Ser  
65 70 75 80  
Ile His Arg Phe Ala Arg Leu Cys Asp Glu Asn Leu Lys Arg Arg Arg  
85 90 95  
Thr Ser Glu Ile Leu Leu Arg Phe Pro Ser Leu Leu Cys Gln Asp Cys  
100 105 110  
Pro Ser Arg His Asp Asp Met Asp Leu Pro Lys Pro Asp Tyr Glu Ile

115 120 125  
Ser Lys Glu Asp Trp Tyr Val Arg Asn Glu Asp Ser Ser Lys Lys Ile  
130 135 140  
Arg  
145

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| accctaagcg tatataaatc atatagtttt cattttttcg tacttcttct ccatcgccgt  | 60  |
| ctaaaaaccc taatctcact ccgcctcctg cgagatccat caacacttac gcaaaaatga  | 120 |
| aggttgttgc tgcgtttttg cttgccgtct tgagcgggaa agcttcccca accactggcg  | 180 |
| atatcaagga tattcttgga tcagttggtg ctgagacaga ggattctcag attgagcttt  | 240 |
| tgttgaagga agtgaaaggg aaagacttgg ctgagctaatt tgctgctgga agggagaagt | 300 |
| tagcttcagt accatcagga ggtggtggtg gtgttgcggt tgcttctgct acatctggag  | 360 |
| gtggaggagg tgggtggtgct cctgctgctg agtccaagaa agaagagaag aaagaagaga | 420 |
| aagaagaatc cgatgatgac atgggtttca gtttgttcga gtaatgcggt atacttggca  | 480 |
| tttggttttg ctgtaccctt tcgaaatctt tatgtcgttg tttagtttgt tgtattcgac  | 540 |
| tatcttctta gactttgctg aaattctcaa gagatttttt Tactcaaaca tcagtcCact  | 600 |
| tgtgattggc atttatattt c                                            |     |

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Val Val Ala Ala Phe Leu Leu Ala Val Leu Ser Gly Lys Ala |  |
| 1 5 10 15                                                       |  |
| Ser Pro Thr Thr Gly Asp Ile Lys Asp Ile Leu Gly Ser Val Gly Ala |  |
| 20 25 30                                                        |  |
| Glu Thr Glu Asp Ser Gln Ile Glu Leu Leu Lys Glu Val Lys Gly     |  |
| 35 40 45                                                        |  |
| Lys Asp Leu Ala Glu Leu Ile Ala Ala Gly Arg Glu Lys Leu Ala Ser |  |
| 50 55 60                                                        |  |
| Val Pro Ser Gly Gly Gly Gly Val Ala Val Ala Ser Ala Thr Ser     |  |
| 65 70 75 80                                                     |  |
| Gly Gly Gly Gly Gly Gly Gly Ala Pro Ala Ala Glu Ser Lys Lys Glu |  |
| 85 90 95                                                        |  |
| Glu Lys Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser |  |
| 100 105 110                                                     |  |
| Leu Phe Glu                                                     |  |
| 115                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..534  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atattcaaag attagaaaca ttcttgatag atacaaaaaa cattttttca gacacaaatt  | 60  |
| cataaaatct ttgccttgag tagatcaaag ttctttacat taatcgttag aagatgagcc  | 120 |
| agtacgatca caaccagtct gcaggagcta acccaccgcc accgatgtct acctgtacat  | 180 |
| caccaccacc gccgattggg taccgcacta accaaccgag tcatggttcg gtagctcagg  | 240 |
| gtaaagtgga aaccaagtct aagggtgacg gattcttcaa aggctgtctt gcggccatgt  | 300 |
| gttgctgttg tgccctggac atttgcttct aagccatttg ggaattggga tggctctattt | 360 |
| atgacgagtt tatgtgaatg tgatgtgaat tattattatt attctctcca gccttattgt  | 420 |
| ataaattctc tattttttgt ttattatttt cttgtaatac tttgtgagac gaacatatta  | 480 |
| tgttttgtat ttggatctct actctctagt acttaaatta atttgtcttg cYtt        |     |

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Gln Tyr Asp His Asn Gln Ser Ala Gly Ala Asn Pro Pro Pro |  |
| 1                  5                  10                  15    |  |
| Pro Met Ser Thr Cys Thr Ser Pro Pro Pro Ile Gly Tyr Pro Thr     |  |
| 20                  25                  30                      |  |
| Asn Gln Pro Ser His Gly Ser Val Ala Gln Gly Lys Val Glu Thr Lys |  |
| 35                  40                  45                      |  |
| Ser Lys Gly Asp Gly Phe Phe Lys Gly Cys Leu Ala Ala Met Cys Cys |  |
| 50                  55                  60                      |  |
| Cys Cys Ala Leu Asp Ile Cys Phe                                 |  |
| 65                  70                                          |  |

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..55  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Thr Cys Thr Ser Pro Pro Pro Pro Ile Gly Tyr Pro Thr Asn |  |
| 1                  5                  10                  15    |  |
| Gln Pro Ser His Gly Ser Val Ala Gln Gly Lys Val Glu Thr Lys Ser |  |
| 20                  25                  30                      |  |
| Lys Gly Asp Gly Phe Phe Lys Gly Cys Leu Ala Ala Met Cys Cys Cys |  |
| 35                  40                  45                      |  |
| Cys Ala Leu Asp Ile Cys Phe                                     |  |
| 50                  55                                          |  |

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids

(2) INFORMATION FOR SEQ ID NO:1482:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..689

(D) OTHER INFORMATION: / Ceres Seq. ID 1570142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aaccaatctc | aaagcaaatt  | aaatacacta | ctacttcttg | agctttttaa | ctacacaaac | 60  |
| aaatggctcc | aagaaccccc  | cttgcaactc | tcgtttctct | caacctcctc | ttcttcactt | 120 |
| acacctctgc | aaccacaggg  | acttgctcta | aaaattccat | agagatcggt | acttggtgta | 180 |
| ctgtgctcaa | tctagtggac  | ctaacattgg | gaaaccacc  | tgtaaagcca | tgttgctcgc | 240 |
| tcatccaagg | cttggtgcac  | cttgaggctg | cggcctgcct | ctgcactcgc | ctcaaagcta | 300 |
| gcattcttgg | aattgtcaat  | attaaccctc | ctatcaactc | cagcgtaact | ctcaatgttt | 360 |
| gtagtaggaa | tgtctcaaag  | agtttccagt | gcgcgtaagt | tgaataccta | tgacatacct | 420 |
| atgaaacaaa | cgaatcatac  | csmtgcttga | acatgttttc | ttacctactt | gttgttggtc | 480 |
| taagatgttt | gttttttctt  | tctttctctg | attgttaata | atgaacgtac | gacgttctga | 540 |
| tgcaaaataa | tggaaaatgg  | ggttggtgtg | acaatcgaca | agtttgata  | tactccttta | 600 |
| ctttgttgtt | cctttgtttt  | gttggtctct | ttctttgtaa | ctgtgtattt | caaatttgct | 660 |
| taataaaaat | ataaaattgat | gttgtagcc  |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1570143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Arg | Thr | Pro | Leu | Ala | Leu | Phe | Val | Ser | Leu | Asn | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Phe | Thr | Tyr | Thr | Ser | Ala | Thr | Thr | Gly | Thr | Cys | Pro | Lys | Asn | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Glu | Ile | Gly | Thr | Cys | Val | Thr | Val | Leu | Asn | Leu | Val | Asp | Leu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Asn | Pro | Pro | Val | Lys | Pro | Cys | Cys | Ser | Leu | Ile | Gln | Gly | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

Ala Asp Leu Glu Ala Ala Cys Leu Cys Thr Ala Leu Lys Ala Ser  
65 70 75 80  
Ile Leu Gly Ile Val Asn Ile Asn Leu Pro Ile Asn Leu Ser Val Leu  
85 90 95  
Leu Asn Val Cys Ser Arg Asn Ala Pro Lys Ser Phe Gln Cys Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..716
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aatcaagcaa tccaaagcga ttaaactac tcaatctcag atctcgtaa acctagaaac    | 60  |
| ctcgagaaaa accgtatcaa tggcgccgaa agcagagaag aagcccgctg agaagaaacc  | 120 |
| agcttccgag aagccggtgg aggagaaatc aaaagccgag aaagctccgg cggagaagaa  | 180 |
| accaaaggcc ggaagaagc tcccgaagga agctggtgcc ggaggcgaca agaagaaaaa   | 240 |
| gatgaagaag aagagtgtcg agacttaca gatctacatc ttcaaggtgc ttaagcaagt   | 300 |
| tcattccgat atcggaatct ccagcaaagc gatggggatc atgaacagtt tcattaacga  | 360 |
| tatcttcgag aagcttgtct aagaggcgct gaagcttgct aggtacaata agadacctac  | 420 |
| gatcacttct cgggagattc agactgctgt gagattggtg cttcctggag agttggcgaa  | 480 |
| gcatgccgtt tctgagggga ctaaagccgt caccgaaattc accagctctt gaataattga | 540 |
| gttaggggtc ttatcatatg gatgttgctc tgcttttaggg ttaatggaat ttggaagatc | 600 |
| tgagttaggg ttttagaatg tctttaagt atctctgttt cgtttggaat ttctacgttt   | 660 |
| tgtaagtact gctgctattg ataatgtttg gagtctatat ttgctctttg tgtccc      |     |

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Lys Gln Ser Lys Ala Ile Lys Pro Thr Gln Ser Gln Ile Ser Leu |  |
| 1 5 10 15                                                       |  |
| Asn Leu Glu Thr Ser Arg Lys Thr Val Ser Met Ala Pro Lys Ala Glu |  |
| 20 25 30                                                        |  |
| Lys Lys Pro Ala Glu Lys Lys Pro Ala Ser Glu Lys Pro Val Glu Glu |  |
| 35 40 45                                                        |  |
| Lys Ser Lys Ala Glu Lys Ala Pro Ala Glu Lys Lys Pro Lys Ala Gly |  |
| 50 55 60                                                        |  |
| Lys Lys Leu Pro Lys Glu Ala Gly Ala Gly Gly Asp Lys Lys Lys Lys |  |
| 65 70 75 80                                                     |  |
| Met Lys Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr Ile Phe Lys Val |  |
| 85 90 95                                                        |  |
| Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Gly |  |
| 100 105 110                                                     |  |
| Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Gln Glu |  |
| 115 120 125                                                     |  |
| Ala Ser Lys Leu Ala Arg Tyr Asn Lys Xaa Pro Thr Ile Thr Ser Arg |  |
| 130 135 140                                                     |  |
| Glu Ile Gln Thr Ala Val Arg Leu Val Leu Pro Gly Glu Leu Ala Lys |  |

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 145 |     | 150 |     | 155 |     | 160 |
| His | Ala | Val | Ser | Glu | Thr | Lys |
|     |     | 165 |     |     | 170 |     |
|     |     |     |     |     |     | 175 |

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

Met Ala Pro Lys Ala Glu Lys Lys Pro Ala Glu Lys Lys Pro Ala Ser  
1 5 10 15  
Glu Lys Pro Val Glu Glu Lys Ser Lys Ala Glu Lys Ala Pro Ala Glu  
20 25 30  
Lys Lys Pro Lys Ala Gly Lys Lys Leu Pro Lys Glu Ala Gly Ala Gly  
35 40 45  
Gly Asp Lys Lys Lys Lys Met Lys Lys Lys Ser Val Glu Thr Tyr Lys  
50 55 60  
Ile Tyr Ile Phe Lys Val Leu Lys Gln Val His Pro Asp Ile Gly Ile  
65 70 75 80  
Ser Ser Lys Ala Met Gly Ile Met Asn Ser Phe Ile Asn Asp Ile Phe  
85 90 95  
Glu Lys Leu Ala Gln Glu Ala Ser Lys Leu Ala Arg Tyr Asn Lys Xaa  
100 105 110  
Pro Thr Ile Thr Ser Arg Glu Ile Gln Thr Ala Val Arg Leu Val Leu  
115 120 125  
Pro Gly Glu Leu Ala Lys His Ala Val Ser Glu Gly Thr Lys Ala Val  
130 135 140  
Thr Lys Phe Thr Ser Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

Met Lys Lys Lys Ser Val Glu Thr Tyr Lys Ile Tyr Ile Phe Lys Val  
1 5 10 15  
Leu Lys Gln Val His Pro Asp Ile Gly Ile Ser Ser Lys Ala Met Gly  
20 25 30  
Ile Met Asn Ser Phe Ile Asn Asp Ile Phe Glu Lys Leu Ala Gln Glu  
35 40 45  
Ala Ser Lys Leu Ala Arg Tyr Asn Lys Xaa Pro Thr Ile Thr Ser Arg  
50 55 60  
Glu Ile Gln Thr Ala Val Arg Leu Val Leu Pro Gly Glu Leu Ala Lys  
65 70 75 80  
His Ala Val Ser Glu Gly Thr Lys Ala Val Thr Lys Phe Thr Ser Ser  
85 90 95



(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..936
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| aactttatca  | cgctattctc  | aaacaagcaa  | agaaccttaa | ccaaaaagaa | aacgtctacg | 60  |
| gagacatatg  | gagaggaaac  | atcacttcgt  | gtaggttcac | aacgcttata | atggagcctg | 120 |
| gatctggtac  | aagctcaagc  | ccctccttga  | atcagccggc | caccgcgtta | ctgctgtcga | 180 |
| actcgccgcc  | tccgggatcg  | acccacgacc  | aatccaggcc | ggtgaaaccg | tcgacgaata | 240 |
| ctccaaaccg  | ttgatcgaaa  | ccctcaaata  | tcttccagag | aacgaagagg | taattctggg | 300 |
| tggattcagc  | ttcggaggca  | tcaacatcgc  | tctcgccggc | gacatatttc | cggcgaagat | 360 |
| taaggttctt  | gtgttcctca  | acgccttctt  | gcccgcacac | acccacgtgc | cttctcacgt | 420 |
| tctggacaag  | tatatggaga  | tgccctggagg | tttgggagat | tgtgagtttt | catctcatga | 480 |
| aacaagaaat  | gggacgatga  | gtttattTga  | agatgggacc | aaaattcatg | aaggcacgtc | 540 |
| tttaccaaaa  | ttgtcccata  | gaggattacg  | agctggcaaa | aatgttgcat | aggcaagggt | 600 |
| cattttttcac | agaggatcta  | tcaaagaaaag | aaaagttag  | cgaggaagga | tatggttcgg | 660 |
| tgcaacgagt  | ttacgttatg  | agtagtgaag  | acaaagccat | cccctgcgat | ttcattcggt | 720 |
| ggatgattga  | taattttcaac | gtctcgaaaag | tctacgagat | cgatggcgga | gatcacatgg | 780 |
| tgatgctctc  | caaaccctca  | aaactctttg  | actctctctc | tgctattgcc | accgattata | 840 |
| tgtaataatc  | ttaagtccgt  | tttacttttt  | tctcatcggt | actaataaaa | caaaccctt  | 900 |
| tttcggggca  | actttcatca  | aaaaacaaaa  | cttatg     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Lys | His | His | Phe | Val | Leu | Val | His | Asn | Ala | Tyr | His | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Trp | Ile | Trp | Tyr | Lys | Leu | Lys | Pro | Leu | Leu | Glu | Ser | Ala | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Arg | Val | Thr | Ala | Val | Glu | Leu | Ala | Ala | Ser | Gly | Ile | Asp | Pro | Arg | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ile | Gln | Ala | Val | Glu | Thr | Val | Asp | Glu | Tyr | Ser | Lys | Pro | Leu | Ile | Glu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Thr | Leu | Lys | Ser | Leu | Pro | Glu | Asn | Glu | Glu | Val | Ile | Leu | Val | Gly | Phe |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  | 80  |
| Ser | Phe | Gly | Gly | Ile | Asn | Ile | Ala | Leu | Ala | Ala | Asp | Ile | Phe | Pro | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ile | Lys | Val | Leu | Val | Phe | Leu | Asn | Ala | Phe | Leu | Pro | Asp | Thr | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| His | Val | Pro | Ser | His | Val | Leu | Asp | Lys | Tyr | Met | Glu | Met | Pro | Gly | Gly |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Leu | Gly | Asp | Cys | Glu | Phe | Ser | Ser | His | Glu | Thr | Arg | Asn | Gly | Thr | Met |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Ser | Leu | Phe | Glu | Asp | Gly | Thr | Lys | Ile | His | Glu | Gly | Thr | Ser | Leu | Pro |

(2) INFORMATION FOR SEQ ID NO:1490:

(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

(2) INFORMATION FOR SEQ ID NO:1491:

(A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

(2) INFORMATION FOR SEQ ID NO:1492:

(A) LENGTH: 1220 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1570170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

|             |            |            |             |            |            |      |
|-------------|------------|------------|-------------|------------|------------|------|
| atttataatca | tccccttgaa | ttttccaagt | tttctccttt  | tgtcttctct | aactattttc | 60   |
| ccttaaaata  | aaaatccaat | ttttctttgt | ttcagtcctc  | tcttctgctc | attgatcttt | 120  |
| taattaactt  | tgattctctc | cgtttatgga | ttaaccattt  | gatcgagata | actctccaag | 180  |
| aaatcgactg  | agttcgtaac | ttgttggtgt | ctgatctttt  | aaagattcaa | ccttttttgg | 240  |
| tccgatcatg  | gctggtgctg | agaatgctgg | tgtcaaagtg  | gactcttctg | gtcagaattt | 300  |
| agacaacaac  | aacactgctg | cttcagctac | cgagacgaca  | aagccgccat | gtcctgatga | 360  |
| tgatcaaagc  | cctaaatctg | actcatccac | tcctcttacc  | atcgattcga | ctcctgaaac | 420  |
| tgacgatcgg  | atcaatgaga | ctgctcaaaa | ggttcagact  | ttaaattggg | ttagtggaaa | 480  |
| tggtgagaga  | gataacaatg | gagagatcaa | agatttggtg  | gatgcgtttt | ctaagcttaa | 540  |
| tccgatggct  | caggagtttg | ttcctccttc | tcttgctcga  | agtcaatctg | gggttttgag | 600  |
| aaatggatta  | gggtttacta | acaattttgc | agccccacct  | aaacttgctg | atgggaatga | 660  |
| tcattttcct  | agaaggagaa | ggagttttgg | ccaaggggaag | cgaagaatga | acaaaaggac | 720  |
| aagcttggtg  | cagaaggatg | atgtaatcag | gacaactgta  | tatgtctctg | acatcgacca | 780  |
| acaggttaca  | gaggagaacc | tcgcaggtgt | ctttattaac  | tgtggacagg | ttgttgattg | 840  |
| tcgtgtatgc  | ggtgatccaa | attctgtcct | tcgtttcgct  | ttcattgaat | ttaccaatga | 900  |
| agagggagct  | agagctgctt | tgagcatgtc | gggtactgtg  | ctaggttttt | accctcttaa | 960  |
| ggttcttctc  | tccaaaacag | ctattgtctc | tgtaaaccgg  | acttttcttc | cacgatctga | 1020 |
| ggatgagcgt  | gagatgtgcg | ttaggactgt | ttactgtacc  | aacattgaca | agcggatcac | 1080 |
| tcaaattgac  | ttgaaaggct | tctttgaaat | gctttgcggg  | gaggttcac  | gtctgaggct | 1140 |
| tggagactat  | caccaccaa  | cccgtattgc | ttttgttgag  | tttgcatg   | cgaaaagcgc | 1200 |

aaCttgCtgc gcttcaactgc

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1570171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Ala | Glu | Asn | Ala | Gly | Val | Lys | Val | Asp | Ser | Ser | Gly | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Leu | Asp | Asn | Asn | Asn | Thr | Ala | Ala | Ser | Ala | Thr | Glu | Thr | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Pro | Pro | Cys | Pro | Asp | Asp | Asp | Gln | Ser | Pro | Lys | Ser | Asp | Ser | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Thr | Ile | Asp | Ser | Thr | Pro | Glu | Thr | Asp | Asp | Arg | Ile | Asn | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ala | Gln | Lys | Val | Gln | Thr | Leu | Asn | Gly | Phe | Ser | Gly | Asn | Gly | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Asp | Asn | Asn | Gly | Glu | Ile | Lys | Asp | Leu | Ala | Asp | Ala | Phe | Ser | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Asn | Pro | Met | Ala | Gln | Glu | Phe | Val | Pro | Pro | Ser | Leu | Ala | Arg | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Ser | Gly | Val | Leu | Arg | Asn | Gly | Leu | Gly | Phe | Thr | Asn | Asn | Phe | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Pro | Lys | Leu | Ala | Asp | Gly | Asn | Asp | His | Phe | Pro | Arg | Arg | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Ser | Phe | Gly | Gln | Gly | Lys | Arg | Arg | Met | Asn | Lys | Arg | Thr | Ser | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Gln | Lys | Asp | Asp | Val | Ile | Arg | Thr | Thr | Val | Tyr | Val | Ser | Asp | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

```
(2) INFORMATION FOR SEQ ID NO:1494:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..225
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570172
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:
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[illegible]

225

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1570173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

Met Asn Lys Arg Thr Ser Leu Ala Gln Lys Asp Asp Val Ile Arg Thr  
1 5 10 15  
Thr Val Tyr Val Ser Asp Ile Asp Gln Gln Val Thr Glu Glu Asn Leu  
20 25 30  
Ala Gly Val Phe Ile Asn Cys Gly Gln Val Val Asp Cys Arg Val Cys  
35 40 45  
Gly Asp Pro Asn Ser Val Leu Arg Phe Ala Phe Ile Glu Phe Thr Asn  
50 55 60  
Glu Glu Gly Ala Arg Ala Ala Leu Ser Met Ser Gly Thr Val Leu Gly  
65 70 75 80  
Phe Tyr Pro Leu Lys Val Leu Pro Ser Lys Thr Ala Ile Ala Pro Val  
85 90 95  
Asn Pro Thr Phe Leu Pro Arg Ser Glu Asp Glu Arg Glu Met Cys Val  
100 105 110  
Arg Thr Val Tyr Cys Thr Asn Ile Asp Lys Arg Ile Thr Gln Ile Asp  
115 120 125  
Leu Lys Gly Phe Phe Glu Met Leu Cys Gly Glu Val His Arg Leu Arg  
130 135 140  
Leu Gly Asp Tyr His His Gln Thr Arg Ile Ala Phe Val Glu Phe Ala  
145 150 155 160  
Met Ala Glu Ser Ala Thr Cys Cys Ala Ser Leu  
165 170

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1460

(D) OTHER INFORMATION: / Ceres Seq. ID 1570183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

atTTTTtgagt tctcagatTTT caaacacaaa agTTTcgtct ccgatttTaat ctttctacgt 60  
cttggtttat gagctcaaag gagaagccca ctctcgaggg tacgcggatt aagaccgcga 120  
aaaggaatat tgctgctcct ctgcaccctg ctgctttttc tgatgcacta gttcagattt 180  
atctggataa tgctggtgat ctggaacttg ttgccagaag tttagagtca tctgatctta 240  
atttctcaag atacggtgat attttctttg aggttgTTTT cattggagga cgtactcaaa 300  
ctggttcagt gaaatctgat gaaggggaac gccaccctta ctctataatc gactgtgaac 360  
caaagcgtga agctatTTTta ccatcagttg tatacatata gaaaattttg cggaggaaaag 420  
ccttccttat taagaacctt gagaatgtta cacggagatt cttacagtca ctggagcttt 480  
ttgaggagaa tgagagggaag aagcttgcaa tattcacagc acttgcatTTT tcacagaagc 540  
tctcaggatt acctgcagag actgtcttcc agccattgct taaggatact cttgttgcca 600  
aagggatagt tctcaatttt gtaacagact tcttcaatga atatttggtt gagaacagtc 660  
ttgatgactt gatttctatt ctgaggcgtg gcaagatgga tgacaaactc ttggagttcc 720  
tgccaccac aaagcggact acagaaagtt ttgccgagca tttcactaag gcaggattga 780  
cagctctggt agagtacaat gaaaggaaaa tatttgaggt gaagctgaag gaaatcaaa 840

```
cggtccttac gagccaagtg acagaggaaa taaacgtaga tgaagtgact gaaatgggtga 900
agcaacacggt gaaagatgca aagctgccag agAactgagg ttgtgcatgt gatctgggat 960
aggataatga atgctgttca atggtctggg aaaaaccagc agcagaattc gaatgctgta 1020
ttacgccaag tgaaaacatg ggcacccctt ctgaacacgc tgtgtagcac cggaacatg 1080
gagatggaac tgatgtataa agtacagatg caatgctatg aggatgcaaa gctgatgaaa 1140
gtgtttcctg aggtagttag atctctGTmt gTaTrmAygg atgtgcttgc ggaagacacc 1200
attctgcact ggtatcgcaa agggaccaac cctaagggca ggcaaacgtt tgtgaaggga 1260
ttggaaccgt ttgtgaattg gctcgaagag gccgaagaag aggagttagt gagacgctct 1320
gcttcttggt ttctcttttt actctcttct aataaaagaa agacaatatt ttacttctct 1380
taacgcaaaa ttcagatgct ctacattggt ggtgacttgg tgtgatctct tttttgaatg 1440
aataagtact tcttttagttg
```

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1570184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

```
Met Ser Ser Lys Glu Lys Pro Thr Leu Gly Gly Thr Arg Ile Lys Thr
1 5 10 15
Arg Lys Arg Asn Ile Ala Ala Pro Leu Asp Pro Ala Ala Phe Ser Asp
20 25 30
Ala Leu Val Gln Ile Tyr Leu Asp Asn Ala Gly Asp Leu Glu Leu Val
35 40 45
Ala Arg Ser Leu Glu Ser Ser Asp Leu Asn Phe Ser Arg Tyr Gly Asp
50 55 60
Ile Phe Phe Glu Val Val Phe Ile Gly Gly Arg Thr Gln Thr Gly Ser
65 70 75 80
Val Lys Ser Asp Glu Gly Glu Arg His Pro Tyr Ser Ile Ile Asp Cys
85 90 95
Glu Pro Lys Arg Glu Ala Ile Leu Pro Ser Val Val Tyr Ile Gln Lys
100 105 110
Ile Leu Arg Arg Lys Ala Phe Leu Ile Lys Asn Leu Glu Asn Val Thr
115 120 125
Arg Arg Phe Leu Gln Ser Leu Glu Leu Phe Glu Glu Asn Glu Arg Lys
130 135 140
Lys Leu Ala Ile Phe Thr Ala Leu Ala Phe Ser Gln Lys Leu Ser Gly
145 150 155 160
Leu Pro Ala Glu Thr Val Phe Gln Pro Leu Leu Lys Asp Thr Leu Val
165 170 175
Ala Lys Gly Ile Val Leu Asn Phe Val Thr Asp Phe Phe Asn Glu Tyr
180 185 190
Leu Val Glu Asn Ser Leu Asp Asp Leu Ile Ser Ile Leu Arg Arg Gly
195 200 205
Lys Met Asp Asp Lys Leu Leu Glu Phe Leu Pro Pro Thr Lys Arg Thr
210 215 220
Thr Glu Ser Phe Ala Glu His Phe Thr Lys Ala Gly Leu Thr Ala Leu
225 230 235 240
Val Glu Tyr Asn Glu Arg Lys Ile Phe Glu Val Lys Leu Lys Glu Ile
245 250 255
Lys Ala Val Leu Thr Ser Gln Val Thr Glu Glu Ile Asn Val Asp Glu
260 265 270
Val Thr Glu Met Val Lys Gln Gln Val Lys Asp Ala Lys Leu Pro Glu
275 280 285
Asn
```

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..557
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| actttacttt | tccggaggaa | tagaaaattg | ggggctaggg | ttcgcaattg | tagttttcga  | 60  |
| gcgaagaaga | tgatcgaggt | ggttctcaac | gatcgtttag | ggaaaaaagt | taggggtgaag | 120 |
| tgtaacRgAt | gatgacacga | tcggtgatct | gaagaagctt | gtcgcggcac | aaaccggaac  | 180 |
| acgagccgag | aagatcagaa | ttcagaagtg | gtacaacatc | tacaaggatc | acatcactct  | 240 |
| caaggactat | gagatccatg | acggcatggg | tcttgagctt | tactacaact | aggccaatcg  | 300 |
| aaggagctaa | gctgaaggag | tggtgttgat | ttggacacct | acataaactc | atatcaacca  | 360 |
| tgttacatct | aaaaaagaca | caagtatggt | gtaagacgtg | ataacttcaa | atttgtggta  | 420 |
| ataataatac | attcactgtc | aatggtttta | aacccttcca | aattgtcaga | ttgatttctg  | 480 |
| gttatctcta | agtttgtagt | atattagtct | ttttggttgt | attgatgtgc | tctttctcca  | 540 |
| aatgttacc  | atcttcc    |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Leu | Phe | Arg | Arg | Asn | Arg | Lys | Leu | Gly | Ala | Arg | Val | Arg | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Ser | Phe | Arg | Ala | Lys | Lys | Met | Ile | Glu | Val | Val | Leu | Asn | Asp | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Gly | Lys | Lys | Val | Arg | Val | Lys | Cys | Asn | Xaa |     |     |     |     |     |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1625
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| gagtaacatc | gagacaaaga | agaaaagcta  | aaaaagagaa  | cccaaagaa   | tcgaatattt | 60  |
| attatttcgc | cccgaagatt | ctattttctga | tcattttacac | ccctaaaaag  | agtagagctt | 120 |
| tcgtgaagcc | accatgtgtg | gaggagctat  | aatctccgat  | ttcatacctc  | cgccgaggtc | 180 |
| cctccgctgc | actaacgagt | ttatctggcc  | ggatctgaaa  | aacaaagtga  | aagcttcaaa | 240 |
| gaagagatcg | aataagcgat | ccgattttctt | cgatcttgac  | gatgatattcg | aagctgattt | 300 |
| ccaaggggtt | aaggatgact | cggtttttga  | ctgcgaagac  | gatgatgatg  | tcttcgtcaa | 360 |
| tgtaagcct  | ttcgtcttca | ccgcaactac  | taagcccgta  | gcttccgctt  | tcgtctccac | 420 |
| tgtaggttca | gcatatgcc  | agaaaactgt  | agagtccgct  | gagcaagctg  | agaaatcttc | 480 |
| taagaggaag | aggaagaatc | agtaccgagg  | gattaggcag  | cgtccttggg  | gaaaatgggc | 540 |

tgccggagatc cgtgatccgA gaaaaggctc ccgagaatgg cttggaacat tcgacactgc 600  
tgaggaagca gcaagagctt atgatgctgc agcacgcaga atccgtggca cgaaagctaa 660  
ggtgaatttt cccgaggaga agaaccctag cgtcgtatcc cagaaacgtc ctagtgtctaa 720  
gactaataat cttcagaaat cagtggctaa accaaacaaa agcgtaaactt tgggttcagca 780  
gccaacacat ctgagtcagc agtaactgcaa caactccttt gacaactcctt ttggtgatata 840  
gagtttcatg gaagagaagc ctcagatgta caacaatcag tttgggttaa caaactcggt 900  
cgatgctgga ggtaacaatg gataaccagta tttcagttcc gatcagggca gtaactcctt 960  
cgactgttct gagttcgggt ggagtgatca cggccctaaa acacccgaga tctcttcaat 1020  
gcttgtcaat aacaacgaag catcatttgt tgaagaaacc aatgcagcca agaagctcaa 1080  
acctaactct gatgagtcag acgatctgat ggcatacctt gacaacgcct tgtgggacac 1140  
cccactagaa gtgaaagcca tgcttggcgc agatgctgggt gctgtgactc aggaagagga 1200  
aaaccagtg gagctatgga gcttagatga gatcaatttc atgctggaag gagacttttg 1260  
aagtgcaga tggttcctta gtttgtaaat aaagctgtgt tggattttgc tgttggggga 1320  
tggtagaagt cacacctcaa gctctatgca ttggtatctc atgagcctct cttccataga 1380  
gagtttctct tttaattttg tcgaaataaa aaaggtgtga tgaagtaaat agaggtataa 1440  
taatatctat ctattaagtc ttgttttgtt ctttcatttt tgtatttctt ttctatttaa 1500  
aagacagttt attagtcttc tgagctctct ttttgatctt tgttatagcg tatcatcacc 1560  
ctcgaaagtg taatgttttg taccocccaaa cttgttttagc attataataa agtctctttg 1620  
gaacc

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1570202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Gly | Gly | Ala | Ile | Ile | Ser | Asp | Phe | Ile | Pro | Pro | Pro | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Val | Thr | Asn | Glu | Phe | Ile | Trp | Pro | Asp | Leu | Lys | Asn | Lys | Val |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ala | Ser | Lys | Lys | Arg | Ser | Asn | Lys | Arg | Ser | Asp | Phe | Phe | Asp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Asp | Asp | Phe | Glu | Ala | Asp | Phe | Gln | Gly | Phe | Lys | Asp | Asp | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asp | Cys | Glu | Asp | Asp | Asp | Asp | Val | Phe | Val | Asn | Val | Lys | Pro | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Phe | Thr | Ala | Thr | Thr | Lys | Pro | Val | Ala | Ser | Ala | Phe | Val | Ser | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Gly | Ser | Ala | Tyr | Ala | Lys | Lys | Thr | Val | Glu | Ser | Ala | Glu | Gln | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | Ser | Ser | Lys | Arg | Lys | Arg | Lys | Asn | Gln | Tyr | Arg | Gly | Ile | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Arg | Pro | Trp | Gly | Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Arg | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Gly | Ser | Arg | Glu | Trp | Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Glu | Ala | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Ala | Tyr | Asp | Ala | Ala | Ala | Arg | Arg | Ile | Arg | Gly | Thr | Lys | Ala | Lys |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Asn | Phe | Pro | Glu | Glu | Lys | Asn | Pro | Ser | Val | Val | Ser | Gln | Lys | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Ser | Ala | Lys | Thr | Asn | Asn | Leu | Gln | Lys | Ser | Val | Ala | Lys | Pro | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Ser | Val | Thr | Leu | Val | Gln | Gln | Pro | Thr | His | Leu | Ser | Gln | Gln | Tyr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Asn | Asn | Ser | Phe | Asp | Asn | Ser | Phe | Gly | Asp | Met | Ser | Phe | Met | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |



Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Thr Asn Ser Phe  
245 250 255  
Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly  
260 265 270  
Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro  
275 280 285  
Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn Asn Glu Ala Ser  
290 295 300  
Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys Pro Asn Ser Asp  
305 310 315 320  
Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp Asp Thr  
325 330 335  
Pro Leu Glu Val Lys Ala Met Leu Gly Ala Asp Ala Gly Ala Val Thr  
340 345 350  
Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu Asp Glu Ile Asn  
355 360 365  
Phe Met Leu Glu Gly Asp Phe  
370 375

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..996
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

|          |      |         |         |       |         |         |         |       |        |         |       |     |
|----------|------|---------|---------|-------|---------|---------|---------|-------|--------|---------|-------|-----|
| aatcaaat | ttt  | gtcatt  | gtgt    | tatt  | caaatt  | ttt     | gagaaa  | tggt  | gagaag | taccaa  | aaggt | 60  |
| cgtcagaa | aaa  | tagaga  | tga     | aaaa  | atggaa  | aacgaa  | agca    | acct  | tcaggt | tacttt  | tctca | 120 |
| aaaaga   | agat | tcggt   | tcttt   | caaaa | aagct   | agtga   | acttt   | gcac  | attaag | tggtgc  | cagag | 180 |
| attctgt  | tga  | ttgtg   | ttctc   | tcttg | gtggg   | aaagt   | gtttt   | cttt  | tgcca  | tccaag  | tgtt  | 240 |
| caagaact | ca   | ttcat   | cgctt   | ttcga | atcct   | aaccata | aatt    | ctgcc | attgt  | ccatcat | cag   | 300 |
| aacaaca  | atc  | tccaact | tgt     | tga   | aaccgt  | ccgat   | tagaa   | atat  | ccaata | tctca   | acaat | 360 |
| atactc   | actg | aggtg   | ctggc   | aaacc | aggaa   | aaggaga | aac     | aga   | agaga  | ggtttt  | ggac  | 420 |
| ctattga  | aag  | aatcc   | agaga   | aca   | agtagga | aactg   | gtatg   | aaaa  | agatgt | gaa     | gatc  | 480 |
| gacatga  | atg  | aaacca  | aacca   | gctga | tatct   | gctctt  | caag    | atgt  | gaaaaa | gaa     | actg  | 540 |
| agagaaa  | tgt  | ctcaat  | atttc   | tcaag | taaa    | gtttc   | gcaga   | attac | tttgg  | tcaa    | agt   | 600 |
| ggcgtg   | attg | gtggt   | ggtaa   | tg    | ttggc   | att     | gatc    | ttttt | g      | atcaa   | aga   | 660 |
| aactata  | atc  | caa     | acatggt | gttt  | cccaat  | cata    | caccac  | caat  | gtttg  | ata     | acaat | 720 |
| gatggag  | ttc  | tcgtt   | ccgat   | atcca | acatg   | aacta   | catgt   | caag  | ttaca  | ctt     | caacc | 780 |
| agctaga  | gtc  | tga     | agctaga | aga   | acatcct | aat     | caatatt | tg    | cg     | ttattt  | tg    | 840 |
| tactgtt  | agg  | attgt   | tcttg   | tatt  | gtgaga  | ctta    | agttt   | tttt  | ttc    | taatt   | tgtt  | 900 |
| cagctg   | gttg | gttt    | tttcatt | ttatt | cg      | ttt     | gttttc  | tttg  | K      | tttt    | g     | 960 |
| gtatcc   | agaa | taa     | atttatt | tatt  | cttttaa | ttttac  |         |       |        |         |       |     |

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

Asn Gln Ile Cys His Leu Phe Ile Gln Ile Phe Glu Lys Met Val Arg  
1 5 10 15

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1570229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Arg | Ser | Thr | Lys | Gly | Arg | Gln | Lys | Ile | Glu | Met | Lys | Lys | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | Glu | Ser | Asn | Leu | Gln | Val | Thr | Phe | Ser | Lys | Arg | Arg | Phe | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Lys | Lys | Ala | Ser | Glu | Leu | Cys | Thr | Leu | Ser | Gly | Ala | Glu | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Ile | Val | Phe | Ser | Pro | Gly | Gly | Lys | Val | Phe | Ser | Phe | Gly | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Val | Gln | Glu | Leu | Ile | His | Arg | Phe | Ser | Asn | Pro | Asn | His | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ala | Ile | Val | His | His | Gln | Asn | Asn | Asn | Leu | Gln | Leu | Val | Glu | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Pro | Asp | Arg | Asn | Ile | Gln | Tyr | Leu | Asn | Asn | Ile | Leu | Thr | Glu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Asn | Gln | Glu | Lys | Glu | Lys | Gln | Lys | Arg | Met | Val | Leu | Asp | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Lys | Glu | Ser | Arg | Glu | Gln | Val | Gly | Asn | Trp | Tyr | Glu | Lys | Asp | Val |

130 135 140  
Lys Asp Leu Asp Met Asn Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln  
145 150 155 160  
Asp Val Lys Lys Lys Leu Val Arg Glu Met Ser Gln Tyr Ser Gln Val  
165 170 175  
Asn Val Ser Gln Asn Tyr Phe Gly Gln Ser Ser Gly Val Ile Gly Gly  
180 185 190  
Gly Asn Val Gly Ile Asp Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn  
195 200 205  
Tyr Asn Pro Asn Met Val Phe Pro Asn His Thr Pro Pro Met Phe Gly  
210 215 220  
Tyr Asn Asn Asp Gly Val Leu Val Pro Ile Ser Asn Met Asn Tyr Met  
225 230 235 240  
Ser Ser Tyr Asn Phe Asn Gln Ser  
245

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1570230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

Met Lys Lys Met Glu Asn Glu Ser Asn Leu Gln Val Thr Phe Ser Lys  
1 5 10 15  
Arg Arg Phe Gly Leu Phe Lys Lys Ala Ser Glu Leu Cys Thr Leu Ser  
20 25 30  
Gly Ala Glu Ile Leu Leu Ile Val Phe Ser Pro Gly Gly Lys Val Phe  
35 40 45  
Ser Phe Gly His Pro Ser Val Gln Glu Leu Ile His Arg Phe Ser Asn  
50 55 60  
Pro Asn His Asn Ser Ala Ile Val His His Gln Asn Asn Asn Leu Gln  
65 70 75 80  
Leu Val Glu Thr Arg Pro Asp Arg Asn Ile Gln Tyr Leu Asn Asn Ile  
85 90 95  
Leu Thr Glu Val Leu Ala Asn Gln Glu Lys Glu Lys Gln Lys Arg Met  
100 105 110  
Val Leu Asp Leu Leu Lys Glu Ser Arg Glu Gln Val Gly Asn Trp Tyr  
115 120 125  
Glu Lys Asp Val Lys Asp Leu Asp Met Asn Glu Thr Asn Gln Leu Ile  
130 135 140  
Ser Ala Leu Gln Asp Val Lys Lys Lys Leu Val Arg Glu Met Ser Gln  
145 150 155 160  
Tyr Ser Gln Val Asn Val Ser Gln Asn Tyr Phe Gly Gln Ser Ser Gly  
165 170 175  
Val Ile Gly Gly Gly Asn Val Gly Ile Asp Leu Phe Asp Gln Arg Arg  
180 185 190  
Asn Ala Phe Asn Tyr Asn Pro Asn Met Val Phe Pro Asn His Thr Pro  
195 200 205  
Pro Met Phe Gly Tyr Asn Asn Asp Gly Val Leu Val Pro Ile Ser Asn  
210 215 220  
Met Asn Tyr Met Ser Ser Tyr Asn Phe Asn Gln Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1062  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570235  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

```
aaaaaaattt gttcgattct cattcttctt ctcacagtcg taaaccctaa aaaaaaaca 60
gagaaatcaa atttcaatct cgaaggatct acaaagaagc atgacgaccg gagatctcgt 120
taatatccat cctactgagc ttaaattccc ctttgagttg aagaaacaaa gttcgtgttc 180
gatgcaattg accaacaaga caactactca atgtgtcgtt tttaaggtta aaacaaccaa 240
tcctcgcaaa tactgtgttc gtccaaacac tgggtgtgtc ttgcccgtg attcctgcaa 300
tgttacagtg acgatgcaag ccagaaaga ggcaccactt gatatgcaat gcaaagacaa 360
gttccttggt cagactgttg ttgtctctga tgggtactact tccaaagaag tcctcgtga 420
aatgttcaac aaggaggctg gtagagtgat tgaggatttc aaactgcgag ttgtttacat 480
tcctgctaatt cctccttcac ctgtccctga aggttctgaa gaaggcaact ctctatggc 540
ttccctcaac gatattgcct ctcaatctgc ctcactcttt gatgacgtgt caaaaacgtt 600
tgaagaaaca agtgagaaat cttcabaggc atggtctatg atttccaaat tgacggagga 660
gaagacttct gctactcaac aaagtcagaa gctccgtctc gaactggaaa tgctgaggaa 720
agaaacAaag caagaagcag tcgggtggtc attccttgct cttgatgctg ctggtgggtc 780
tgctcggttg cgtgattggc tacttattga accggatata aacgccatgg ggtagcttc 840
atcatccttt taatcatcaa atcttgcaaa gttcttaaga tttttgacca gattttcgt 900
aaayggcggg ggtttttttt taaaagtttc atatttaagc tgtaaaatca gtagctgtag 960
cacaggaaca ggtgtgattt tgtggcaggt ttcttggtat tgatttaaac acactttcga 1020
gtctgtagta agatctcaag agtcgttctt atgattggaa tt
```

(2) INFORMATION FOR SEQ ID NO:1507:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..250  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

```
Met Thr Thr Gly Asp Leu Val Asn Ile His Pro Thr Glu Leu Lys Phe
1 5 10 15
Pro Phe Glu Leu Lys Lys Gln Ser Ser Cys Ser Met Gln Leu Thr Asn
20 25 30
Lys Thr Thr Thr Gln Cys Val Ala Phe Lys Val Lys Thr Thr Asn Pro
35 40 45
Arg Lys Tyr Cys Val Arg Pro Asn Thr Gly Val Val Leu Pro Gly Asp
50 55 60
Ser Cys Asn Val Thr Val Thr Met Gln Ala Gln Lys Glu Ala Pro Leu
65 70 75 80
Asp Met Gln Cys Lys Asp Lys Phe Leu Val Gln Thr Val Val Val Ser
85 90 95
Asp Gly Thr Thr Ser Lys Glu Val Leu Ala Glu Met Phe Asn Lys Glu
100 105 110
Ala Gly Arg Val Ile Glu Asp Phe Lys Leu Arg Val Val Tyr Ile Pro
115 120 125
Ala Asn Pro Pro Ser Pro Val Pro Glu Gly Ser Glu Glu Gly Asn Ser
130 135 140
Pro Met Ala Ser Leu Asn Asp Ile Ala Ser Gln Ser Ala Ser Leu Phe
145 150 155 160
Asp Asp Val Ser Lys Thr Phe Glu Glu Thr Ser Glu Lys Ser Ser Xaa
165 170 175
Ala Trp Ser Met Ile Ser Lys Leu Thr Glu Glu Lys Thr Ser Ala Thr
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |
| Gln | Gln | Ser | Gln | Lys | Leu | Arg | Leu | Glu | Leu | Glu | Met | Leu | Arg | Lys | Glu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Thr | Lys | Gln | Glu | Ala | Val | Gly | Trp | Ser | Phe | Leu | Ala | Leu | Asp | Ala | Ala |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gly | Gly | Ser | Ala | Arg | Leu | Arg | Asp | Trp | Leu | Leu | Ile | Glu | Pro | Asp | Ile |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Asn | Ala | Met | Gly | Leu | Ala | Ser | Ser | Ser | Phe |     |     |     |     |     |     |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1570237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Leu | Thr | Asn | Lys | Thr | Thr | Thr | Cys | Val | Ala | Phe | Lys | Val |     |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Thr | Thr | Asn | Pro | Arg | Lys | Tyr | Cys | Val | Arg | Pro | Asn | Thr | Gly | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Val | Leu | Pro | Gly | Asp | Ser | Cys | Asn | Val | Thr | Val | Thr | Met | Gln | Ala | Gln |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Lys | Glu | Ala | Pro | Leu | Asp | Met | Gln | Cys | Lys | Asp | Lys | Phe | Leu | Val | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Val | Val | Val | Ser | Asp | Gly | Thr | Thr | Ser | Lys | Glu | Val | Leu | Ala | Glu |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Met | Phe | Asn | Lys | Glu | Ala | Gly | Arg | Val | Ile | Glu | Asp | Phe | Lys | Leu | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Val | Val | Tyr | Ile | Pro | Ala | Asn | Pro | Pro | Ser | Pro | Val | Pro | Glu | Gly | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Glu | Gly | Asn | Ser | Pro | Met | Ala | Ser | Leu | Asn | Asp | Ile | Ala | Ser | Gln |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ser | Ala | Ser | Leu | Phe | Asp | Asp | Val | Ser | Lys | Thr | Phe | Glu | Glu | Thr | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Lys | Ser | Ser | Xaa | Ala | Trp | Ser | Met | Ile | Ser | Lys | Leu | Thr | Glu | Glu |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Lys | Thr | Ser | Ala | Thr | Gln | Gln | Ser | Gln | Lys | Leu | Arg | Leu | Glu | Leu | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Met | Leu | Arg | Lys | Glu | Thr | Lys | Gln | Glu | Ala | Val | Gly | Trp | Ser | Phe | Leu |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ala | Leu | Asp | Ala | Ala | Gly | Gly | Ser | Ala | Arg | Leu | Arg | Asp | Trp | Leu | Leu |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Ile | Glu | Pro | Asp | Ile | Asn | Ala | Met | Gly | Leu | Ala | Ser | Ser | Ser | Phe |     |  |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

Met Gln Ala Gln Lys Glu Ala Pro Leu Asp Met Gln Cys Lys Asp Lys  
1 5 10 15  
Phe Leu Val Gln Thr Val Val Val Ser Asp Gly Thr Thr Ser Lys Glu  
20 25 30  
Val Leu Ala Glu Met Phe Asn Lys Glu Ala Gly Arg Val Ile Glu Asp  
35 40 45  
Phe Lys Leu Arg Val Val Tyr Ile Pro Ala Asn Pro Pro Ser Pro Val  
50 55 60  
Pro Glu Gly Ser Glu Glu Gly Asn Ser Pro Met Ala Ser Leu Asn Asp  
65 70 75 80  
Ile Ala Ser Gln Ser Ala Ser Leu Phe Asp Asp Val Ser Lys Thr Phe  
85 90 95  
Glu Glu Thr Ser Glu Lys Ser Ser Xaa Ala Trp Ser Met Ile Ser Lys  
100 105 110  
Leu Thr Glu Glu Lys Thr Ser Ala Thr Gln Gln Ser Gln Lys Leu Arg  
115 120 125  
Leu Glu Leu Glu Met Leu Arg Lys Glu Thr Lys Gln Glu Ala Val Gly  
130 135 140  
Trp Ser Phe Leu Ala Leu Asp Ala Ala Gly Gly Ser Ala Arg Leu Arg  
145 150 155 160  
Asp Trp Leu Leu Ile Glu Pro Asp Ile Asn Ala Met Gly Leu Ala Ser  
165 170 175  
Ser Ser Phe

(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| atcaagttaa  | aaaaaaaaaca | gaaggagaaa | tggcaataag  | ttttagaact  | ctagctcttt | 60   |
| tgacctctc   | ggtgttacta  | atttccatat | ctctcggcgt  | cgtcacagca  | acagagtcgc | 120  |
| agaggaatga  | agggggggtg  | cttacaatgt | acgagcaatg  | gcttgtagag  | aatgggaagT | 180  |
| aactataacg  | gtcttgagag  | gaaggagaga | cggttcaaga  | tcttcaaaga  | caacttgaag | 240  |
| cgcacgaag   | aacacaattc  | agatccaaac | cggagttatg  | aacgcgggtt  | gaacaagttt | 300  |
| tcggatctaa  | cggctgatga  | gtttcaagct | agttacttag  | gtgggaagat  | ggaaaagaaa | 360  |
| agcctatcag  | atgtagcgga  | gaggtatcag | tacaaagaag  | gagatgtttt  | acctgatgaa | 420  |
| gttgattgga  | gggagagagg  | agcagttggt | ccaagagtca  | aaagacaagg  | agagtgtgga | 480  |
| agttgttggg  | cgtttgccgc  | gactgagcgg | tggaaaggtat | aaaccagatc  | acaaccggag | 540  |
| aattagtatc  | tttatcgga   | caagaactca | ttgactgcga  | tagagggaac  | gacaactttg | 600  |
| gatgtgctgg  | tggtggagca  | gtatgggcct | ttgagttcat  | taaggagaac  | ggtggtattg | 660  |
| tatccgatga  | agtttatggt  | tataccggtg | aagatactgc  | cgcattgcaag | gccattgaga | 720  |
| tgaaaaccac  | tcgggttggt  | accattaatg | gtcatgaggt  | tgttcctgta  | aacgatgaga | 780  |
| tgtctttgaa  | gaaagctggt  | gcttatcaac | ctattagtgt  | tatgatataca | gctgcaaaca | 840  |
| tgagcgacta  | caaatctggt  | gtgtataaag | gagcatgtag  | taattttgtgg | ggagatcaca | 900  |
| atgtgtcta   | tgtggggtat  | ggaacatcat | cagatgaagg  | agactactgg  | cttattcgta | 960  |
| attcttgggg  | vccagagtgg  | ggagaaggcg | ggtaccttag  | gcttcaacgt  | aacttccatg | 1020 |
| aaccaaccgg  | gaaatgtgca  | gtcgtgttag | ctcctgtata  | cccaatcaag  | tcgaactctt | 1080 |
| catctcattt  | gttgtctcca  | agtgtgttta | aattgggtgt  | tttattttgtt | tttcagttga | 1140 |
| ttagtttggc  | cttgctttga  | aatatacttt | tatcgggtgtt | caagtttcgtt | ggtttttggt | 1200 |
| ttaataaaagg | aaacaagatt  | cgtc       |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..116  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570240  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

Met Gly Ser Asn Tyr Asn Gly Leu Gly Glu Lys Glu Arg Arg Phe Lys  
1                  5                  10                  15  
Ile Phe Lys Asp Asn Leu Lys Arg Ile Glu Glu His Asn Ser Asp Pro  
          20                  25                  30  
Asn Arg Ser Tyr Glu Arg Gly Leu Asn Lys Phe Ser Asp Leu Thr Ala  
          35                  40                  45  
Asp Glu Phe Gln Ala Ser Tyr Leu Gly Gly Lys Met Glu Lys Lys Ser  
50                  55                  60  
Leu Ser Asp Val Ala Glu Arg Tyr Gln Tyr Lys Glu Gly Asp Val Leu  
65                  70                  75                  80  
Pro Asp Glu Val Asp Trp Arg Glu Arg Gly Ala Val Val Pro Arg Val  
          85                  90                  95  
Lys Arg Gln Gly Glu Cys Gly Ser Cys Trp Ala Phe Ala Ala Thr Glu  
          100                  105                  110  
Arg Trp Lys Val  
          115

(2) INFORMATION FOR SEQ ID NO:1512:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 146 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..146  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570241  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

Met Lys Thr Thr Arg Val Val Thr Ile Asn Gly His Glu Val Val Pro  
1                  5                  10                  15  
Val Asn Asp Glu Met Ser Leu Lys Lys Ala Val Ala Tyr Gln Pro Ile  
          20                  25                  30  
Ser Val Met Ile Ser Ala Ala Asn Met Ser Asp Tyr Lys Ser Gly Val  
          35                  40                  45  
Tyr Lys Gly Ala Cys Ser Asn Leu Trp Gly Asp His Asn Val Leu Ile  
50                  55                  60  
Val Gly Tyr Gly Thr Ser Ser Asp Glu Gly Asp Tyr Trp Leu Ile Arg  
65                  70                  75                  80  
Asn Ser Trp Xaa Pro Glu Trp Gly Glu Gly Tyr Leu Arg Leu Gln  
          85                  90                  95  
Arg Asn Phe His Glu Pro Thr Gly Lys Cys Ala Val Ala Val Ala Pro  
          100                  105                  110  
Val Tyr Pro Ile Lys Ser Asn Ser Ser Ser His Leu Leu Ser Pro Ser  
          115                  120                  125  
Val Phe Lys Leu Val Val Leu Phe Val Phe Gln Leu Ile Ser Leu Ala  
130                  135                  140  
Leu Leu  
145

(2) INFORMATION FOR SEQ ID NO:1513:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 126 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

```
Met Ser Leu Lys Lys Ala Val Ala Tyr Gln Pro Ile Ser Val Met Ile
1 5 10 15
Ser Ala Ala Asn Met Ser Asp Tyr Lys Ser Gly Val Tyr Lys Gly Ala
 20 25 30
Cys Ser Asn Leu Trp Gly Asp His Asn Val Leu Ile Val Gly Tyr Gly
 35 40 45
Thr Ser Ser Asp Glu Gly Asp Tyr Trp Leu Ile Arg Asn Ser Trp Xaa
 50 55 60
Pro Glu Trp Gly Glu Gly Gly Tyr Leu Arg Leu Gln Arg Asn Phe His
65 70 75 80
Glu Pro Thr Gly Lys Cys Ala Val Ala Val Ala Pro Val Tyr Pro Ile
 85 90 95
Lys Ser Asn Ser Ser Ser His Leu Leu Ser Pro Ser Val Phe Lys Leu
 100 105 110
Val Val Leu Phe Val Phe Gln Leu Ile Ser Leu Ala Leu Leu
 115 120 125
```

(2) INFORMATION FOR SEQ ID NO:1514:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1387 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1387  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

```
acgttctcag agttagttac acagctttca acgatgaate agctcgcgct ttcaagatcc 60
ggttacaccg ccgccgtgag gttttctccct atgcttttcg cagctgtttc gaagatctta 120
tcattctctg ccgccgcatt caccgtccgc aacttcagct ctaccggaag tcctctcacc 180
agctaccaaa tcaataaacc ttccgcgtca aaatccttca cttccaggct tctccaccaa 240
tcctcctccg ccggtactcc tccgcaacaa cttttcggcg cccgtagctt ctcatctccc 300
agcagtgatt tcaacagcta ccacattaat ccgccgtcta actggggaat ccgaatcgtg 360
ccggagagga aagcttgtgt gattgagcgg tttggtaaatt tccacacgac tttgccggcg 420
gggattcact tccttgttcc gtttgtggat cgtatcgctt atgttcattc tctaaaggaa 480
gaagcgattc ctattggtaa tcagactgcg attacaaagg ataacgtag catccacatc 540
gatggttttc tctacgttaa gatttgtgat cctaagttgg cttcttatgg cgttgagaat 600
ccgatctatg ctgttatgca gttggctcag actacaatgc gtagtgagct cggtaaaatt 660
actcttgaca agacttttga ggaacgggac actctcaatg agaagattgt ggaagccatc 720
aatgttgctg caaaagattg gggctcttcag tgcccttagtt atgagatcag ggatatcatg 780
cctcctaatt gagtgagagt tgctatggaa atgcaagctg aagctgaacg taaaaagaga 840
gccagattc ttgagtctga aggagaacgt caagcccata tcaatagagc tgatggtaag 900
aaaagttctg taatcttgga atcagaagct gcaatgatgg accaagtcaa tcgtgcacaa 960
ggtaggctg aagcaatatt agctagagca caagcaacag ccaaRgggac tggccatggg 1020
atctcaatcc ctcaagggaag ctgggtggaga ggaggctgcg agtttgagag ttgctggagca 1080
atacattcaa gcttttgcca aaattgctaa ggagggtaca acaatgctgc ttYccgagta 1140
atgtcgacaa tcctgctagc atgatcgctc aAgcttttagg aatgtacaaa ggcttgtcaa 1200
caaaggtccc aacagtgggt tcagggaaac ttctggagta gaatcctcta ctaacgtggg 1260
tgttgcaaaa cttgaataga agctataatg tagctgaacc tagggaacaa ctattctttt 1320
gatttgtcca ggcttttagc catttttcagt ttgtttattt cttcatatga gaaacagtta 1380
tcttacc
```

(2) INFORMATION FOR SEQ ID NO:1515:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 369 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..369  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570248  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

Thr Phe Ser Glu Leu Val Thr Gln Leu Ser Thr Met Asn Gln Leu Ala  
1 5 10 15  
Leu Ser Arg Ser Gly Tyr Thr Ala Ala Val Arg Phe Leu Pro Met Leu  
20 25 30  
Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu Ala Ala Ala Ser Thr  
35 40 45  
Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu Thr Ser Tyr Gln Ile  
50 55 60  
Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser Arg Leu Leu His Gln  
65 70 75 80  
Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu Phe Gly Ala Arg Ser  
85 90 95  
Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr His Ile Asn Pro Pro  
100 105 110  
Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg Lys Ala Cys Val Ile  
115 120 125  
Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro Ala Gly Ile His Phe  
130 135 140  
Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val His Ser Leu Lys Glu  
145 150 155 160  
Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile Thr Lys Asp Asn Val  
165 170 175  
Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys Ile Val Asp Pro Lys  
180 185 190  
Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr Ala Val Met Gln Leu  
195 200 205  
Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Ile Thr Leu Asp Lys  
210 215 220  
Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys Ile Val Glu Ala Ile  
225 230 235 240  
Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys Leu Ser Tyr Glu Ile  
245 250 255  
Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val Ala Met Glu Met Gln  
260 265 270  
Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser Glu Gly  
275 280 285  
Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly Lys Lys Ser Ser Val  
290 295 300  
Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln Val Asn Arg Ala Gln  
305 310 315 320  
Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala Xaa Gly  
325 330 335  
Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser Trp Trp Arg Gly Gly  
340 345 350  
Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser Ser Phe Trp Gln Asn  
355 360 365  
Cys

- (2) INFORMATION FOR SEQ ID NO:1516:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 358 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..358  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570249  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

Met Asn Gln Leu Ala Leu Ser Arg Ser Gly Tyr Thr Ala Ala Val Arg  
1 5 10 15  
Phe Leu Pro Met Leu Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu  
20 25 30  
Ala Ala Ala Ser Thr Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu  
35 40 45  
Thr Ser Tyr Gln Ile Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser  
50 55 60  
Arg Leu Leu His Gln Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu  
65 70 75 80  
Phe Gly Ala Arg Ser Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr  
85 90 95  
His Ile Asn Pro Pro Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg  
100 105 110  
Lys Ala Cys Val Ile Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro  
115 120 125  
Ala Gly Ile His Phe Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val  
130 135 140  
His Ser Leu Lys Glu Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile  
145 150 155 160  
Thr Lys Asp Asn Val Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys  
165 170 175  
Ile Val Asp Pro Lys Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr  
180 185 190  
Ala Val Met Gln Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys  
195 200 205  
Ile Thr Leu Asp Lys Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys  
210 215 220  
Ile Val Glu Ala Ile Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys  
225 230 235 240  
Leu Ser Tyr Glu Ile Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val  
245 250 255  
Ala Met Glu Met Gln Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile  
260 265 270  
Leu Glu Ser Glu Gly Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly  
275 280 285  
Lys Lys Ser Ser Val Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln  
290 295 300  
Val Asn Arg Ala Gln Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln  
305 310 315 320  
Ala Thr Ala Xaa Gly Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser  
325 330 335  
Trp Trp Arg Gly Gly Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser  
340 345 350  
Ser Phe Trp Gln Asn Cys  
355

- (2) INFORMATION FOR SEQ ID NO:1517:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1570250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

Met Leu Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu Ala Ala Ala  
1 5 10 15  
Ser Thr Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu Thr Ser Tyr  
20 25 30  
Gln Ile Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser Arg Leu Leu  
35 40 45  
His Gln Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu Phe Gly Ala  
50 55 60  
Arg Ser Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr His Ile Asn  
65 70 75 80  
Pro Pro Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg Lys Ala Cys  
85 90 95  
Val Ile Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro Ala Gly Ile  
100 105 110  
His Phe Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val His Ser Leu  
115 120 125  
Lys Glu Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile Thr Lys Asp  
130 135 140  
Asn Val Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys Ile Val Asp  
145 150 155 160  
Pro Lys Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr Ala Val Met  
165 170 175  
Gln Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Ile Thr Leu  
180 185 190  
Asp Lys Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys Ile Val Glu  
195 200 205  
Ala Ile Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys Leu Ser Tyr  
210 215 220  
Glu Ile Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val Ala Met Glu  
225 230 235 240  
Met Gln Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser  
245 250 255  
Glu Gly Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly Lys Lys Ser  
260 265 270  
Ser Val Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln Val Asn Arg  
275 280 285  
Ala Gln Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala  
290 295 300  
Xaa Gly Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser Trp Trp Arg  
305 310 315 320  
Gly Gly Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser Ser Phe Trp  
325 330 335  
Gln Asn Cys

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1412

(D) OTHER INFORMATION: / Ceres Seq. ID 1570265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| actccgagcg  | tttccctttct | cacaagccaa | tggcgcaatt | tactaattcc | atcaattatc  | 60   |
| tctttttctgt | ttctctctta  | ttatttgtat | cgttccactg | cttatgtttt | cgttttttcat | 120  |
| tgggttcagc  | ttgttcaaac  | tccaccgacg | accaacagat | tcaacaccat | caccaccgga  | 180  |
| aatgggttgg  | tccctcaggc  | cacaaagtca | tcaccgtctc | acttaacggc | cacgctcagt  | 240  |
| ttcgctccgt  | ccaagacgct  | gtggattcca | taccaaagav | caataacaag | agcatcacia  | 300  |
| tcaagattgc  | tcccggattt  | tacagagaga | aagtgggtgg | tccagctaca | aaaccgtaca  | 360  |
| tAaacgttca  | aaggagctgg  | tagggatgtg | accgctatag | agtggcacga | ccgtgcgtcc  | 420  |
| gaccttggcg  | ctaaccggtca | acagttacgt | acctatcaaa | ccgcttccgt | caccgtctac  | 480  |
| gctaattatt  | tcaccgctag  | aaacattagc | ttcacggtag | tctattcaat | tctaacgcaa  | 540  |
| ttatatatat  | agggaaactt  | tcacaaaaat | gcgagtcttt | ctttatttta | ttttaaattg  | 600  |
| tgaagaatac  | tgcgccggct  | ccattgccgg | ggatgcaagg | gtggcaagcg | gtggcggtta  | 660  |
| ggatctccgg  | cgacaaagct  | ttcttttccg | gctgogggtt | ttacggtgca | caagacactt  | 720  |
| tatgcgacga  | tgctggccgt  | cattacttca | aggagtgtta | cattgaaggc | tctatcgact  | 780  |
| ttatctttgg  | taatggccgc  | tccatgtata | aagattgtga | gttgcatctg | atagcgtcaa  | 840  |
| gattcgggtc  | gatagcggcg  | catggtagga | catgcccgga | agagaaaacg | ggtttcgcgt  | 900  |
| tcgtgggttg  | tcgggtaaca  | ggtacgggtc | cattgtacgt | gggccggggc | atgggaCcaa  | 960  |
| tactcacgta  | tcgtttacgc  | ctacacttac | tttgatgctc | tcgtcgctca | cggtgggttg  | 1020 |
| gacgattggg  | accacaaaatc | caacaaaagc | aagacggcat | ttttcggagt | gtacaattgc  | 1080 |
| tatgggccag  | gagcagcagc  | gacgagaggc | gtgtcttggg | ctagagcttt | ggactatgaa  | 1140 |
| tcggcccatc  | catttatcgc  | taagagcttc | gttaatggga | gacattggat | cgctcctcga  | 1200 |
| gatgcttaac  | caacttcaaa  | ccttggcggg | gtttcttttc | ctaattcctc | ggttctctcc  | 1260 |
| agtcccaagt  | cctaaaaagct | tactatat   | ttatcattcg | tttatttctt | ttattgttta  | 1320 |
| ttttttccaa  | tttatattata | cattgtgtga | tagtacaaca | aagtattgct | tcttcttcat  | 1380 |
| ctgtatccat  | ttcagttaaa  | tgttttgagc | tt         |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Arg | Phe | Leu | Ser | His | Lys | Pro | Met | Ala | Gln | Phe | Thr | Asn | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Tyr | Leu | Phe | Ser | Val | Ser | Leu | Leu | Leu | Phe | Val | Ser | Phe | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Leu | Cys | Phe | Arg | Phe | Ser | Leu | Val | Ala | Ala | Cys | Ser | Asn | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | Asp | Gln | Gln | Ile | Gln | His | His | His | Arg | Lys | Trp | Val | Gly | Pro |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Gly | His | Lys | Val | Ile | Thr | Val | Ser | Leu | Asn | Gly | His | Ala | Gln | Phe |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Val | Gln | Asp | Ala | Val | Asp | Ser | Ile | Pro | Lys | Xaa | Asn | Asn | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ile | Thr | Ile | Lys | Ile | Ala | Pro | Gly | Phe | Tyr | Arg | Glu | Lys | Val | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Val | Pro | Ala | Thr | Lys | Pro | Tyr | Ile | Asn | Val | Gln | Arg | Ser | Trp |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Met Pro Gly Arg Glu Asn Gly Phe Arg Val Arg Gly Leu Ser Gly Asn  
1 5 10 15  
Arg Tyr Gly Ser Ile Val Arg Gly Pro Gly His Gly Thr Asn Thr His  
20 25 30  
Val Ser Phe Thr Pro Thr Leu Thr Leu Met Leu Ser Ser Leu Thr Val  
35 40 45  
Val Gly Thr Ile Gly Thr Thr Asn Pro Thr Lys Ala Arg Arg His Phe  
50 55 60  
Ser Glu Cys Thr Ile Ala Met Gly Gln Glu Gln Arg Arg Glu Ala  
65 70 75 80  
Cys Leu Gly Leu Glu Leu Trp Thr Met Asn Arg Pro Ile His Leu Ser  
85 90 95  
Leu Arg Ala Ser Leu Met Gly Asp Ile Gly Ser Leu Leu Glu Met Leu  
100 105 110  
Asn Gln Leu Gln Thr Leu Ala Gly Phe Leu Phe Leu Ile Pro Arg Phe  
115 120 125  
Leu Pro Val Pro Ser Pro Lys Ser Leu Leu Tyr Phe Tyr His Ser Phe  
130 135 140  
Ile Ser Phe Ile Val Tyr Phe Phe Gln Phe Ile Tyr Thr Leu Cys Asp  
145 150 155 160  
Ser Thr Thr Lys Tyr Cys Phe Phe Phe Ile Cys Ile His Phe Ser  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1570268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met Leu Ser Ser Leu Thr Val Val Gly Thr Ile Gly Thr Thr Asn Pro  
1 5 10 15  
Thr Lys Ala Arg Arg His Phe Ser Glu Cys Thr Ile Ala Met Gly Gln  
20 25 30  
Glu Gln Gln Arg Arg Glu Ala Cys Leu Gly Leu Glu Leu Trp Thr Met  
35 40 45  
Asn Arg Pro Ile His Leu Ser Leu Arg Ala Ser Leu Met Gly Asp Ile  
50 55 60  
Gly Ser Leu Leu Glu Met Leu Asn Gln Leu Gln Thr Leu Ala Gly Phe  
65 70 75 80  
Leu Phe Leu Ile Pro Arg Phe Leu Pro Val Pro Ser Pro Lys Ser Leu  
85 90 95  
Leu Tyr Phe Tyr His Ser Phe Ile Ser Phe Ile Val Tyr Phe Phe Gln  
100 105 110  
Phe Ile Tyr Thr Leu Cys Asp Ser Thr Thr Lys Tyr Cys Phe Phe Phe  
115 120 125  
Ile Cys Ile His Phe Ser  
130

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 973 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..973  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570289  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| gaacaatatt | cacagagatt | ttcgatctta  | accgagaaaa | ggaagaaatg | gctgggtccat | 60  |
| cgacaacttc | aaacgcacca | aagcagagga  | agagagtcga | agccgagact | agcagcaaca  | 120 |
| cttctactac | cttacgtcgc | gctaaagacg  | gaagcgcttt | cgctctctgt | gaaggatgta  | 180 |
| acaagagtgt | agctgtagcg | cttataagca  | tgcacaattg | cagtctcgat | gctaagatca  | 240 |
| gagtgaatct | cgaagcacia | gttgtggaga  | cacaagcaga | ggctaagaag | aagcctgcag  | 300 |
| agaagaagaa | gacaacatct | gatggacctt  | agccaaagag | acttaagaaa | accaatgatg  | 360 |
| agaagaagag | ctcttcaact | tcaaacaagc  | ccaagcgacc | tctcactgcc | ttctttatct  | 420 |
| tcagtgtgta | tttccgtaaa | acgtttaagt  | cagagcataa | tggttcatta | gctaaggatg  | 480 |
| ctgcaaagat | cgggtgtgag | aagtgggaagt | ctttgactga | ggaagagaag | aaagtttatc  | 540 |
| tggataaagc | tgctgaactt | aaggcagagt  | ataAcaagtc | actggaaagc | aatgatgctg  | 600 |
| atgaggaaga | ggaagatgag | gagaagcaat  | ctgatgatgt | tgatgatgct | gaggagaaac  | 660 |
| aagttgacga | tgatgatgaa | gttgaggaga  | aagaagttga | gaacacagat | gatgacaaga  | 720 |
| aagaagctga | aggtaaagaa | gaggaggaag  | aagagatttt | ggatgactac | tagaaatgtt  | 780 |
| atgctcgttc | ttgtgggtct | agtcttactg  | aaatcggttt | atctctaata | gttgcgatgc  | 840 |
| attgtaaatg | aagcctttat | tagtgaaagt  | agtttatttg | aagttaagtt | gtgagcaagt  | 900 |
| ggtttttttg | tagttcactg | aaatggtaat  | gccttttgtt | taaacaagta | atgaagctta  | 960 |
| tgtttttcgt | ttt        |             |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1523:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 256 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..256  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570290  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Phe | Thr | Glu | Ile | Phe | Asp | Leu | Asn | Arg | Glu | Lys | Glu | Met |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Gly | Pro | Ser | Thr | Thr | Ser | Asn | Ala | Pro | Lys | Gln | Arg | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     | Val |
| Glu | Ala | Glu | Thr | Ser | Ser | Asn | Thr | Ser | Thr | Thr | Leu | Arg | Arg | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Lys |
| Asp | Gly | Ser | Ala | Phe | Ala | Leu | Cys | Glu | Gly | Cys | Asn | Lys | Ser | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     | Ala |
| Val | Ala | Leu | Ile | Ser | Met | His | Asn | Cys | Ser | Leu | Asp | Ala | Lys | Ile |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | Arg |
| Val | Asn | Leu | Glu | Ala | Gln | Val | Val | Glu | Thr | Gln | Ala | Glu | Ala | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | Lys |
| Lys | Pro | Ala | Glu | Lys | Lys | Lys | Thr | Thr | Ser | Asp | Gly | Pro | Lys | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Lys |
| Arg | Leu | Lys | Lys | Thr | Asn | Asp | Glu | Lys | Lys | Ser | Ser | Ser | Thr | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     | Asn |
| Lys | Pro | Lys | Arg | Pro | Leu | Thr | Ala | Phe | Phe | Ile | Phe | Met | Ser | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     | Phe |
| Arg | Lys | Thr | Phe | Lys | Ser | Glu | His | Asn | Gly | Ser | Leu | Ala | Lys | Asp |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     | Ala |
| Ala | Lys | Ile | Gly | Gly | Glu | Lys | Trp | Lys | Ser | Leu | Thr | Glu | Glu | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 | Lys |
| Lys | Val | Tyr | Leu | Asp | Lys | Ala | Ala | Glu | Leu | Lys | Ala | Glu | Tyr | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Lys |
| Ser | Leu | Glu | Ser | Asn | Asp | Ala | Asp | Glu | Glu | Glu | Glu | Asp | Glu | Glu |

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
|                                                                 | 195 |     | 200 |     | 205 |
| Gln Ser Asp Asp Val Asp Asp Ala Glu Glu Lys Gln Val Asp Asp Asp |     |     |     |     |     |
| 210                                                             |     | 215 |     | 220 |     |
| Asp Glu Val Glu Glu Lys Glu Val Glu Asn Thr Asp Asp Asp Lys Lys |     |     |     |     |     |
| 225                                                             |     | 230 |     | 235 | 240 |
| Glu Ala Glu Gly Lys Glu Glu Glu Glu Glu Glu Ile Leu Asp Asp Tyr |     |     |     |     |     |
|                                                                 | 245 |     | 250 |     | 255 |

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1570291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Pro | Ser | Thr | Thr | Ser | Asn | Ala | Pro | Lys | Gln | Arg | Lys | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Glu | Ala | Glu | Thr | Ser | Ser | Asn | Thr | Ser | Thr | Thr | Leu | Arg | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asp | Gly | Ser | Ala | Phe | Ala | Leu | Cys | Glu | Gly | Cys | Asn | Lys | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Ala | Leu | Ile | Ser | Met | His | Asn | Cys | Ser | Leu | Asp | Ala | Lys | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Val | Asn | Leu | Glu | Ala | Gln | Val | Val | Glu | Thr | Gln | Ala | Glu | Ala | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Lys | Pro | Ala | Glu | Lys | Lys | Lys | Thr | Thr | Ser | Asp | Gly | Pro | Lys | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Arg | Leu | Lys | Lys | Thr | Asn | Asp | Glu | Lys | Lys | Ser | Ser | Ser | Thr | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Lys | Pro | Lys | Arg | Pro | Leu | Thr | Ala | Phe | Phe | Ile | Phe | Met | Ser | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Arg | Lys | Thr | Phe | Lys | Ser | Glu | His | Asn | Gly | Ser | Leu | Ala | Lys | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Lys | Ile | Gly | Gly | Glu | Lys | Trp | Lys | Ser | Leu | Thr | Glu | Glu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Lys | Val | Tyr | Leu | Asp | Lys | Ala | Ala | Glu | Leu | Lys | Ala | Glu | Tyr | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Ser | Leu | Glu | Ser | Asn | Asp | Ala | Asp | Glu | Glu | Glu | Glu | Asp | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gln | Ser | Asp | Asp | Val | Asp | Asp | Ala | Glu | Glu | Lys | Gln | Val | Asp | Asp |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Asp | Glu | Val | Glu | Glu | Lys | Glu | Val | Glu | Asn | Thr | Asp | Asp | Asp | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Glu | Ala | Glu | Gly | Lys | Glu | Glu | Glu | Glu | Glu | Glu | Ile | Leu | Asp | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..187  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

Met His Asn Cys Ser Leu Asp Ala Lys Ile Arg Val Asn Leu Glu Ala  
1 5 10 15  
Gln Val Val Glu Thr Gln Ala Glu Ala Lys Lys Lys Pro Ala Glu Lys  
20 25 30  
Lys Lys Thr Thr Ser Asp Gly Pro Lys Pro Lys Arg Leu Lys Lys Thr  
35 40 45  
Asn Asp Glu Lys Lys Ser Ser Ser Thr Ser Asn Lys Pro Lys Arg Pro  
50 55 60  
Leu Thr Ala Phe Phe Ile Phe Met Ser Asp Phe Arg Lys Thr Phe Lys  
65 70 75 80  
Ser Glu His Asn Gly Ser Leu Ala Lys Asp Ala Ala Lys Ile Gly Gly  
85 90 95  
Glu Lys Trp Lys Ser Leu Thr Glu Glu Glu Lys Lys Val Tyr Leu Asp  
100 105 110  
Lys Ala Ala Glu Leu Lys Ala Glu Tyr Asn Lys Ser Leu Glu Ser Asn  
115 120 125  
Asp Ala Asp Glu Glu Glu Glu Asp Glu Glu Lys Gln Ser Asp Asp Val  
130 135 140  
Asp Asp Ala Glu Glu Lys Gln Val Asp Asp Asp Asp Glu Val Glu Glu  
145 150 155 160  
Lys Glu Val Glu Asn Thr Asp Asp Asp Lys Lys Glu Ala Glu Gly Lys  
165 170 175  
Glu Glu Glu Glu Glu Glu Ile Leu Asp Asp Tyr  
180 185

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..795  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

gttcccaact ccttacgcgc tctctctcta tctcttttagc tttctctttc tagcggcgaa 60  
catTgggtta tccggtgggg tacactgagc tctctctccc aagaatcttc cttcacttac 120  
tctctctctt aggcctaata cgaacactca tagacacggg ttttcggata ttgggtctac 180  
ccgactttct cgaatccgac ccggttttat cgtcatcgtc atggctggaa ccaccgtata 240  
tgtccacggc ggcgcacatc caccaagaaa gctcattttt cttcccagtg gcggcgaggc 300  
tagctggaga aatcttgccc gtcacagat tctcggaact aactcgaccc ggattcggat 360  
ccggatccga ttgctgcgcg gtgtgcctcc acgagttcga gaacgaagac gagatccgac 420  
ggctgacgaa ttgtcaacac atatttcacc ggagctgttt agaccgttgg atgatgggtt 480  
ataatcagat gacgtgtcca cttttagtaa cgccgtttat ttctgatgag ttacaagttg 540  
cttttaacca acgagtttgg tctgaatctg aacttctcgc agaatcaaat tagaatcttt 600  
cttgtttggg tgggaattagt ttctactaat gagaaaatta atttctatct tttttttttt 660  
tttgtttaat ctttagctga gtgggtgata tatgtaaata taaaaattat aggtggtgat 720  
gcttagtaaa ttagaagaat gaaatttgta ttatccgttg aggaataaaa agaatgaat 780  
ggaaatctta atttt

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1570302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

Met Ala Gly Thr Thr Val Tyr Val His Gly Gly Ala Ser Ser Pro Arg  
1 5 10 15  
Lys Leu Ile Phe Leu Pro Ser Gly Gly Glu Ala Ser Trp Arg Asn Leu  
20 25 30  
Ala Arg His Gln Ile Leu Gly Thr Asn Ser Thr Arg Ile Arg Ile Arg  
35 40 45  
Ile Arg Leu Leu Arg Gly Val Pro Pro Arg Val Arg Glu Arg Arg Arg  
50 55 60  
Asp Pro Thr Ala Asp Glu Leu Ser Thr His Ile Ser Pro Glu Leu Phe  
65 70 75 80  
Arg Pro Leu Asp Asp Gly Leu  
85

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1570303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

Met Ser Thr Ala Ala His His His Gln Ser Ser Phe Phe Phe Pro  
1 5 10 15  
Val Ala Ala Arg Leu Ala Gly Glu Ile Leu Pro Val Ile Arg Phe Ser  
20 25 30  
Glu Leu Thr Arg Pro Gly Phe Gly Ser Gly Ser Asp Cys Cys Ala Val  
35 40 45  
Cys Leu His Glu Phe Glu Asn Glu Asp Glu Ile Arg Arg Leu Thr Asn  
50 55 60  
Cys Gln His Ile Phe His Arg Ser Cys Leu Asp Arg Trp Met Met Gly  
65 70 75 80  
Tyr Asn Gln Met Thr Cys Pro Leu Cys Arg Thr Pro Phe Ile Ser Asp  
85 90 95  
Glu Leu Gln Val Ala Phe Asn Gln Arg Val Trp Ser Glu Ser Glu Leu  
100 105 110  
Leu Ala Glu Ser Asn  
115

(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..627

(D) OTHER INFORMATION: / Ceres Seq. ID 1570308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| cataatcctc  | aaaaatctca | actttatctc | ccaaaacaca  | aaacaaaaaa  | aatggcttc  | 60  |
| cactgctctc  | tcaagcgcca | tcgtcggaac | ttcattcattc | cgtcggttccc | cagctccaat | 120 |
| cagctctccgt | tcccttccat | cagccaacac | acaatccctc  | ttcggtctca  | aatcaggcac | 180 |
| cgctcggtggt | ggacgtgtca | cagccatggc | tacatacaag  | gtcaagttca  | tcacaccaga | 240 |

aggtagagcta gaggttgagt gtgacgacga cgtotacgtt cttgatgctg ctgaggaagc 300  
tggaatcgat ttgccttact cttgcogtgc tggttcttgt tgcagctgtg ctggtaaagt 360  
tgtgtctgga tctgttgatc agtctgacca gagtttcctt gatgatgaac agattggtga 420  
agggtttgtt ctcaacttggtg ctgcttacct tacctctgat gttaccattg aaaCccacaa 480  
agaagaagac attgtttaag cctcacctac tcaccagctt ttgatggttt aaaaatcatg 540  
tctttataat tgagtttggt gttacaaaac tattgttata tggtgttatt gttcctgggt 600  
tggtcacca tcaatcgatg acatttt

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1570309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Ile Ile Leu Lys Asn Leu Asn Phe Ile Ser Gln Asn Thr Lys Gln Lys  
1 5 10 15  
Lys Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe  
20 25 30  
Ile Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala  
35 40 45  
Asn Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly  
50 55 60  
Arg Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu  
65 70 75 80  
Gly Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala  
85 90 95  
Ala Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser  
100 105 110  
Cys Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser  
115 120 125  
Asp Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu  
130 135 140  
Thr Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys  
145 150 155 160  
Glu Glu Asp Ile Val  
165

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1570310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe Ile  
1 5 10 15  
Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala Asn  
20 25 30  
Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly Arg  
35 40 45  
Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly  
50 55 60

Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala  
65 70 75 80  
Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys  
85 90 95  
Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp  
100 105 110  
Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr  
115 120 125  
Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys Glu  
130 135 140  
Glu Asp Ile Val  
145

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly Glu Leu Glu  
1 5 10 15  
Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala Glu Glu Ala  
20 25 30  
Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys Ser Ser Cys  
35 40 45  
Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp Gln Ser Phe  
50 55 60  
Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr Cys Ala Ala  
65 70 75 80  
Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys Glu Glu Asp Ile  
85 90 95  
Val

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..637
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tyttCtctct CtCttcacac acttcacact ttcaatatac actctcatta tgactaccga  | 60  |
| agagaaagag atcctcgccg ccaaattgga agaacagaag atcgatctcg ataagcccga  | 120 |
| agttgaggac gatgatgata acgaagacga tgactctgat gacgatgata aggatgatga  | 180 |
| cgaggctgat ggactagatg gagaggcagg aggtaagtca aaacaaagca gaagtgaaga  | 240 |
| gaagagtcgc aaagccatgc tcaagcttgg catgaaaccc atcactggtg ttagccgagt  | 300 |
| caccgtcaaa aagagcaaga atatcttgg ttgtcatatca aagcctgatg tgttcaagag  | 360 |
| tccagcatca gacacatatg tgatctttgg agaggcgaag atcgaggatt tgagctctca  | 420 |
| gatccagtcg caagcagcag agcaattcaa ggcaccagat ctcagcaatg tgatctcaaa  | 480 |
| gggtgagtca tcgagcgctg cagtggttca ggatgatgag gaggttgacg aggaaggtgt  | 540 |
| tgagccaaag gacattgagt tggatgatgac tcaagcagga gtgtctaggc caaatgctgt | 600 |
| gaaggctctc aaggctgcag atggagatat tgtctct                           |     |

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1570316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

Xaa 1 Leu Ser Leu Phe Thr His Phe Thr Leu Ser Ile Tyr Thr Leu Ile  
5 10 15  
Met Thr Thr Glu Glu Lys Glu Ile Leu Ala Ala Lys Leu Glu Glu Gln  
20 25 30  
Lys Ile Asp Leu Asp Lys Pro Glu Val Glu Asp Asp Asp Asn Glu  
35 40 45  
Asp Asp Asp Ser Asp Asp Asp Asp Lys Asp Asp Asp Glu Ala Asp Gly  
50 55 60  
Leu Asp Gly Glu Ala Gly Gly Lys Ser Lys Gln Ser Arg Ser Glu Lys  
65 70 75 80  
Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr Gly  
85 90 95  
Val Ser Arg Val Thr Val Lys Lys Ser Lys Asn Ile Leu Phe Val Ile  
100 105 110  
Ser Lys Pro Asp Val Phe Lys Ser Pro Ala Ser Asp Thr Tyr Val Ile  
115 120 125  
Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Ser Gln Ile Gln Ser Gln  
130 135 140  
Ala Ala Glu Gln Phe Lys Ala Pro Asp Leu Ser Asn Val Ile Ser Lys  
145 150 155 160  
Gly Glu Ser Ser Ser Ala Ala Val Val Gln Asp Asp Glu Glu Val Asp  
165 170 175  
Glu Glu Gly Val Glu Pro Lys Asp Ile Glu Leu Val Met Thr Gln Ala  
180 185 190  
Gly Val Ser Arg Pro Asn Ala Val Lys Ala Leu Lys Ala Ala Asp Gly  
195 200 205  
Asp Ile Val Ser  
210

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1570317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

Met Thr Thr Glu Glu Lys Glu Ile Leu Ala Ala Lys Leu Glu Glu Gln  
1 5 10 15  
Lys Ile Asp Leu Asp Lys Pro Glu Val Glu Asp Asp Asp Asp Asn Glu  
20 25 30  
Asp Asp Asp Ser Asp Asp Asp Asp Lys Asp Asp Asp Glu Ala Asp Gly  
35 40 45  
Leu Asp Gly Glu Ala Gly Gly Lys Ser Lys Gln Ser Arg Ser Glu Lys  
50 55 60  
Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr Gly

65 70 75 80  
Val Ser Arg Val Thr Val Lys Lys Ser Lys Asn Ile Leu Phe Val Ile  
85 90 95  
Ser Lys Pro Asp Val Phe Lys Ser Pro Ala Ser Asp Thr Tyr Val Ile  
100 105 110  
Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Ser Gln Ile Gln Ser Gln  
115 120 125  
Ala Ala Glu Gln Phe Lys Ala Pro Asp Leu Ser Asn Val Ile Ser Lys  
130 135 140  
Gly Glu Ser Ser Ser Ala Ala Val Val Gln Asp Asp Glu Glu Val Asp  
145 150 155 160  
Glu Glu Gly Val Glu Pro Lys Asp Ile Glu Leu Val Met Thr Gln Ala  
165 170 175  
Gly Val Ser Arg Pro Asn Ala Val Lys Ala Leu Lys Ala Ala Asp Gly  
180 185 190  
Asp Ile Val Ser  
195

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1570318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

Met Leu Lys Leu Gly Met Lys Pro Ile Thr Gly Val Ser Arg Val Thr  
1 5 10 15  
Val Lys Lys Ser Lys Asn Ile Leu Phe Val Ile Ser Lys Pro Asp Val  
20 25 30  
Phe Lys Ser Pro Ala Ser Asp Thr Tyr Val Ile Phe Gly Glu Ala Lys  
35 40 45  
Ile Glu Asp Leu Ser Ser Gln Ile Gln Ser Gln Ala Glu Gln Phe  
50 55 60  
Lys Ala Pro Asp Leu Ser Asn Val Ile Ser Lys Gly Glu Ser Ser Ser  
65 70 75 80  
Ala Ala Val Val Gln Asp Asp Glu Glu Val Asp Glu Glu Gly Val Glu  
85 90 95  
Pro Lys Asp Ile Glu Leu Val Met Thr Gln Ala Gly Val Ser Arg Pro  
100 105 110  
Asn Ala Val Lys Ala Leu Lys Ala Ala Asp Gly Asp Ile Val Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1131

(D) OTHER INFORMATION: / Ceres Seq. ID 1570339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

aaccaaatac aaaccctagc cgccttattc gtcttcttcg ttctctagtt ttttctcag 60  
tctctgttct tagatccctt gtagtttcca aatcttccga taaaaatgtc gggtaaagga 120  
gaaggaccag ctatcggtat cgatcttggt accacttact cttgcgtcgg agtatggcaa 180  
cacgaccgtg ttgagatcat tgctaattgat caaggaaaca gaaccacgcc atcttacgtt 240

(2) INFORMATION FOR SEO ID NO:1538:

(A) LENGTH: 342 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1570340

|            |            |            |            |            |     |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Ser        | Gly        | Lys        | Gly<br>5   | Glu | Gly        | Pro        | Ala        | Ile<br>10  | Gly        | Ile        | Asp        | Leu        | Gly<br>15  | Thr        |
| Thr        | Tyr        | Ser        | Cys<br>20  | Val        | Gly | Val        | Trp        | Gln<br>25  | His        | Asp        | Arg        | Val        | Glu<br>30  | Ile        | Ile        |
| Ala        | Asn        | Asp        | Gln<br>35  | Gly        | Asn | Arg        | Thr<br>40  | Thr        | Pro        | Ser        | Tyr        | Val<br>45  | Ala        | Phe        | Thr        |
| Asp        | Ser<br>50  | Glu        | Arg        | Leu        | Ile | Gly<br>55  | Asp        | Ala        | Ala        | Lys        | Asn<br>60  | Gln        | Val        | Ala        | Met        |
| Asn<br>65  | Pro        | Val        | Asn        | Thr<br>70  | Val | Phe        | Asp        | Ala        | Lys        | Arg<br>75  | Leu        | Ile        | Gly        | Arg        | Arg<br>80  |
| Phe        | Ser        | Asp        | Ser        | Ser<br>85  | Val | Gln        | Ser        | Asp        | Met<br>90  | Lys        | Leu        | Trp        | Pro        | Phe        | Lys        |
| Ile        | Gln        | Ala        | Gly<br>100 | Pro        | Ala | Asp        | Lys        | Pro<br>105 | Met        | Ile        | Tyr        | Val        | Glu<br>110 | Tyr        | Lys        |
| Gly        | Glu        | Glu<br>115 | Lys        | Glu        | Phe | Ala        | Ala<br>120 | Glu        | Glu        | Ile        | Ser        | Ser<br>125 | Met        | Val        | Leu        |
| Ile        | Lys<br>130 | Met        | Arg        | Glu        | Ile | Ala<br>135 | Glu        | Ala        | Tyr        | Leu        | Ser<br>140 | Val        | Thr        | Ile        | Lys        |
| Asn<br>145 | Ala        | Val        | Val        | Thr<br>150 | Val | Pro        | Ala        | Tyr        | Phe        | Asn<br>155 | Asp        | Ser        | Gln        | Arg        | Gln<br>160 |
| Ala        | Thr        | Lys        | Asp<br>165 | Ala        | Gly | Val        | Ile        | Ala        | Gly<br>170 | Leu        | Asn        | Val        | Met        | Arg        | Ile        |
| Ile        | Asn        | Glu        | Pro<br>180 | Thr        | Ala | Ala        | Ala<br>185 | Ile        | Ala        | Tyr        | Gly        | Leu        | Asp<br>190 | Lys        | Lys        |
| Ala        | Thr        | Ser<br>195 | Val        | Gly        | Glu | Lys        | Asn<br>200 | Val        | Leu        | Ile        | Phe        | Asp<br>205 | Leu        | Gly        | Gly        |
| Gly        | Thr<br>210 | Phe        | Asp        | Val        | Ser | Leu<br>215 | Leu        | Thr        | Ile        | Glu        | Glu<br>220 | Gly        | Ile        | Phe        | Glu        |
| Val<br>225 | Lys        | Ala        | Thr        | Ala<br>230 | Gly | Asp        | Thr        | His        | Leu        | Gly<br>235 | Gly        | Glu        | Asp        | Phe        | Asp<br>240 |
| Asn        | Arg        | Met        | Val        | Asn<br>245 | His | Phe        | Val        | Gln        | Glu<br>250 | Phe        | Lys        | Arg        | Lys        | Ser<br>255 | Lys        |
| Lys        | Asp        | Ile        | Thr<br>260 | Gly        | Asn | Pro        | Arg        | Ala<br>265 | Leu        | Arg        | Arg        | Leu        | Arg<br>270 | Thr        | Ser        |

Cys Glu Arg Ala Lys Arg Thr Leu Ser Ser Thr Ala Gln Thr Thr Ile  
275 280 285  
Glu Ile Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Ser Thr Ile Thr  
290 295 300  
Arg Ala Arg Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Lys Cys Met  
305 310 315 320  
Glu Pro Val Glu Lys Cys Leu Arg Asp Ala Lys Met Asp Lys Ser Thr  
325 330 335  
Val His Asp Val Val Leu  
340

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1570341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

Met Asn Pro Val Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg  
1 5 10 15  
Arg Phe Ser Asp Ser Ser Val Gln Ser Asp Met Lys Leu Trp Pro Phe  
20 25 30  
Lys Ile Gln Ala Gly Pro Ala Asp Lys Pro Met Ile Tyr Val Glu Tyr  
35 40 45  
Lys Gly Glu Glu Lys Glu Phe Ala Ala Glu Glu Ile Ser Ser Met Val  
50 55 60  
Leu Ile Lys Met Arg Glu Ile Ala Glu Ala Tyr Leu Ser Val Thr Ile  
65 70 75 80  
Lys Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg  
85 90 95  
Gln Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu Asn Val Met Arg  
100 105 110  
Ile Ile Asn Glu Pro Thr Ala Ala Ile Ala Tyr Gly Leu Asp Lys  
115 120 125  
Lys Ala Thr Ser Val Gly Glu Lys Asn Val Leu Ile Phe Asp Leu Gly  
130 135 140  
Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Glu Glu Gly Ile Phe  
145 150 155 160  
Glu Val Lys Ala Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe  
165 170 175  
Asp Asn Arg Met Val Asn His Phe Val Gln Glu Phe Lys Arg Lys Ser  
180 185 190  
Lys Lys Asp Ile Thr Gly Asn Pro Arg Ala Leu Arg Arg Leu Arg Thr  
195 200 205  
Ser Cys Glu Arg Ala Lys Arg Thr Leu Ser Ser Thr Ala Gln Thr Thr  
210 215 220  
Ile Glu Ile Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Ser Thr Ile  
225 230 235 240  
Thr Arg Ala Arg Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Lys Cys  
245 250 255  
Met Glu Pro Val Glu Lys Cys Leu Arg Asp Ala Lys Met Asp Lys Ser  
260 265 270  
Thr Val His Asp Val Val Leu  
275

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..253  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570342  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

Met Lys Leu Trp Pro Phe Lys Ile Gln Ala Gly Pro Ala Asp Lys Pro  
1 5 10 15  
Met Ile Tyr Val Glu Tyr Lys Gly Glu Lys Glu Phe Ala Ala Glu  
20 25 30  
Glu Ile Ser Ser Met Val Leu Ile Lys Met Arg Glu Ile Ala Glu Ala  
35 40 45  
Tyr Leu Ser Val Thr Ile Lys Asn Ala Val Val Thr Val Pro Ala Tyr  
50 55 60  
Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Val Ile Ala  
65 70 75 80  
Gly Leu Asn Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile  
85 90 95  
Ala Tyr Gly Leu Asp Lys Lys Ala Thr Ser Val Gly Glu Lys Asn Val  
100 105 110  
Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Thr  
115 120 125  
Ile Glu Glu Gly Ile Phe Glu Val Lys Ala Thr Ala Gly Asp Thr His  
130 135 140  
Leu Gly Gly Glu Asp Phe Asp Asn Arg Met Val Asn His Phe Val Gln  
145 150 155 160  
Glu Phe Lys Arg Lys Ser Lys Lys Asp Ile Thr Gly Asn Pro Arg Ala  
165 170 175  
Leu Arg Arg Leu Arg Thr Ser Cys Glu Arg Ala Lys Arg Thr Leu Ser  
180 185 190  
Ser Thr Ala Gln Thr Thr Ile Glu Ile Asp Ser Leu Tyr Glu Gly Ile  
195 200 205  
Asp Phe Tyr Ser Thr Ile Thr Arg Ala Arg Phe Glu Glu Leu Asn Met  
210 215 220  
Asp Leu Phe Arg Lys Cys Met Glu Pro Val Glu Lys Cys Leu Arg Asp  
225 230 235 240  
Ala Lys Met Asp Lys Ser Thr Val His Asp Val Val Leu  
245 250

(2) INFORMATION FOR SEQ ID NO:1541:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 921 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..921  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

aatccatata tacccttctc cattagcttt tgttcttctg ttccaattcc aattccttct 60  
gaaatattca tcgcaattcg tatcggttta aagtaaaaaa gcaatgggag gtggtaaaga 120  
caagcatcat gatgagcaag agaaaggatt tcatggtttt ccaggagggt gacattaccc 180  
acctgctcaa ggaggttaac ctccacaagg ttaccaccca caacaagggt atcctccagc 240  
tgagggttac ccacctgccc gatatactcc tgggtgcttac cctgctgcgc ccggtgggta 300  
tcctcctgca cctggagggtt acctcctgcg tggctatcct gcacctggag ctcaccattc 360  
aggacattct ggtggtggac tcggaggcat gatagcaggt gcagctgggt cagccgcagc 420  
agcttatgga gctcaccatg ttggtcacgc ctctcacaac cttacgggc atgctgtagg 480



acatggaggg tatggccatg cccctgctca tggctttggc catggtggtc atggtaaatt 540  
caagcacgga aagcatggag gcaaattcaa gcacggaaag catggaaagc acgggaaaca 600  
tggcatgttt ggaggaggag gcaaattcaa gaagtgaag taatctcaaa aacccacct 660  
ttgatcctct cctccagtat agtctcatta cctgaccgat gtttctaata atcccccttc 720  
aaacatatatt cattttaact atgtcggttt agagattact ggttgaggaa ataattggag 780  
agtgctagta taaaccttat ggtatctgca gcagagggtt ctttaatctc tcaatagtag 840  
atgctttgaa acttatctat aatttNggta ttgtaatgac agtttgtgtt tggGtttttt 900  
cttcagtatc ttctttgttt g

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met Gly Gly Gly Lys Asp Lys His His Asp Glu Gln Glu Lys Gly Phe  
1 5 10 15  
His Gly Phe Pro Gly Gly Gly His Tyr Pro Pro Ala Gln Gly Gly Tyr  
20 25 30  
Pro Pro Gln Gly Tyr Pro Pro Gln Gln Gly Tyr Pro Pro Ala Gly Gly  
35 40 45  
Tyr Pro Pro Ala Gly Tyr Pro Pro Gly Ala Tyr Pro Ala Ala Pro Gly  
50 55 60  
Gly Tyr Pro Pro Ala Pro Gly Gly Tyr Pro Pro Ala Gly Tyr Pro Ala  
65 70 75 80  
Pro Gly Ala His His Ser Gly His Ser Gly Gly Gly Leu Gly Gly Met  
85 90 95  
Ile Ala Gly Ala Ala Gly Ala Ala Ala Ala Tyr Gly Ala His His  
100 105 110  
Val Gly His Ala Ser His Asn Pro Tyr Gly His Ala Val Gly His Gly  
115 120 125  
Gly Tyr Gly His Ala Pro Ala His Gly Phe Gly His Gly Gly His Gly  
130 135 140  
Lys Phe Lys His Gly Lys His Gly Gly Lys Phe Lys His Gly Lys His  
145 150 155 160  
Gly Lys His Gly Lys His Gly Met Phe Gly Gly Gly Gly Lys Phe Lys  
165 170 175  
Lys Trp Lys

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2432

(D) OTHER INFORMATION: / Ceres Seq. ID 1570349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

acctattctc actaacaac tctgaacaaa ccaaaaaaaaa ctcttctttt ttctatcttt 60  
cacgcgttga agattcttga ttttctttct tctccttcct tacacgacca ctgatatgtg 120  
tcggtgactg aaaccatctg ttctcttttg cctctgattt atcgatatgt tttaaagaaa 180  
aacggtgttt gaaacttttg taatttaagg ttcacaaat actcagatct tgtctgagaa 240  
attaagctga aatctgataa atgggtttgt ttaaattcat cttcttgta tctcttctat 300

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| ggagtttcta  | cagtttaggc | tcatctcagc  | tacaagcttc  | acaagcacia  | gtttttcttc  | 360  |
| agctgaaaaa  | acacttagaa | tatccacaac  | agctagaatc  | ttggtatgat  | cacagaacca  | 420  |
| atttctgcta  | cttacaagca | acaccatcga  | tgaacatcac  | ttgtttctct  | aattcagctc  | 480  |
| cagagctaaa  | catcttcggg | gataagtcac  | cagaaaaagc  | caaaaagcttt | gatgggtttg  | 540  |
| ctatctctaa  | tgttacttta | tctgatggat  | tctccattga  | atcatttggt  | actacactgt  | 600  |
| caaggctaaa  | atctcttagg | gttcttactc  | tggcttctct  | agggatttgg  | ggctgtctcc  | 660  |
| ctgagaaact  | tcatcggtta | tcttcacttg  | agtatttggg  | tttgagcaat  | aactttctgt  | 720  |
| ttgggttcagt | accacctaag | ttgtctacaa  | tggtaaagct  | tgaaactttt  | cagatttgat  | 780  |
| cataactttct | tcaatggcac | attacctagc  | tggtttgatt  | cgtattgggt  | tctcaaagtt  | 840  |
| cttagcttta  | aaagtaataa | gctatcagga  | gagctacatt  | cttcattact  | ctcgttggtc  | 900  |
| acaatcgagt  | atatcgattt | gagagcaaat  | tctctgagtg  | gttcacttcc  | ggatgatctg  | 960  |
| aaatgtggaa  | gcaaactctg | gtttatcgac  | atttccgaca  | ataagttaac  | cggaaaaactt | 1020 |
| cctcgttgct  | taagcagcaa | gcaagatatt  | gcgttgagat  | tcaatggaaa  | ctgtttatct  | 1080 |
| ctagagaaac  | agcaacatcc | agaatctttt  | tgtgttaaag  | aagttcgcgc  | tgccgctaaa  | 1140 |
| gctgaagcaa  | aagcagaagc | agaggctgca  | aatgaatcag  | gaaaaagaaa  | atggaagaaa  | 1200 |
| ggagctttta  | tcggcttaat | cgttgggtata | tcaatggcgg  | tattggtttt  | agtctgctgt  | 1260 |
| gtattttatct | tgctcagaag | aaaaggagta  | acaaagaagc  | atgtccacca  | taatactgtc  | 1320 |
| caagataatc  | atccaactac | tggattttct  | tccgagatac  | tctcaaacgc  | aaggtagatt  | 1380 |
| tctgaaacat  | ccaagtttgg | ttcagaggac  | ttaccgggtat | gtagacaggt  | tagcttagaa  | 1440 |
| gagatagtta  | aagctacaaa | gaacttcgat  | aagactatga  | tactcgggtg  | aagctcctta  | 1500 |
| tatggcacgc  | tttacaaaag | aaatcttgag  | aatggaacaa  | aagtggcaat  | aagatgctta  | 1560 |
| ccttcacatc  | agaaatactc | gataaggaat  | cttaaaactgc | ggttggattt  | gctcgcgaa   | 1620 |
| cttagacacc  | cgaatcttgt | ctgcttggtg  | ggtcattgca  | tagatttggt  | aggaaaagat  | 1680 |
| gattacagcg  | ttgagaaagt | ctttttgatt  | tatgagtaca  | ttccaaatgg  | aaacttccaa  | 1740 |
| tcttgtctct  | cagataatag | ttcaggtaag  | ggatgaatt   | ggtcagagag  | gcttaatgtt  | 1800 |
| ctcacagggt  | ttgcaaaaag | tggtcatctt  | cttcacactg  | gagttattcc  | tggattcttc  | 1860 |
| agcaatagac  | tcaagactaa | caacgttttg  | cttaaccaac  | atcggtttgt  | gaagctgagt  | 1920 |
| gattatgggt  | tghccattgt | ctctgaagca  | accagacata  | acacagaaat  | cgcaaaatca  | 1980 |
| tggaacatgt  | caaggctaga | agacgatgtt  | tacagctttg  | gattgattct  | tctacaatca  | 2040 |
| atcgttggac  | catctgtatc | cgcaagagaa  | gaagcatttc  | tacgagacga  | actggcatcg  | 2100 |
| ttggagagcg  | aagaaggag  | gagaagaatg  | gtgaatccga  | cagtacaagc  | cacttgctga  | 2160 |
| aacggatcac  | tgataagagt | gataactctg  | atgaacaaat  | gtgtttcacc  | tgaatcttta  | 2220 |
| agccgaccgt  | ccttcgaaga | tatcttggtg  | aatttacagt  | atgcttctca  | gttgcaagct  | 2280 |
| gcttctgatg  | gtgaccagt  | ttaatatatt  | catagcttct  | tcttctctta  | gtaaaaaatt  | 2340 |
| caaacgaact  | ttttaatgct | ttaaagattc  | gtgtaatgtg  | tgtgtacgaa  | aatcccctgt  | 2400 |
| tatttatgta  | acgattggga | aaaatggaaa  | tt          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Leu | Val | Leu | Val | Cys | Cys | Val | Phe | Ile | Leu | Leu | Arg | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gly | Val | Thr | Lys | Lys | His | Val | His | His | Asn | Thr | Val | Gln | Asp | Asn |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| His | Pro | Thr | Thr | Gly | Phe | Ser | Ser | Glu | Ile | Leu | Ser | Asn | Ala | Arg | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Glu | Thr | Ser | Lys | Phe | Gly | Ser | Glu | Asp | Leu | Pro | Val | Cys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Phe | Ser | Leu | Glu | Glu | Ile | Val | Lys | Ala | Thr | Lys | Asn | Phe | Asp | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Met | Ile | Leu | Gly | Glu | Ser | Ser | Leu | Tyr | Gly | Thr | Leu | Tyr | Lys | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Leu | Glu | Asn | Gly | Thr | Lys | Val | Ala | Ile | Arg | Cys | Leu | Pro | Ser | Ser |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: lin

FEATURE:

(B) LOCATION: 1..275

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1545:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Gly | Glu | Ser | Ser | Leu | Tyr | Gly | Thr | Leu | Tyr | Lys | Gly | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Glu | Asn | Gly | Thr | Lys | Val | Ala | Ile | Arg | Cys | Leu | Pro | Ser | Ser | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Ser | Ile | Arg | Asn | Leu | Lys | Leu | Arg | Leu | Asp | Leu | Leu | Ala | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Arg | His | Pro | Asn | Leu | Val | Cys | Leu | Leu | Gly | His | Cys | Ile | Asp | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Lys | Asp | Asp | Tyr | Ser | Val | Glu | Lys | Val | Phe | Leu | Ile | Tyr | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Ile | Pro | Asn | Gly | Asn | Phe | Gln | Ser | Cys | Leu | Ser | Asp | Asn | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Lys | Gly | Met | Asn | Trp | Ser | Glu | Arg | Leu | Asn | Val | Leu | Thr | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Lys | Ala | Val | His | Phe | Leu | His | Thr | Gly | Val | Ile | Pro | Gly | Phe | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ser Asn Arg Leu Lys Thr Asn Asn Val Leu Leu Asn Gln His Arg Phe  
130 135 140  
Val Lys Leu Ser Asp Tyr Gly Leu Xaa Ile Val Ser Glu Ala Thr Arg  
145 150 155 160  
His Asn Thr Glu Ile Ala Lys Ser Trp Gln Met Ser Arg Leu Glu Asp  
165 170 175  
Asp Val Tyr Ser Phe Gly Leu Ile Leu Leu Gln Ser Ile Val Gly Pro  
180 185 190  
Ser Val Ser Ala Arg Glu Glu Ala Phe Leu Arg Asp Glu Leu Ala Ser  
195 200 205  
Leu Glu Ser Glu Glu Gly Arg Arg Arg Met Val Asn Pro Thr Val Gln  
210 215 220  
Ala Thr Cys Arg Asn Gly Ser Leu Ile Arg Val Ile Thr Leu Met Asn  
225 230 235 240  
Lys Cys Val Ser Pro Glu Ser Leu Ser Arg Pro Ser Phe Glu Asp Ile  
245 250 255  
Leu Trp Asn Leu Gln Tyr Ala Ser Gln Leu Gln Ala Ala Ser Asp Gly  
260 265 270  
Asp Gln Cys  
275

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| acagtaataa tcaagtcaga gccggcgaas ttgccgtttc cgccgttgga gaggaattat   | 60  |
| agtcatgaag cttatttcac ttgtcagaaa cgttcgttct cgccaatgtc aaccggaagt   | 120 |
| tatctggtct ttgcaagttc gtttcttgca gcaagattct gtctcgaaag cttaaaccctaa | 180 |
| gaaatacaaaa taccgcgtcag tttatgatcc gtatggtcct agaccccagc cttcaagcaa | 240 |
| aatcatggag ctagctgagc gtatagctgc tttatctcca gaagaaagaa aacagattgg   | 300 |
| tcctgcactc aatgaacacc tgaggcttcc aaaacaacag atgatttcac cggacggcat   | 360 |
| tggagcaaaa caagataacc gagctgggaa agtagaggag aagaaggaga agacggcttt   | 420 |
| cgatgtgaag ttggagaagt ttaatgcata tgataagatc aaagtgataa aagaagtga    | 480 |
| aacgttcaca agtttggtc tgaaggaagc gaaagagctt gtggagaaag tcccggctat    | 540 |
| tcttaaacaa ggtgtgacaa aggaagaagc taatgaaatc atagccaaga tcaaagctgt   | 600 |
| tggtggagtc gcagttatgg agtaggtgac ttttgacact tcaattgttt ttttgtttga   | 660 |
| ttcactattt ggtattgtga tcacatcttg gtacttaagg tagatgtttt gtaataacaa   | 720 |
| atcgattact tgacattgag ttttcaagaa ctttggDtca attgtttgcc ttctctttgc   | 780 |

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

Met Lys Leu Ile Ser Leu Val Arg Asn Val Arg Ser Arg Gln Cys Gln  
1 5 10 15  
Pro Glu Val Ile Trp Ser Leu Gln Val Arg Phe Leu Gln Gln Asp Ser

20 25 30  
Val Ser Lys Ala Lys Pro Lys Lys Tyr Lys Tyr Pro Ser Val Tyr Asp  
35 40 45  
Pro Tyr Gly Pro Arg Pro Gln Pro Ser Ser Lys Ile Met Glu Leu Ala  
50 55 60  
Glu Arg Ile Ala Ala Leu Ser Pro Glu Glu Arg Lys Gln Ile Gly Pro  
65 70 75 80  
Ala Leu Asn Glu His Leu Arg Leu Pro Lys Gln Gln Met Ile Ser Ser  
85 90 95  
Asp Gly Ile Gly Ala Lys Gln Asp Thr Gly Ala Gly Lys Val Glu Glu  
100 105 110  
Lys Lys Glu Lys Thr Ala Phe Asp Val Lys Leu Glu Lys Phe Asn Ala  
115 120 125  
Ser Asp Lys Ile Lys Val Ile Lys Glu Val Arg Thr Phe Thr Ser Leu  
130 135 140  
Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys Val Pro Ala Ile Leu  
145 150 155 160  
Lys Gln Gly Val Thr Lys Glu Glu Ala Asn Glu Ile Ile Ala Lys Ile  
165 170 175  
Lys Ala Val Gly Gly Val Ala Val Met Glu  
180 185

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

Met Glu Leu Ala Glu Arg Ile Ala Ala Leu Ser Pro Glu Glu Arg Lys  
1 5 10 15  
Gln Ile Gly Pro Ala Leu Asn Glu His Leu Arg Leu Pro Lys Gln Gln  
20 25 30  
Met Ile Ser Ser Asp Gly Ile Gly Ala Lys Gln Asp Thr Gly Ala Gly  
35 40 45  
Lys Val Glu Glu Lys Lys Glu Lys Thr Ala Phe Asp Val Lys Leu Glu  
50 55 60  
Lys Phe Asn Ala Ser Asp Lys Ile Lys Val Ile Lys Glu Val Arg Thr  
65 70 75 80  
Phe Thr Ser Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys Val  
85 90 95  
Pro Ala Ile Leu Lys Gln Gly Val Thr Lys Glu Glu Ala Asn Glu Ile  
100 105 110  
Ile Ala Lys Ile Lys Ala Val Gly Gly Val Ala Val Met Glu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met Ile Ser Ser Asp Gly Ile Gly Ala Lys Gln Asp Thr Gly Ala Gly  
1 5 10 15  
Lys Val Glu Glu Lys Lys Glu Lys Thr Ala Phe Asp Val Lys Leu Glu  
20 25 30  
Lys Phe Asn Ala Ser Asp Lys Ile Lys Val Ile Lys Glu Val Arg Thr  
35 40 45  
Phe Thr Ser Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys Val  
50 55 60  
Pro Ala Ile Leu Lys Gln Gly Val Thr Lys Glu Glu Ala Asn Glu Ile  
65 70 75 80  
Ile Ala Lys Ile Lys Ala Val Gly Gly Val Ala Val Met Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

ctttttctct ttcacatcgt tctttctctc gcaaaccctaa attctctcag cgccggtcaa 60  
atacttgctct ctctctctct ctctctttca ctcttgctct gtctccttcg aagctgtttg 120  
ttctgtaaga aagatggaag caggtggcgc gtacaatcca cgcactgttg aagaggtgtt 180  
tagggatttt aagggtcgta gagctggcat gattaaggct ttaaccactg atgttcagga 240  
gtttttccga ctttgtgatc ccgaaaagga gaacctttgc ctttacggac atccaaatga 300  
gcactgggaa gtgaatttgc cagctgaaga ggttcctcct gagctcccag agcctgtctt 360  
gggtatcaat tttgccagag acgggatggc ggaaaaggat tggttgtccc ttgttgctgt 420  
ccacagtgat gcttggtctt ttgctgttgc tttctttttt ggagccagggt ttggatttga 480  
caaagctgat aggaagaggc ttttcaatat ggtgaatgac ctccaacaa tctttgaggt 540  
tgtagctggc actgctaaga aacaaggaaa agataagtcc tctgtttcca acaacagcag 600  
caacagatcc aaatcaagct ccaagcgagg atctgaatcc cgtgccaaagt tctcaaagcc 660  
ggagccgaaa gatgatgagg aggaggaaga ggaagggtgt gaagaggagg atgaggatga 720  
gcaaggtgaa acacagtgtg gagcatgttg tgagagctat gcagctgatg agttctggat 780  
ttgctgtgac ctctgtgaga tgtggtttca tggaaagtgt gtttaagataa caccagcaag 840  
agctgagcac atcaagcaat acaagtgcct ttcttgagc aaAcaaaagg gctcgttctt 900  
aaatttggtg accgctcgct tctgtgtatc tacctttgca tatgatgatg aacagcttaa 960  
ctgtttgggt tagatcagat ttgtcatatg gatttggtta ttttaggaag acattttagt 1020  
tttttcattg ttacattttg gcgattgaag ggataactct ttgtttaggg gtaatgatct 1080  
ttgtctctgt tttatgtttg tttattaaca ttcttcaaac tcaatcaaaa gtattttggt 1140  
tagtctt

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

Phe Phe Ser Phe Thr Ser Phe Phe Leu Ser Gln Thr Gln Ile Leu Ser  
1 5 10 15  
Ala Pro Val Lys Tyr Leu Ser Leu Ser Leu Ser Leu Phe His Ser Cys  
20 25 30  
Leu Val Ser Phe Glu Ala Val Cys Ser Val Arg Lys Met Glu Ala Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |     |     |     |     |     |     |     |     |     |     |
| Gly | Ala | Tyr | Asn | Pro | Arg | Thr | Val | Glu | Glu | Val | Phe | Arg | Asp | Phe | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Arg | Arg | Ala | Gly | Met | Ile | Lys | Ala | Leu | Thr | Thr | Asp | Val | Gln | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Phe | Arg | Leu | Cys | Asp | Pro | Glu | Lys | Glu | Asn | Leu | Cys | Leu | Tyr | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| His | Pro | Asn | Glu | His | Trp | Glu | Val | Asn | Leu | Pro | Ala | Glu | Glu | Val | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Glu | Leu | Pro | Glu | Pro | Val | Leu | Gly | Ile | Asn | Phe | Ala | Arg | Asp | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Ala | Glu | Lys | Asp | Trp | Leu | Ser | Leu | Val | Ala | Val | His | Ser | Asp | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Leu | Leu | Ala | Val | Ala | Phe | Phe | Phe | Gly | Ala | Arg | Phe | Gly | Phe | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Ala | Asp | Arg | Lys | Arg | Leu | Phe | Asn | Met | Val | Asn | Asp | Leu | Pro | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Phe | Glu | Val | Val | Ala | Gly | Thr | Ala | Lys | Lys | Gln | Gly | Lys | Asp | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Val | Ser | Asn | Asn | Ser | Ser | Asn | Arg | Ser | Lys | Ser | Ser | Ser | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Gly | Ser | Glu | Ser | Arg | Ala | Lys | Phe | Ser | Lys | Pro | Glu | Pro | Lys | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Glu | Glu | Glu | Glu | Glu | Glu | Gly | Val | Glu | Glu | Glu | Asp | Glu | Asp | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Gly | Glu | Thr | Gln | Cys | Gly | Ala | Cys | Gly | Glu | Ser | Tyr | Ala | Ala | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Phe | Trp | Ile | Cys | Cys | Asp | Leu | Cys | Glu | Met | Trp | Phe | His | Gly | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Val | Lys | Ile | Thr | Pro | Ala | Arg | Ala | Glu | His | Ile | Lys | Gln | Tyr | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Pro | Ser | Cys | Ser | Lys | Gln | Lys | Gly | Ser | Phe | Leu | Asn | Leu | Leu | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Ala | Arg | Phe | Cys | Val | Ser | Thr | Phe | Ala | Tyr | Asp | Asp | Glu | Gln | Leu | Asn |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Cys | Leu | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1570368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Gly | Gly | Ala | Tyr | Asn | Pro | Arg | Thr | Val | Glu | Glu | Val | Phe |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Asp | Phe | Lys | Gly | Arg | Arg | Ala | Gly | Met | Ile | Lys | Ala | Leu | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Gln | Glu | Phe | Phe | Arg | Leu | Cys | Asp | Pro | Glu | Lys | Glu | Asn | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Cys | Leu | Tyr | Gly | His | Pro | Asn | Glu | His | Trp | Glu | Val | Asn | Leu | Pro | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Glu | Val | Pro | Pro | Glu | Leu | Pro | Glu | Pro | Val | Leu | Gly | Ile | Asn | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Arg | Asp | Gly | Met | Ala | Glu | Lys | Asp | Trp | Leu | Ser | Leu | Val | Ala | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |

His Ser Asp Ala Trp Leu Leu Ala Val Ala Phe Phe Phe Gly Ala Arg  
100 105 110  
Phe Gly Phe Asp Lys Ala Asp Arg Lys Arg Leu Phe Asn Met Val Asn  
115 120 125  
Asp Leu Pro Thr Ile Phe Glu Val Val Ala Gly Thr Ala Lys Lys Gln  
130 135 140  
Gly Lys Asp Lys Ser Ser Val Ser Asn Asn Ser Ser Asn Arg Ser Lys  
145 150 155 160  
Ser Ser Ser Lys Arg Gly Ser Glu Ser Arg Ala Lys Phe Ser Lys Pro  
165 170 175  
Glu Pro Lys Asp Asp Glu Glu Glu Glu Glu Gly Val Glu Glu Glu  
180 185 190  
Asp Glu Asp Glu Gln Gly Glu Thr Gln Cys Gly Ala Cys Gly Glu Ser  
195 200 205  
Tyr Ala Ala Asp Glu Phe Trp Ile Cys Cys Asp Leu Cys Glu Met Trp  
210 215 220  
Phe His Gly Lys Cys Val Lys Ile Thr Pro Ala Arg Ala Glu His Ile  
225 230 235 240  
Lys Gln Tyr Lys Cys Pro Ser Cys Ser Lys Gln Lys Gly Ser Phe Leu  
245 250 255  
Asn Leu Leu Thr Ala Arg Phe Cys Val Ser Thr Phe Ala Tyr Asp Asp  
260 265 270  
Glu Gln Leu Asn Cys Leu Val  
275

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1570369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

Met Ile Lys Ala Leu Thr Thr Asp Val Gln Glu Phe Phe Arg Leu Cys  
1 5 10 15  
Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly His Pro Asn Glu His  
20 25 30  
Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu  
35 40 45  
Pro Val Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Ala Glu Lys Asp  
50 55 60  
Trp Leu Ser Leu Val Ala Val His Ser Asp Ala Trp Leu Leu Ala Val  
65 70 75 80  
Ala Phe Phe Phe Gly Ala Arg Phe Gly Phe Asp Lys Ala Asp Arg Lys  
85 90 95  
Arg Leu Phe Asn Met Val Asn Asp Leu Pro Thr Ile Phe Glu Val Val  
100 105 110  
Ala Gly Thr Ala Lys Lys Gln Gly Lys Asp Lys Ser Ser Val Ser Asn  
115 120 125  
Asn Ser Ser Asn Arg Ser Lys Ser Ser Ser Lys Arg Gly Ser Glu Ser  
130 135 140  
Arg Ala Lys Phe Ser Lys Pro Glu Pro Lys Asp Asp Glu Glu Glu Glu  
145 150 155 160  
Glu Glu Gly Val Glu Glu Glu Asp Glu Asp Glu Gln Gly Glu Thr Gln  
165 170 175  
Cys Gly Ala Cys Gly Glu Ser Tyr Ala Ala Asp Glu Phe Trp Ile Cys  
180 185 190  
Cys Asp Leu Cys Glu Met Trp Phe His Gly Lys Cys Val Lys Ile Thr



```

 195 200 205
Pro Ala Arg Ala Glu His Ile Lys Gln Tyr Lys Cys Pro Ser Cys Ser
 210 215 220
Lys Gln Lys Gly Ser Phe Leu Asn Leu Leu Thr Ala Arg Phe Cys Val
 225 230 235 240
Ser Thr Phe Ala Tyr Asp Asp Glu Gln Leu Asn Cys Leu Val
 245 250
```

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1386 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1386

(D) OTHER INFORMATION: / Ceres Seq. ID 1570370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

```

gtaatttctt aggaaagtca ttttgataga ggcacagata aacacagcac cgcaaaaagc 60
acagaagcag agaaagacga agacaaaaca aaaaagcttc cccaagaac aaaaagttag 120
catagatgaa gagtcttcgg gttttgtagt ttttgtaaaa cagaaaaaaa aaaaagagaa 180
gaagagatgg gaggttgctg ttgttgttct tcttcacgaa gagctgatgt agataatgga 240
cctgcgtact actactaccc aagggaaca gaagagcgtg tgcctttAtc ttccgctcat 300
aacaggactt cctctgcaat ctctactggt gttgtagtag tagacmcaaa cttagagaca 360
tcatctcctg atgcttatat accaccgcca ctgcctaccc ctttcgatgt gcctataggg 420
attcctcaaa caccagctag tgggtgaagag gctacttggt ttgatataag agaggtttcg 480
gtggactctg ctaataccga gtctgctcaa gaaacagttg atggtattac tctcgggggt 540
ccaactacat gctcacataa agagacagat agcaaaatcc aaacagagat tgatcttgaa 600
tctactgaag aaatagaccc gaagctatca aaagctgttt ttataccaat agaggaagag 660
gaggattgtc ccataatggtt ggaagaatat gatatcgaga acccgaaact tgtagccaaa 720
tgtgatcacc attttcacct tgcattgcat ctagaatgga tggagagaag tgaaacctgc 780
cccgtctgca acaaggaaat ggtatttgac tctactcttg actagcaacc cgcaaatgcc 840
gcatcttaga aggtctcaat ctctctgtat cagaagaaag aaattggagW acaagagaaa 900
aacttaaaaa gaaaaaatgg gtaagaatac actaatagct gatcaciaag ttggatttac 960
gaaacatgtc agtgttgata tatatatggt tgtgtacaga cgtttcaaat cgtctacaaa 1020
aaaacggaga ttaagaatta gagtttggtc ttttagattca cttctgtgaa taaaaaacga 1080
gacaaaactg ataatttttc ttctagatgt ttttaatttt gtaattcttg tttataggtt 1140
attttaggag tgtttttaaag ctgggggttc aatttgggtt tgattcagtt ttttcttgag 1200
tttaagaaaa atattaatca aactgaaatt gagagtttgt tatgtatgga ttgggtttat 1260
tacggttcga ttttagtttg gtttagtgct tatttatatt ctttatattg ttctgtgata 1320
tgtaatatga aaattgttta tacttactag tttgtagtgt ttatgtttta gatttcttag 1380
ttcttc
```

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1570371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

```

Met Gly Gly Cys Cys Cys Ser Ser Arg Arg Ala Asp Val Asp
 1 5 10 15
Asn Gly Pro Ala Tyr Tyr Tyr Tyr Pro Arg Ala Thr Glu Glu Arg Val
 20 25 30
Pro Leu Ser Ser Ala His Asn Arg Thr Ser Ser Ala Ile Ser Thr Gly
 35 40 45
```

Val Val Val Val Asp Xaa Asn Leu Glu Thr Ser Ser Pro Asp Ala Tyr  
50 55 60  
Ile Pro Pro Pro Leu Pro Thr Pro Phe Asp Val Pro Ile Gly Ile Pro  
65 70 75 80  
Gln Thr Pro Ala Ser Gly Glu Glu Ala Thr Cys Val Asp Ile Arg Glu  
85 90 95  
Val Ser Val Asp Ser Ala Asn Thr Glu Ser Ala Gln Glu Thr Val Asp  
100 105 110  
Gly Ile Thr Leu Gly Val Pro Thr Thr Cys Ser His Lys Glu Thr Asp  
115 120 125  
Ser Lys Ile Gln Thr Glu Ile Asp Leu Glu Ser Thr Glu Glu Ile Asp  
130 135 140  
Pro Lys Leu Ser Lys Ala Val Phe Ile Pro Ile Glu Glu Glu Glu Asp  
145 150 155 160  
Cys Pro Ile Cys Leu Glu Glu Tyr Asp Ile Glu Asn Pro Lys Leu Val  
165 170 175  
Ala Lys Cys Asp His His Phe His Leu Ala Cys Ile Leu Glu Trp Met  
180 185 190  
Glu Arg Ser Glu Thr Cys Pro Val Cys Asn Lys Glu Met Val Phe Asp  
195 200 205  
Ser Thr Leu Asp  
210

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

```
ctcttgcttc ttttcaactca caatctcaca gcaaagcctc tcgttgctag aggaatcaaa 60
caatgggtggt tgtgaagtcc accaagtcga atgcttactt caagaggtag caagtgaagt 120
tcaggagaag aagagatgga aagactgact acagggcaag gatccgtctt atcaaccaag 180
acaagaacaa gtacaataca cctaagtatc gttttgttgt ccggtttacc aacaaagaca 240
tagtggcaca gattgtatct gcaagcattg ctgggtgacat tgtaaagct tctgcttacg 300
cacatgaact gcctcagtat ggtctcactg ttggtcttac aaactatgct gcagcttact 360
gtactggcct ttttttggtt cgccgtgttt taaagatggt ggaaatggat gacgagtatg 420
agggaaacgt tgaggccact ggagaggact tttccgttga gccaaactgat tcaaggagac 480
ctttccgtgc ttttcttgat gttggactta tcaggaccac aacaggaaac cgtgtgttcg 540
gtgctcttaa ggggtgcttt gatgggtggtc ttgatatccc tcacagtac aagagatttg 600
ctgggttcca caaggagaac aagcaacttg atgctgaaat ccacaggaaac tacatctatg 660
gtggccatgt ctcaaactac atgaagctgt tgggagaaga tgagccagag aagttacaaa 720
ctcacttcag tgcttacatc aagaaaggag ttgaagctga gagcattgag gagttgtaca 780
agaaggttca cgcagctatt cgtgctgrcc ccaaCcsaag gaaaaccgtg aaacctgctc 840
ccaagcaaca caagaggtag aacttgaaga aacttactta cgaggagagg aagaacaagt 900
tgatcgagag agtcaggcat tgaatggagc aggtgggtgat gatgatgatg aggacgatga 960
asagtaaata agtcaagcct tctttatctc atgcctcttg tagtttttta tcttttgagc 1020
ttaatgcctc aaattttctg ttttcagact aaaacactca gcttttgtgt tcacatttta 1080
attgtgttcg aggattttga tattgaggat acattttctt tgaagtatca ttatcttatt 1140
attacctcca tcataatttt caagaatttg tatgacaata gtttgatgac ttgattttat 1200
ctgtagtttg ctattgttaa atgtaagaac tgtagactt catctat
```

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Val | Lys | Ser | Thr | Lys | Ser | Asn | Ala | Tyr | Phe | Lys | Arg | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Val | Lys | Phe | Arg | Arg | Arg | Arg | Asp | Gly | Lys | Thr | Asp | Tyr | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Arg | Leu | Ile | Asn | Gln | Asp | Lys | Asn | Lys | Tyr | Asn | Thr | Pro | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Arg | Phe | Val | Val | Arg | Phe | Thr | Asn | Lys | Asp | Ile | Val | Ala | Gln | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Ala | Ser | Ile | Ala | Gly | Asp | Ile | Val | Lys | Ala | Ser | Ala | Tyr | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Glu | Leu | Pro | Gln | Tyr | Gly | Leu | Thr | Val | Gly | Leu | Thr | Asn | Tyr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Tyr | Cys | Thr | Gly | Leu | Leu | Leu | Ala | Arg | Arg | Val | Leu | Lys | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Met | Asp | Asp | Glu | Tyr | Glu | Gly | Asn | Val | Glu | Ala | Thr | Gly | Glu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asp | Phe | Ser | Val | Glu | Pro | Thr | Asp | Ser | Arg | Arg | Pro | Phe | Arg | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asp | Val | Gly | Leu | Ile | Arg | Thr | Thr | Thr | Gly | Asn | Arg | Val | Phe | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Leu | Lys | Gly | Ala | Leu | Asp | Gly | Gly | Leu | Asp | Ile | Pro | His | Ser | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Arg | Phe | Ala | Gly | Phe | His | Lys | Glu | Asn | Lys | Gln | Leu | Asp | Ala | Glu |
|     | 180 |     |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | His | Arg | Asn | Tyr | Ile | Tyr | Gly | Gly | His | Val | Ser | Asn | Tyr | Met | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Gly | Glu | Asp | Glu | Pro | Glu | Lys | Leu | Gln | Thr | His | Phe | Ser | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Ile | Lys | Lys | Gly | Val | Glu | Ala | Glu | Ser | Ile | Glu | Glu | Leu | Tyr | Lys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Val | His | Ala | Ala | Ile | Arg | Ala | Xaa | Pro | Asn | Xaa | Arg | Lys | Thr | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Lys | Pro | Ala | Pro | Lys | Gln | His | Lys | Arg | Tyr | Asn | Leu | Lys | Lys | Leu | Thr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Glu | Glu | Arg | Lys | Asn | Lys | Leu | Ile | Glu | Arg | Val | Arg | His |     |     |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1570374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Met | Asp | Glu | Tyr | Glu | Gly | Asn | Val | Glu | Ala | Thr | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Phe | Ser | Val | Glu | Pro | Thr | Asp | Ser | Arg | Arg | Pro | Phe | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Leu | Leu | Asp | Val | Gly | Leu | Ile | Arg | Thr | Thr | Thr | Gly | Asn | Arg | Val |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Leu | Lys | Gly | Ala | Leu | Asp | Gly | Gly | Leu | Asp | Ile | Pro | His |

50 55 60  
Asp Lys Arg Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala  
65 70 75 80  
Glu Ile His Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met  
85 90 95  
Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser  
100 105 110  
Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr  
115 120 125  
Lys Lys Val His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr  
130 135 140  
Val Lys Pro Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu  
145 150 155 160  
Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1570375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly Glu Asp Phe  
1 5 10 15  
Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala Leu Leu Asp  
20 25 30  
Val Gly Leu Ile Arg Thr Thr Thr Gly Asn Arg Val Phe Gly Ala Leu  
35 40 45  
Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser Asp Lys Arg  
50 55 60  
Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala Glu Ile His  
65 70 75 80  
Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met Lys Leu Leu  
85 90 95  
Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser Ala Tyr Ile  
100 105 110  
Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr Lys Lys Val  
115 120 125  
His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr Val Lys Pro  
130 135 140  
Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu Thr Tyr Glu  
145 150 155 160  
Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His  
165 170

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1724

(D) OTHER INFORMATION: / Ceres Seq. ID 1570376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

aatttttagt ctccctccgc gtagaagctt ctccgagact tgtctctgct ttgattgaag 60  
aagacgcttg atcgaaaatt cccttagatt tcgtaaatag ggttttacag aaggtgagat 120  
tacacagaga tcggatttgc gaaaaaaaat aatgggaagt ccaaagaaga acgagaacaa 180  
aggcttcttc gccgccatga cttctggctt ctccatgttc ggtaccgccg tgtcgagatc 240  
cgtaaacggc gtgcaaggta atgaaggagt tgaggtcata aatccagaag gtggcaagga 300  
agatgctgaa gaggaagctc agaaaggaag gtggaaggac gaggaacgag atagttacta 360  
gaagatgatg cagaaatata taggttcgga tattacgtca atggtgactc ttcctgttgt 420  
tatatttgag cctatgacta tgctccagaa gatggctgag ataatggagt attctcattt 480  
gttggatcaa gcagatgaat gcgaagatcc atacttgctt ttagtatatg cttcatcatg 540  
ggctatatct gtttactatg ccttccaacg aacttggaag cttttcaatc ctattcttgg 600  
ggagacatat gagatggta accatgggtg gatttctttt atttctgagc aggttagcca 660  
tcatccacca atgagtgttg gtcattgccg gaacgagcac ttcatttacg acatcacatc 720  
aaagttgaaa actRaacttt tgggtaactc tgttgatgtt taccctgtgg gaagaacgcg 780  
tgtaaccctc aagaaagatg gtgtgggttct ggatttgggt ccgcctctca ctaagattca 840  
caatctaata tttggacgaa cctgggttga ctcacctggg gaaatggtca tgacaaattt 900  
aaccactgga gacaaagttg tgctttatatt ccagccatgt ggctgggttc gttctggccg 960  
ctatgaagtt gatggctacg tttacagcgc agctgaagaa ccgaaaatca tgatgacagg 1020  
aaaatggaat gagaaaatga gctaccaacc ttgtgatgcc gaagggaac cccttccagg 1080  
aacagagctg aaagaggtgt ggcatttggc tgatgtcccc aaaaacgaca aatttcagta 1140  
cactcacttt gctcacaaga taaacagctt cgacacagcg cctgctaagc tcttggttc 1200  
agactcagct atccgtcctg atagatatct ccttgagcag ggtgacctt ctaaagctgg 1260  
ttccgagaaa cacagccttg aggagagaca aagccgaaaa gagaccaga gagacaaagg 1320  
gacaaaagtt cactccaaga tggttcgatc taacggatga gatcacacct actccatggg 1380  
gagatataga agtataccaa tacaacggga agtacaatga acaccgagac acggcagaga 1440  
gctcaagtag tgccccaac gaaacggacc tcaaactgat cgagtttaac ccttggcaat 1500  
atggtaatat ctcaaccgaa tgaagtaact cttatagttt aatttgttat ctctatatac 1560  
gaatgctgtg attcatgttc acttggaagt gattcccatg ttgtttttaa ctttgtttca 1620  
gactgaaaaa tctgattatg tagtttgagt gataaaacat aagttttgtg tttctgtctc 1680  
attgtatctt tgttccattt cgatcaatag taattatggt tggt

(2) INFORMATION FOR SEQ ID NO:1561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

Met Met Gln Lys Tyr Ile Gly Ser Asp Ile Thr Ser Met Val Thr Leu  
1 5 10 15  
Pro Val Val Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu  
20 25 30  
Ile Met Glu Tyr Ser His Leu Leu Asp Gln Ala Asp Glu Cys Glu Asp  
35 40 45  
Pro Tyr Leu Arg Leu Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr  
50 55 60  
Tyr Ala Phe Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu  
65 70 75 80  
Thr Tyr Glu Met Val Asn His Gly Gly Ile Ser Phe Ile Ser Glu Gln  
85 90 95  
Val Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His  
100 105 110  
Phe Ile Tyr Asp Ile Thr Ser Lys Leu Lys Thr Xaa Leu Leu Gly Asn  
115 120 125  
Ser Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Lys  
130 135 140  
Asp Gly Val Val Leu Asp Leu Val Pro Pro Leu Thr Lys Ile His Asn  
145 150 155 160

Leu Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Val Met  
165 170 175  
Thr Asn Leu Thr Thr Gly Asp Lys Val Leu Tyr Phe Gln Pro Cys  
180 185 190  
Gly Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Ser  
195 200 205  
Ala Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys Trp Asn Glu Lys  
210 215 220  
Met Ser Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro Leu Pro Gly Thr  
225 230 235 240  
Glu Leu Lys Glu Val Trp His Leu Ala Asp Val Pro Lys Asn Asp Lys  
245 250 255  
Phe Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala  
260 265 270  
Pro Ala Lys Leu Leu Ala Ser Asp Ser Arg Ile Arg Pro Asp Arg Tyr  
275 280 285  
Ser Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser Glu Lys His Ser  
290 295 300  
Leu Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg Asp Lys Gly Thr  
305 310 315 320  
Lys Val His Ser Lys Met Val Arg Ser Asn Gly  
325 330

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1570378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

Met Gln Lys Tyr Ile Gly Ser Asp Ile Thr Ser Met Val Thr Leu Pro  
1 5 10 15  
Val Val Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Ile  
20 25 30  
Met Glu Tyr Ser His Leu Leu Asp Gln Ala Asp Glu Cys Glu Asp Pro  
35 40 45  
Tyr Leu Arg Leu Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr  
50 55 60  
Ala Phe Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr  
65 70 75 80  
Tyr Glu Met Val Asn His Gly Gly Ile Ser Phe Ile Ser Glu Gln Val  
85 90 95  
Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe  
100 105 110  
Ile Tyr Asp Ile Thr Ser Lys Leu Lys Thr Xaa Leu Leu Gly Asn Ser  
115 120 125  
Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Lys Asp  
130 135 140  
Gly Val Val Leu Asp Leu Val Pro Pro Leu Thr Lys Ile His Asn Leu  
145 150 155 160  
Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Val Met Thr  
165 170 175  
Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly  
180 185 190  
Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Ser Ala  
195 200 205  
Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys Trp Asn Glu Lys Met

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 210                     | 215                 | 220                 |
| Ser Tyr Gln Pro Cys Asp | Ala Glu Gly Glu Pro | Leu Pro Gly Thr Glu |
| 225                     | 230                 | 235                 |
| Leu Lys Glu Val Trp His | Leu Ala Asp Val Pro | Lys Asn Asp Lys Phe |
| 245                     | 250                 | 255                 |
| Gln Tyr Thr His Phe Ala | His Lys Ile Asn Ser | Phe Asp Thr Ala Pro |
| 260                     | 265                 | 270                 |
| Ala Lys Leu Leu Ala Ser | Asp Ser Arg Ile Arg | Pro Asp Arg Tyr Ser |
| 275                     | 280                 | 285                 |
| Leu Glu Gln Gly Asp Leu | Ser Lys Ala Gly Ser | Glu Lys His Ser Leu |
| 290                     | 295                 | 300                 |
| Glu Glu Arg Gln Ser Arg | Lys Glu Asp Gln Arg | Asp Lys Gly Thr Lys |
| 305                     | 310                 | 315                 |
| Val His Ser Lys Met Val | Arg Ser Asn Gly     |                     |
| 325                     | 330                 |                     |

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..319

(D) OTHER INFORMATION: / Ceres Seq. ID 1570379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Val Thr Leu Pro Val Val Ile Phe Glu Pro Met Thr Met Leu Gln |             |
| 1                                                               | 5 10 15     |
| Lys Met Ala Glu Ile Met Glu Tyr Ser His Leu Leu Asp Gln Ala Asp |             |
|                                                                 | 20 25 30    |
| Glu Cys Glu Asp Pro Tyr Leu Arg Leu Val Tyr Ala Ser Ser Trp Ala |             |
|                                                                 | 35 40 45    |
| Ile Ser Val Tyr Tyr Ala Phe Gln Arg Thr Trp Lys Pro Phe Asn Pro |             |
|                                                                 | 50 55 60    |
| Ile Leu Gly Glu Thr Tyr Glu Met Val Asn His Gly Gly Ile Ser Phe |             |
| 65                                                              | 70 75 80    |
| Ile Ser Glu Gln Val Ser His His Pro Pro Met Ser Ala Gly His Ala |             |
|                                                                 | 85 90 95    |
| Glu Asn Glu His Phe Ile Tyr Asp Ile Thr Ser Lys Leu Lys Thr Xaa |             |
|                                                                 | 100 105 110 |
| Leu Leu Gly Asn Ser Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val |             |
|                                                                 | 115 120 125 |
| Thr Leu Lys Lys Asp Gly Val Val Leu Asp Leu Val Pro Pro Leu Thr |             |
|                                                                 | 130 135 140 |
| Lys Ile His Asn Leu Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly |             |
| 145                                                             | 150 155 160 |
| Glu Met Val Met Thr Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr |             |
|                                                                 | 165 170 175 |
| Phe Gln Pro Cys Gly Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly |             |
|                                                                 | 180 185 190 |
| Tyr Val Tyr Ser Ala Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys |             |
|                                                                 | 195 200 205 |
| Trp Asn Glu Lys Met Ser Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro |             |
|                                                                 | 210 215 220 |
| Leu Pro Gly Thr Glu Leu Lys Glu Val Trp His Leu Ala Asp Val Pro |             |
| 225                                                             | 230 235 240 |
| Lys Asn Asp Lys Phe Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser |             |
|                                                                 | 245 250 255 |
| Phe Asp Thr Ala Pro Ala Lys Leu Leu Ala Ser Asp Ser Arg Ile Arg |             |
|                                                                 | 260 265 270 |

Pro Asp Arg Tyr Ser Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser  
275 280 285  
Glu Lys His Ser Leu Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg  
290 295 300  
Asp Lys Gly Thr Lys Val His Ser Lys Met Val Arg Ser Asn Gly  
305 310 315

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

ataagatcca aaaccataaa actaggtttc acactttctc tctaaacact gtctcttttc 60  
tccgatacat atcccgccgc ttccctgtg tttttcttcg ccgtccgtcg ttcttttcaa 120  
ctccttagct gcgatattaa agtctagaca caatgagagg aaggagctac acgccatcac 180  
caccaagggg ttatggaagg aggggcccga gccctagccc tcggggccgg tttgggtgga 240  
gtcgtgacag tgatctccca accagtcttt tggttcgcaa cttacgtcat gattgcaggc 300  
aagaagacct caggaggcca tttgagcagt ttggtccgt caaggacatc taccttccta 360  
gggattacta tactggagat ccaagggggt ttggattcat tcagtttatg gatcctgctg 420  
atgctgctga ggctaaacat caaatggatg gttatcttct tcttggtcgt gagttgactg 480  
tcgtatttgc tgaagaaaac cggaagaagc caactgagat gagaacaagg gatcgagggtg 540  
gaaggagcaa cagattccag gacagaagac gttctcctcc tcggtactct cggctctcctc 600  
ctcgccgtgg tcgtagatca cgatcacgta gctgcggcta taattctcct cccgctaaaa 660  
gacatcaatc taggtctgtc tcacctcagg atagacgata tgagaaggag aggtcatact 720  
ctcgctcacc accccataat ggctcaaggg ttgcgagtgg aagtcctggg agagtgaaga 780  
gccacagcag aagcccaaga agaagcgtga gcccaagaaa aaacaggagc tacacgccag 840  
aacaagcaag gagccaaagc cctgtcccta ggcagagcag gagcccgacc ccagtcctc 900  
gtggagcaca aaatggagac cgttctccaa gccagtgatt tAacaccatg tatctctcta 960  
ctcttcagtt tttcagttct gttctgtttg atcagatatt ttgtttgcct cagattgata 1020  
tttccctact tagacagata tttgtagtgc tattgggtatt ttgctttatg tttgatccat 1080  
ggatgatctt gagacagtat tttgaagtag catgtgttat ttgtcatctt atcttttttag 1140  
atctcatcta acattgttat ggtgaaaaag atggtcctat tacgggagct ttttg

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

Met Arg Gly Arg Ser Tyr Thr Pro Ser Pro Pro Arg Gly Tyr Gly Arg  
1 5 10 15  
Arg Gly Arg Ser Pro Ser Pro Arg Gly Arg Phe Gly Gly Ser Arg Asp  
20 25 30  
Ser Asp Leu Pro Thr Ser Leu Leu Val Arg Asn Leu Arg His Asp Cys  
35 40 45  
Arg Gln Glu Asp Leu Arg Arg Pro Phe Glu Gln Phe Gly Pro Val Lys  
50 55 60  
Asp Ile Tyr Leu Pro Arg Asp Tyr Tyr Thr Gly Asp Pro Arg Gly Phe  
65 70 75 80  
Gly Phe Ile Gln Phe Met Asp Pro Ala Asp Ala Ala Glu Ala Lys His



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Gln | Met | Asp | Gly | Tyr | Leu | Leu | Leu | Gly | Arg | Glu | Leu | Thr | Val | Val | Phe |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ala | Glu | Glu | Asn | Arg | Lys | Lys | Pro | Thr | Glu | Met | Arg | Thr | Arg | Asp | Arg |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Gly | Gly | Arg | Ser | Asn | Arg | Phe | Gln | Asp | Arg | Arg | Arg | Ser | Pro | Pro | Arg |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Tyr | Ser | Arg | Ser | Pro | Pro | Arg | Arg | Gly | Arg | Arg | Ser | Arg | Ser | Arg | Ser |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Cys | Gly | Tyr | Asn | Ser | Pro | Pro | Ala | Lys | Arg | His | Gln | Ser | Arg | Ser | Val |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Ser | Pro | Gln | Asp | Arg | Arg | Tyr | Glu | Lys | Glu | Arg | Ser | Tyr | Ser | Arg | Ser |  |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |  |  |
| Pro | Pro | His | Asn | Gly | Ser | Arg | Val | Arg | Ser | Gly | Ser | Pro | Gly | Arg | Val |  |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |
| Lys | Ser | His | Ser | Arg | Ser | Pro | Arg | Arg | Ser | Val | Ser | Pro | Arg | Lys | Asn |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |  |  |
| Arg | Ser | Tyr | Thr | Pro | Glu | Gln | Ala | Arg | Ser | Gln | Ser | Pro | Val | Pro | Arg |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Gln | Ser | Arg | Ser | Pro | Thr | Pro | Val | Pro | Arg | Gly | Ala | Gln | Asn | Gly | Asp |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |  |
| Arg | Ser | Pro | Ser | Gln |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1570382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Asp | Pro | Ala | Asp | Ala | Ala | Glu | Ala | Lys | His | Gln | Met | Asp | Gly | Tyr |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Leu | Leu | Leu | Gly | Arg | Glu | Leu | Thr | Val | Phe | Ala | Glu | Glu | Asn | Arg |     |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Lys | Lys | Pro | Thr | Glu | Met | Arg | Thr | Arg | Asp | Arg | Gly | Gly | Arg | Ser | Asn |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Arg | Phe | Gln | Asp | Arg | Arg | Arg | Ser | Pro | Pro | Arg | Tyr | Ser | Arg | Ser | Pro |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Pro | Arg | Arg | Gly | Arg | Arg | Ser | Arg | Ser | Arg | Ser | Cys | Gly | Tyr | Asn | Ser |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Pro | Pro | Ala | Lys | Arg | His | Gln | Ser | Arg | Ser | Val | Ser | Pro | Gln | Asp | Arg |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Arg | Tyr | Glu | Lys | Glu | Arg | Ser | Tyr | Ser | Arg | Ser | Pro | Pro | His | Asn | Gly |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ser | Arg | Val | Arg | Ser | Gly | Ser | Pro | Gly | Arg | Val | Lys | Ser | His | Ser | Arg |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ser | Pro | Arg | Arg | Ser | Val | Ser | Pro | Arg | Lys | Asn | Arg | Ser | Tyr | Thr | Pro |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Glu | Gln | Ala | Arg | Ser | Gln | Ser | Pro | Val | Pro | Arg | Gln | Ser | Arg | Ser | Pro |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Thr | Pro | Val | Pro | Arg | Gly | Ala | Gln | Asn | Gly | Asp | Arg | Ser | Pro | Ser | Gln |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..164
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570383
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

Met Asp Gly Tyr Leu Leu Leu Gly Arg Glu Leu Thr Val Val Phe Ala  
1 5 10 15  
Glu Glu Asn Arg Lys Lys Pro Thr Glu Met Arg Thr Arg Asp Arg Gly  
20 25 30  
Gly Arg Ser Asn Arg Phe Gln Asp Arg Arg Arg Ser Pro Pro Arg Tyr  
35 40 45  
Ser Arg Ser Pro Pro Arg Arg Gly Arg Arg Ser Arg Ser Arg Ser Cys  
50 55 60  
Gly Tyr Asn Ser Pro Pro Ala Lys Arg His Gln Ser Arg Ser Val Ser  
65 70 75 80  
Pro Gln Asp Arg Arg Tyr Glu Lys Glu Arg Ser Tyr Ser Arg Ser Pro  
85 90 95  
Pro His Asn Gly Ser Arg Val Arg Ser Gly Ser Pro Gly Arg Val Lys  
100 105 110  
Ser His Ser Arg Ser Pro Arg Arg Ser Val Ser Pro Arg Lys Asn Arg  
115 120 125  
Ser Tyr Thr Pro Glu Gln Ala Arg Ser Gln Ser Pro Val Pro Arg Gln  
130 135 140  
Ser Arg Ser Pro Thr Pro Val Pro Arg Gly Ala Gln Asn Gly Asp Arg  
145 150 155 160  
Ser Pro Ser Gln

(2) INFORMATION FOR SEQ ID NO:1568:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1358 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1358
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570384
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

aatcgtttcc acgaaaacaa gtagagagag tgatttcgagt ttccaatca taaaaatcag 60  
cgaagaagat cttcgttctt gttcattctg tgaggtttca ttgttaaaat cgaaacgaat 120  
ctcaggttgg agtaatcctt gggagagatc cgatttccgt ttccatggcg attcgggtgg 180  
cggagctgtg tatcgtaactg ttgcgtcttt cctacgccat vtgcgtcctt gccgggaaga 240  
gttactacga tgtgttgcaa gtccccgaaag gtgcatctga tgaacagatc aagagagctt 300  
ataggaaact agctttgaag tatcatcccg ataagaatca aggaaatgag gaagcgactc 360  
gcaaattcgc tgagatcaac aatgcttatg aagtgttatc ggatgaggag aagagggaga 420  
tatataacaa gtatggtgaa gagggactta aacagtttcc tgcaaataga ggaagaggag 480  
gagKaggagg cggcatgaat atgcaggaca tcttcagctc attttttggg ggaggttcga 540  
tgagggaaga agagaagggt gtcaaggggg atgacgtaat tgtggaactt gaggcaactc 600  
tagaagattt gtacatggga ggctctatga aggtatggag ggaaaagaat gtgataaaac 660  
cagctcctgg aaagagaaag tgtaactgca ggaacgaggt ctatcacaga caaattggtc 720  
ctggaatggt ccaacagatg acagagcagg tctgtgacaa atgccctaata gtcaaataacg 780  
aacgggaggg atactttgtg acagttgata tcgagaaagg aatgaaagat ggagaagaag 840  
tgtctttcta tgaagacggc gaaAcccCat tcttgacgggT gaccctgggT gaccttaagt 900  
tccgaatcag aactgcacca catgcccggt tTcagaaggg atggcaacga tctacacatg 960  
aacgtgaaca ttacactggt tgaggcgcta gttgggtttg agaaatcatt caaacacttg 1020

gatgatcacg aagttgacat cagttccaag ggaattacaa agccgaagga agtaaagaag 1080  
ttcaaaggag aagggatgcc acttcactac agcacaaga aaggcaacct ctttgtcact 1140  
tttgaggttt tgtttccgtc ttctctcact gacgatcaga agaagaagat taaagaagtc 1200  
tttgcttagt gctcttctct cgctttcgct ctctctctct ttagaagttt ggggattaaa 1260  
gagaagaaca tgtgatggtc ctaatgtata acatgattag gttttaatat agaaagaaaa 1320  
aagatatggg gagacaaagt cggaaggacg ttttgacc

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1570385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

Met Ala Ile Arg Trp Ser Glu Leu Cys Ile Val Leu Phe Ala Leu Ser  
1 5 10  
Tyr Ala Xaa Cys Val Leu Ala Gly Lys Ser Tyr Tyr Asp Val Leu Gln  
20 25 30  
Val Pro Lys Gly Ala Ser Asp Glu Gln Ile Lys Arg Ala Tyr Arg Lys  
35 40 45  
Leu Ala Leu Lys Tyr His Pro Asp Lys Asn Gln Gly Asn Glu Glu Ala  
50 55 60  
Thr Arg Lys Phe Ala Glu Ile Asn Asn Ala Tyr Glu Val Leu Ser Asp  
65 70 75 80  
Glu Glu Lys Arg Glu Ile Tyr Asn Lys Tyr Gly Glu Glu Gly Leu Lys  
85 90 95  
Gln Phe Ser Ala Asn Gly Gly Arg Gly Gly Xaa Gly Gly Gly Met Asn  
100 105 110  
Met Gln Asp Ile Phe Ser Ser Phe Phe Gly Gly Gly Ser Met Glu Glu  
115 120 125  
Glu Glu Lys Val Val Lys Gly Asp Asp Val Ile Val Glu Leu Glu Ala  
130 135 140  
Thr Leu Glu Asp Leu Tyr Met Gly Gly Ser Met Lys Val Trp Arg Glu  
145 150 155 160  
Lys Asn Val Ile Lys Pro Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg  
165 170 175  
Asn Glu Val Tyr His Arg Gln Ile Gly Pro Gly Met Phe Gln Gln Met  
180 185 190  
Thr Glu Gln Val Cys Asp Lys Cys Pro Asn Val Lys Tyr Glu Arg Glu  
195 200 205  
Gly Tyr Phe Val Thr Val Asp Ile Glu Lys Gly Met Lys Asp Gly Glu  
210 215 220  
Glu Val Ser Phe Tyr Glu Asp Gly Glu Thr Pro Phe Leu Thr Val Thr  
225 230 235 240  
Leu Val Asp Leu Lys Phe Arg Ile Arg Thr Ala Pro His Ala Arg Phe  
245 250 255  
Gln Lys Gly Trp Gln Arg Ser Thr His Glu Arg Glu His Tyr Thr Gly  
260 265 270

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1570386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Met | Gln | Asp | Ile | Phe | Ser | Ser | Phe | Phe | Gly | Gly | Gly | Ser | Met |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Glu | Glu | Lys | Val | Val | Lys | Gly | Asp | Asp | Val | Ile | Val | Glu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Thr | Leu | Glu | Asp | Leu | Tyr | Met | Gly | Gly | Ser | Met | Lys | Val | Trp |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Lys | Asn | Val | Ile | Lys | Pro | Ala | Pro | Gly | Lys | Arg | Lys | Cys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Arg | Asn | Glu | Val | Tyr | His | Arg | Gln | Ile | Gly | Pro | Gly | Met | Phe | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Met | Thr | Glu | Gln | Val | Cys | Asp | Lys | Cys | Pro | Asn | Val | Lys | Tyr | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Glu | Gly | Tyr | Phe | Val | Thr | Val | Asp | Ile | Glu | Lys | Gly | Met | Lys | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Glu | Glu | Val | Ser | Phe | Tyr | Glu | Asp | Gly | Glu | Thr | Pro | Phe | Leu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Thr | Leu | Val | Asp | Leu | Lys | Phe | Arg | Ile | Arg | Thr | Ala | Pro | His | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Phe | Gln | Lys | Gly | Trp | Gln | Arg | Ser | Thr | His | Glu | Arg | Glu | His | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1570387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asp | Ile | Phe | Ser | Ser | Phe | Phe | Gly | Gly | Gly | Ser | Met | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Lys | Val | Val | Lys | Gly | Asp | Asp | Val | Ile | Val | Glu | Leu | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Glu | Asp | Leu | Tyr | Met | Gly | Gly | Ser | Met | Lys | Val | Trp | Arg | Glu |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | Asn | Val | Ile | Lys | Pro | Ala | Pro | Gly | Lys | Arg | Lys | Cys | Asn | Cys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Glu | Val | Tyr | His | Arg | Gln | Ile | Gly | Pro | Gly | Met | Phe | Gln | Gln | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Glu | Gln | Val | Cys | Asp | Lys | Cys | Pro | Asn | Val | Lys | Tyr | Glu | Arg | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Tyr | Phe | Val | Thr | Val | Asp | Ile | Glu | Lys | Gly | Met | Lys | Asp | Gly | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Val | Ser | Phe | Tyr | Glu | Asp | Gly | Glu | Thr | Pro | Phe | Leu | Thr | Val | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Asp | Leu | Lys | Phe | Arg | Ile | Arg | Thr | Ala | Pro | His | Ala | Arg | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Lys | Gly | Trp | Gln | Arg | Ser | Thr | His | Glu | Arg | Glu | His | Tyr | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1879

(D) OTHER INFORMATION: / Ceres Seq. ID 1570388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

```
acagcaaaaa gccactctcc tttctctctc tctcttggtc ctctgcatcc atggccacca 60
agctcgacac cagtagctta cttttggccc tcttggtcaa atgtagcctc cttactcaaa 120
ccaatcttgc tctctctctc ctctgtagct ccctagcttc tctcgctctt tctctcttct 180
tctggtctca tcccggagga cccgcatggg gaaagtactt cctccaccgc cgccgtcaaa 240
ccaccgtgat acccgggcca agaggcttac cttttgtcgg aagcatgtct ctcatgtcaa 300
acactctggc tcaccgttgc atagccgcaa cgcagagaa atttagagcc gaacggttaa 360
tggcggttag tttgggagaa actcgctgga tgcgcacgtg caatcctgat gttagctaaag 420
agattctaaa cagtccggtt ttcgctgacc gcccggttaa ggaatcagct tattccctca 480
tgtttaaccg tgctatcggt ttcgctcctt acggcggtta ctggcgaacc ttgagaaaaa 540
tcgctcttaa tcattctttc agcccgaac agattaaacg ttccgaaacg cagagaagcg 600
tgatcgcgaa tcaaatcgtg aagtgtctca caaacagag taacaccaa ggtctctgtt 660
tcgcacgtga cttgatcaaa acggcatcgc ttaataacat gatgtgctct gttttcggaa 720
aagaatacga gcttgaggaa gagcatgaag aagtgaagtga gctacgtgaa ttggtggaag 780
aaggttatga tttactcggt acactgaatt ggaccgatca tctcccatgg ctctctgaat 840
ttgatcctca aagaatccgg tctagatgct ctaatctcgt cccaaaagta aaccggtttg 900
tgaaccggat tatctctgac caccgtgaac aaactcgtga ctcaccgagt gacttcggtg 960
acgtattgct ctctctcgat ggtcctgata aattatccga ccctgatatc atcgccgttc 1020
tatgggaaat gatattcaga ggaactgaca cgggtggctgt tttgatcgag tggattcttg 1080
ctaggatggt ccttcattca gatattcaat cgaaggttca caatgagctt gatcaaactc 1140
tgggacgata aagggtgtgc gaagagtctg acgtggtgtc tctagtatat ctaacggctg 1200
tggtgaaaga agtcttgagg cttcaccgcg caggccact actctcatgg gcccggttag 1260
caatcacaga cacgatcatc gacggtcgtc gtgttcgggc ggggaccacc gcaatggtga 1320
acatgtgggc tattgcacac gatccacacg tgtgggagaa tccggttgag tttaaaccgc 1380
aacgttttgt agccaaggaa ggtgagggtt agttctcggg tcttggtgtc gatttgaggc 1440
ttgcaccgtt cgggtccggt cgtcgggttt gccccgggaa gaatcttggt ttgaccaccg 1500
tgacgttttg gactgcgacg cttttgcatg agtttgaaNt Ggctgacgcc gtccgatgag 1560
aagaccgttg acttgccga gaaactgagg ctctcgtgtg agatggctaa tcctcttgct 1620
gctaaattac gcccaggcgc cagttttagt gtatgataag ggtaaggcta tacacagata 1680
cagtggtaac taaagcgaag gaaaattagt gtgaatttaa agcaaaagaa taaaataaag 1740
aacaagaaaa gtaaaggaaa caaaaaaaa gaatcataca aaaaatacta ataagaatgg 1800
taatgaagct tttatattaa actaacatct tgatacgtgt tgtatatatg atgaaaacat 1860
taatgtcaca aagaaaagc
```

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..518

(D) OTHER INFORMATION: / Ceres Seq. ID 1570389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

```
Ser Lys Lys Pro Leu Ser Phe Leu Ser Leu Ser Cys Ser Ser Ala Ser
1 5 10 15
Met Ala Thr Lys Leu Asp Thr Ser Ser Leu Leu Leu Ala Leu Leu Ser
20 25 30
Lys Cys Ser Leu Leu Thr Gln Thr Asn Leu Ala Leu Ser Leu Leu Val
```



(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1570390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Lys | Leu | Asp | Thr | Ser | Ser | Leu | Leu | Ala | Leu | Leu | Ser |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Cys | Ser | Leu | Leu | Thr | Gln | Thr | Asn | Leu | Ala | Leu | Ser | Leu | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Leu | Ala | Ser | Leu | Ala | Leu | Ser | Leu | Phe | Phe | Trp | Ser | His | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Gly | Pro | Ala | Trp | Gly | Lys | Tyr | Phe | Leu | His | Arg | Arg | Arg | Gln | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Val | Ile | Pro | Gly | Pro | Arg | Gly | Leu | Pro | Phe | Val | Gly | Ser | Met | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Met | Ser | Asn | Thr | Leu | Ala | His | Arg | Cys | Ile | Ala | Ala | Thr | Ala | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Phe | Arg | Ala | Glu | Arg | Leu | Met | Ala | Phe | Ser | Leu | Gly | Glu | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ile | Val | Thr | Cys | Asn | Pro | Asp | Val | Ala | Lys | Glu | Ile | Leu | Asn | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Val | Phe | Ala | Asp | Arg | Pro | Val | Lys | Glu | Ser | Ala | Tyr | Ser | Leu | Met |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Phe | Asn | Arg | Ala | Ile | Gly | Phe | Ala | Pro | Tyr | Gly | Val | Tyr | Trp | Arg | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Arg | Lys | Ile | Ala | Ser | Asn | His | Leu | Phe | Ser | Pro | Lys | Gln | Ile | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Ser | Glu | Thr | Gln | Arg | Ser | Val | Ile | Ala | Asn | Gln | Ile | Val | Lys | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Thr | Lys | Gln | Ser | Asn | Thr | Lys | Gly | Leu | Cys | Phe | Ala | Arg | Asp | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Lys | Thr | Ala | Ser | Leu | Asn | Asn | Met | Met | Cys | Ser | Val | Phe | Gly | Lys |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Tyr | Glu | Leu | Glu | Glu | Glu | His | Glu | Glu | Val | Ser | Glu | Leu | Arg | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Val | Glu | Glu | Gly | Tyr | Asp | Leu | Leu | Gly | Thr | Leu | Asn | Trp | Thr | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Leu | Pro | Trp | Leu | Ser | Glu | Phe | Asp | Pro | Gln | Arg | Ile | Arg | Ser | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Cys | Ser | Asn | Leu | Val | Pro | Lys | Val | Asn | Arg | Phe | Val | Asn | Arg | Ile | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Asp | His | Arg | Glu | Gln | Thr | Arg | Asp | Ser | Pro | Ser | Asp | Phe | Val | Asp |
|     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Val | Leu | Leu | Ser | Leu | Asp | Gly | Pro | Asp | Lys | Leu | Ser | Asp | Pro | Asp | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Ala | Val | Leu | Trp | Glu | Met | Ile | Phe | Arg | Gly | Thr | Asp | Thr | Val | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Leu | Ile | Glu | Trp | Ile | Leu | Ala | Arg | Met | Val | Leu | His | Pro | Asp | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Ser | Thr | Val | His | Asn | Glu | Leu | Asp | Gln | Ile | Val | Gly | Arg | Ser | Arg |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Ala | Val | Glu | Glu | Ser | Asp | Val | Val | Ser | Leu | Val | Tyr | Leu | Thr | Ala | Val |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Val | Lys | Glu | Val | Leu | Arg | Leu | His | Pro | Pro | Gly | Pro | Leu | Leu | Ser | Trp |

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Met<br>1 | Ser | Leu | Met | Ser<br>5 | Asn | Thr | Leu | Ala | His<br>10 | Arg | Cys | Ile | Ala | Ala<br>15 | Thr |
| Ala      | Glu | Lys | Phe | Arg      | Ala | Glu | Arg | Leu | Met       | Ala | Phe | Ser | Leu | Gly       | Glu |
|          |     |     | 20  |          |     |     |     | 25  |           |     |     |     | 30  |           |     |
| Thr      | Arg | Val | Ile | Val      | Thr | Cys | Asn | Pro | Asp       | Val | Ala | Lys | Glu | Ile       | Leu |
|          |     |     | 35  |          |     |     | 40  |     |           |     |     | 45  |     |           |     |
| Asn      | Ser | Pro | Val | Phe      | Ala | Asp | Arg | Pro | Val       | Lys | Glu | Ser | Ala | Tyr       | Ser |
|          |     |     |     |          |     | 55  |     |     |           |     | 60  |     |     |           |     |
| Leu      | Met | Phe | Asn | Arg      | Ala | Ile | Gly | Phe | Ala       | Pro | Tyr | Gly | Val | Tyr       | Trp |
| 65       |     |     |     |          | 70  |     |     |     |           | 75  |     |     |     |           | 80  |
| Arg      | Thr | Leu | Arg | Lys      | Ile | Ala | Ser | Asn | His       | Leu | Phe | Ser | Pro | Lys       | Gln |
|          |     |     |     | 85       |     |     |     |     | 90        |     |     |     |     | 95        |     |
| Ile      | Lys | Arg | Ser | Glu      | Thr | Gln | Arg | Ser | Val       | Ile | Ala | Asn | Gln | Ile       | Val |
|          |     |     | 100 |          |     |     |     | 105 |           |     |     |     | 110 |           |     |
| Lys      | Cys | Leu | Thr | Lys      | Gln | Ser | Asn | Thr | Lys       | Gly | Leu | Cys | Phe | Ala       | Arg |
|          |     |     | 115 |          |     |     | 120 |     |           |     |     | 125 |     |           |     |
| Asp      | Leu | Ile | Lys | Thr      | Ala | Ser | Leu | Asn | Asn       | Met | Met | Cys | Ser | Val       | Phe |
|          |     |     |     |          |     | 135 |     |     |           |     | 140 |     |     |           |     |
| Gly      | Lys | Glu | Tyr | Glu      | Leu | Glu | Glu | Glu | His       | Glu | Glu | Val | Ser | Glu       | Leu |
| 145      |     |     |     |          | 150 |     |     |     |           | 155 |     |     |     |           | 160 |
| Arg      | Glu | Leu | Val | Glu      | Glu | Gly | Tyr | Asp | Leu       | Leu | Gly | Thr | Leu | Asn       | Trp |
|          |     |     |     | 165      |     |     |     |     | 170       |     |     |     |     | 175       |     |
| Thr      | Asp | His | Leu | Pro      | Trp | Leu | Ser | Glu | Phe       | Asp | Pro | Gln | Arg | Ile       | Arg |
|          |     |     | 180 |          |     |     |     | 185 |           |     |     |     | 190 |           |     |
| Ser      | Arg | Cys | Ser | Asn      | Leu | Val | Pro | Lys | Val       | Asn | Arg | Phe | Val | Asn       | Arg |
|          |     |     | 195 |          |     |     | 200 |     |           |     |     | 205 |     |           |     |
| Ile      | Ile | Ser | Asp | His      | Arg | Glu | Gln | Thr | Arg       | Asp | Ser | Pro | Ser | Asp       | Phe |
|          |     |     | 210 |          |     | 215 |     |     |           |     | 220 |     |     |           |     |
| Val      | Asp | Val | Leu | Leu      | Ser | Leu | Asp | Gly | Pro       | Asp | Lys | Leu | Ser | Asp       | Pro |
| 225      |     |     |     |          | 230 |     |     |     |           | 235 |     |     |     |           | 240 |
| Asp      | Ile | Ile | Ala | Val      | Leu | Trp | Glu | Met | Ile       | Phe | Arg | Gly | Thr | Asp       | Thr |
|          |     |     |     | 245      |     |     |     |     | 250       |     |     |     |     | 255       |     |
| Val      | Ala | Val | Leu | Ile      | Glu | Trp | Ile | Leu | Ala       | Arg | Met | Val | Leu | His       | Pro |
|          |     |     | 260 |          |     |     |     | 265 |           |     |     |     | 270 |           |     |



Asp Ile Gln Ser Thr Val His Asn Glu Leu Asp Gln Ile Val Gly Arg  
275 280 285  
Ser Arg Ala Val Glu Glu Ser Asp Val Val Ser Leu Val Tyr Leu Thr  
290 295 300  
Ala Val Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu  
305 310 315 320  
Ser Trp Ala Arg Leu Ala Ile Thr Asp Thr Ile Ile Asp Gly Arg Arg  
325 330 335  
Val Pro Ala Gly Thr Thr Ala Met Val Asn Met Trp Ala Ile Ala His  
340 345 350  
Asp Pro His Val Trp Glu Asn Pro Leu Glu Phe Lys Pro Glu Arg Phe  
355 360 365  
Val Ala Lys Glu Gly Glu Val Glu Phe Ser Val Leu Gly Ser Asp Leu  
370 375 380  
Arg Leu Ala Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Lys Asn  
385 390 395 400  
Leu Gly Leu Thr Thr Val Thr Phe Trp Thr Ala Thr Leu Leu His Glu  
405 410 415  
Phe Glu Xaa Ala Asp Ala Val Arg  
420

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| gtcctaggaa  | gagcacaagc | ctccacaagt  | ggtgttgccct | ctctgttccct | aactcctttc  | 60   |
| tcttatataa  | aattgtgtat | cctccataca  | tacaacaaag  | agagaaactt  | ttgatatggg  | 120  |
| gttaaagatg  | tcagaatcag | ccaagcctta  | ctttgcaatg  | gtttgtcttc  | aattcggata  | 180  |
| cgccggcatg  | aacctcgtga | cgaaggttgt  | gctagaccgc  | ggcatgagcc  | attacgtcct  | 240  |
| tgtggccttac | cgtaatgcct | ttgccacggc  | tgctatcgca  | cctttttgctc | tactctccga  | 300  |
| gaggaaagtg  | aggccgaaga | tgacatttcc  | aatattcatg  | cagatTTTTTg | ttctagctct  | 360  |
| tctcgggcct  | ttgatcgatc | aaaacttata  | ttacgcctgt  | ctcaaactta  | cttcaccaac  | 420  |
| ttttgccggc  | gcagtcacaa | atatcgttcc  | agctttgacc  | tttatcattt  | ccataatttg  | 480  |
| caggatggag  | aaggtggaga | tgagaaaagt  | aagattccaa  | gcaaaaagtgg | tggggacatt  | 540  |
| agtgatagtg  | gttggagcca | tgttgatgat  | tttattcaaa  | attcctctaa  | tGcacctttc  | 600  |
| tccgatctca  | cctcaccggc | catgctttgt  | cgccggcagg  | tgaggactac  | ctcaaagcca  | 660  |
| ccgtcttcct  | cctcatcgcc | tcattttctt  | ggccttcctt  | tttcgttctt  | caggcggcta  | 720  |
| cgttgaagag  | atactcatct | cacctttcat  | tatcgacgat  | ggtgtgtttc  | atggggcacgt | 780  |
| tacagtccac  | agccttaacg | tttgtgatgg  | agccaaacct  | ttctgcatgg  | aacattggct  | 840  |
| ttgacatgaa  | ccttcttgcc | tctgcttatg  | cgggcataat  | gtcgtcgagc  | atagcgtact  | 900  |
| acgttcaagg  | aatgatgacg | aagcaaaaaga | gtgttatctt  | tgttactgct  | tttaatcctc  | 960  |
| ttgtttgtcat | aatcggatcc | atcattggct  | tcctcatcct  | caaccaaact  | ttaaaccttg  | 1020 |
| gcgggggttct | tggaatggca | attttagtgg  | tgggagtttg  | cacggttctt  | tggggaaagg  | 1080 |
| aaggagatat  | cgatgaagaa | gagaacattg  | aggagaagtt  | tgtagaaatt  | gtcaagtgtt  | 1140 |
| gcaaccgctg  | cgatatcaag | gttctctcga  | tgatgccaaag | aatcgatgag  | gaagtagacg  | 1200 |
| ttgaaatgca  | atccgcagga | acagctaaag  | tggcggtggy  | tttctcgtaa  | cctctcgtgt  | 1260 |
| gtggaaaaag  | atgttcacga | ccttaattag  | atcttttcaa  | gtcttttttt  | tttaacaaaa  | 1320 |
| ttttagatag  | aggagcaact | ttttctttgt  | tctatatcat  | tgctccaact  | ttttattttc  | 1380 |
| tttgtagggtt | ttgttttata | atcttcatta  | gaagggtaat  | tattattatt  | aaataaatgt  | 1440 |
| tcc         |            |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570413  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

Met Gly Leu Lys Met Ser Glu Ser Ala Lys Pro Tyr Phe Ala Met Val  
1 5 10 15  
Cys Leu Gln Phe Gly Tyr Ala Gly Met Asn Leu Val Thr Lys Val Val  
20 25 30  
Leu Asp Arg Gly Met Ser His Tyr Val Leu Val Ala Tyr Arg Asn Ala  
35 40 45  
Phe Ala Thr Ala Ala Ile Ala Pro Phe Ala Leu Leu Ser Glu Arg Lys  
50 55 60  
Val Arg Pro Lys Met Thr Phe Pro Ile Phe Met Gln Ile Phe Val Leu  
65 70 75 80  
Ala Leu Leu Gly Pro Leu Ile Asp Gln Asn Leu Tyr Tyr Ala Cys Leu  
85 90 95  
Lys Leu Thr Ser Pro Thr Phe Ala Gly Ala Val Thr Asn Ile Val Pro  
100 105 110  
Ala Leu Thr Phe Ile Ile Ser Ile Ile Cys Arg Met Glu Lys Val Glu  
115 120 125  
Met Arg Lys Val Arg Phe Gln Ala Lys Val Val Gly Thr Leu Val Ile  
130 135 140  
Val Val Gly Ala Met Leu Met Ile Leu Phe Lys Ile Pro Leu Met His  
145 150 155 160  
Leu Ser Pro Ile Ser Pro His Arg Pro Cys Phe Val Ala Gly Arg  
165 170 175

- (2) INFORMATION FOR SEQ ID NO:1578:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..171  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570414  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

Met Ser Glu Ser Ala Lys Pro Tyr Phe Ala Met Val Cys Leu Gln Phe  
1 5 10 15  
Gly Tyr Ala Gly Met Asn Leu Val Thr Lys Val Val Leu Asp Arg Gly  
20 25 30  
Met Ser His Tyr Val Leu Val Ala Tyr Arg Asn Ala Phe Ala Thr Ala  
35 40 45  
Ala Ile Ala Pro Phe Ala Leu Leu Ser Glu Arg Lys Val Arg Pro Lys  
50 55 60  
Met Thr Phe Pro Ile Phe Met Gln Ile Phe Val Leu Ala Leu Leu Gly  
65 70 75 80  
Pro Leu Ile Asp Gln Asn Leu Tyr Tyr Ala Cys Leu Lys Leu Thr Ser  
85 90 95  
Pro Thr Phe Ala Gly Ala Val Thr Asn Ile Val Pro Ala Leu Thr Phe  
100 105 110  
Ile Ile Ser Ile Ile Cys Arg Met Glu Lys Val Glu Met Arg Lys Val  
115 120 125  
Arg Phe Gln Ala Lys Val Val Gly Thr Leu Val Ile Val Val Gly Ala  
130 135 140  
Met Leu Met Ile Leu Phe Lys Ile Pro Leu Met His Leu Ser Pro Ile

(2) INFORMATION FOR SEO ID NO:1579:

(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..163

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1579:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..916

(D) OTHER INFORMATION: / Ceres Seq. ID 1570422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| aagcgaagC  | tttattcggt  | tgcttgagct | cgaagagtg  | gaaacaaaa  | tggaggaaga | 60  |
| agagcacgag | gtttacgggt  | gagaaatccc | tgaagtcggc | gatacggatg | ttcccgatcc | 120 |
| ggatatcgat | atgtctgcag  | cogatgagga | cgccgttacg | gagcttgctg | agatgaagag | 180 |
| gagattaaag | gagatggag   | aagaagctgc | tgcgctacga | gagatgcaag | caaaagtcga | 240 |
| aaaagaaatg | ggagctactc  | aagatcctgc | tagtatggct | gcaaatcaag | aaggaaagga | 300 |
| ggaggtggat | gctcgatcag  | tttatgttgg | caatgtcgac | tatgcctgta | cacctgaaga | 360 |
| agtgcaacta | cattttccaaa | catgcggaac | agtcaaccgg | gtaaccattc | taatggacaa | 420 |
| gtttggacag | ccaaagggat  | ttgcttatgt | ggagtttgta | gaagtggag  | ccgtgcaaga | 480 |
| agctctgcag | ctgaatgaat  | cagagcttca | tggtcgtcaa | ctgaaggtct | cgcctaagcg | 540 |
| aaccaatggt | cctggcaatga | aacagatca  | tctgtggcgt | ttcaaccctt | caatgggata | 600 |
| ccgcttttcg | agcagcatttg | tgccctcgta | tttttatctc | ccatatggat | acgggaaggc | 660 |
| tcctaggttc | agaagqccaa  | tcgggtacat | qccttaccaa | tagaaaccgt | accggaataa | 720 |

gaagaactat gacagagatg atgccgaggt cgtccctcca tttcgagctt tatatatgaa 780  
tatgactttg ctgcacctg aacttaattt tgaatctgtc atgtacggat gagattataa 840  
gcttttgttt ctttagatta tgattatatt tggtcgatat tactttcagt ttatatcttt 900  
gttagtactt tcttcc

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1570423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

Lys Arg Ser Phe Ile Arg Leu Leu Glu Leu Arg Arg Val Glu Thr Lys  
1 5 10 15  
Met Glu Glu Glu Glu His Glu Val Tyr Gly Gly Glu Ile Pro Glu Val  
20 25 30  
Gly Asp Thr Asp Val Pro Asp Pro Asp Ile Asp Met Ser Ala Ala Asp  
35 40 45  
Glu Asp Ala Val Thr Glu Leu Ala Glu Met Lys Arg Arg Leu Lys Glu  
50 55 60  
Met Glu Glu Glu Ala Ala Ala Leu Arg Glu Met Gln Ala Lys Val Glu  
65 70 75 80  
Lys Glu Met Gly Ala Thr Gln Asp Pro Ala Ser Met Ala Ala Asn Gln  
85 90 95  
Glu Gly Lys Glu Glu Val Asp Ala Arg Ser Val Tyr Val Gly Asn Val  
100 105 110  
Asp Tyr Ala Cys Thr Pro Glu Glu Val Gln Leu His Phe Gln Thr Cys  
115 120 125  
Gly Thr Val Asn Arg Val Thr Ile Leu Met Asp Lys Phe Gly Gln Pro  
130 135 140  
Lys Gly Phe Ala Tyr Val Glu Phe Val Glu Val Glu Ala Val Gln Glu  
145 150 155 160  
Ala Leu Gln Leu Asn Glu Ser Glu Leu His Gly Arg Gln Leu Lys Val  
165 170 175  
Ser Pro Lys Arg Thr Asn Val Pro Gly Met Lys Gln Tyr His Pro Gly  
180 185 190  
Arg Phe Asn Pro Ser Met Gly Tyr Arg Phe Arg Arg Pro Phe Val Pro  
195 200 205  
Pro Tyr Phe Tyr Ser Pro Tyr Gly Tyr Gly Lys Ala Pro Arg Phe Arg  
210 215 220  
Arg Pro Met Arg Tyr Met Pro Tyr Gln  
225 230

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1570424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

Met Glu Glu Glu Glu His Glu Val Tyr Gly Gly Glu Ile Pro Glu Val  
1 5 10 15  
Gly Asp Thr Asp Val Pro Asp Pro Asp Ile Asp Met Ser Ala Ala Asp

(2) INFORMATION FOR SEQ ID NO:1583:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1570425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

|            |            |            |            |            |           |            |            |            |            |            |           |           |            |            |            |
|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|
| Met<br>1   | Ser        | Ala        | Ala        | Asp<br>5   | Glu       | Asp        | Ala        | Val        | Thr<br>10  | Glu        | Leu       | Ala       | Glu        | Met<br>15  | Lys        |
| Arg        | Arg        | Leu        | Lys<br>20  | Glu        | Met       | Glu        | Glu        | Glu        | Ala        | Ala        | Ala       | Leu       | Arg        | Glu        | Met        |
| Gln        | Ala        | Lys<br>35  | Val        | Glu        | Lys       | Glu        | Met<br>40  | Gly        | Ala        | Thr        | Gln       | Asp<br>45 | Pro        | Ala        | Ser        |
| Met        | Ala<br>50  | Ala        | Asn        | Gln        | Glu       | Gly<br>55  | Lys        | Glu        | Glu        | Val        | Asp<br>60 | Ala       | Arg        | Ser        | Val        |
| Tyr<br>65  | Val        | Gly        | Asn        | Val        | Asp<br>70 | Tyr        | Ala        | Cys        | Thr        | Pro        | Glu       | Glu       | Val        | Gln        | Leu<br>80  |
| His        | Phe        | Gln        | Thr<br>85  | Cys        | Gly       | Thr        | Val        | Asn        | Arg<br>90  | Val        | Thr       | Ile       | Leu        | Met<br>95  | Asp        |
| Lys        | Phe        | Gly        | Gln<br>100 | Pro        | Lys       | Gly        | Phe        | Ala<br>105 | Tyr        | Val        | Glu       | Phe       | Val        | Glu        | Val        |
| Glu        | Ala        | Val<br>115 | Gln        | Glu        | Ala       | Leu        | Gln<br>120 | Leu        | Asn        | Glu        | Ser       | Glu       | Leu        | His        | Gly        |
| Arg        | Gln<br>130 | Leu        | Lys        | Val        | Ser       | Pro<br>135 | Lys        | Arg        | Thr        | Asn        | Val       | Pro       | Gly        | Met        | Lys        |
| Gln<br>145 | Tyr        | His        | Pro        | Gly<br>150 | Arg       | Phe        | Asn        | Pro        | Ser        | Met<br>155 | Gly       | Tyr       | Arg        | Phe        | Arg<br>160 |
| Arg        | Pro        | Phe        | Val<br>165 | Pro        | Pro       | Tyr        | Phe        | Tyr        | Ser<br>170 | Pro        | Tyr       | Gly       | Tyr        | Gly<br>175 | Lys        |
| Ala        | Pro        | Arg<br>180 | Phe        | Arg        | Arg       | Pro        | Met        | Arg<br>185 | Tyr        | Met        | Pro       | Tyr       | Gln<br>190 |            |            |

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..617
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aatatataac | ttttaaacaat | tgaagctaac | ttctcacaag | tcaccacccat | ttctctctag | 60  |
| aaaaaatctg | aaaaacaaaa  | ccatctcaaa | gtttcttgag | aagaaaaaaa  | gggtcaagaa | 120 |
| agatgcctaa | agacaggaat  | atcggaatcg | ccatggattt | ctcagagagc  | agcaagaacg | 180 |
| ctctgaaatg | ggcgatcgag  | aacttagcag | acaaaggaga | cacgatttac  | atcatccaca | 240 |
| ctctaccact | ctctggcgat  | gaatctcgta | actccctctg | gttcaaattc  | ggttctcctc | 300 |
| tcataccggt | ggcagagttt  | agggaaaccg | agattatgga | gaaatacggg  | gtcaaaaccg | 360 |
| acatcgcatg | tcttgatatg  | ctcgacactg | gttcgaggga | gaaagagggt  | catgtagtga | 420 |
| ccaagttata | ctggggagat  | gcaagagaga | agcttggtga | tgctgttaaa  | gatcttaaac | 480 |
| tcgattctat | tgtcatggga  | agcagaggac | tcagtgtctt | tcaaaggata  | ataatgggaa | 540 |
| gcgtgaGcag | ctttgtgatc  | caacacgcgc | cttgccctgt | caccgttgtc  | aaggataacg | 600 |
| aataaacgat | tctcact     |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Lys | Asp | Arg | Asn | Ile | Gly | Ile | Ala | Met | Asp | Phe | Ser | Glu | Ser |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Ser | Lys | Asn | Ala | Leu | Lys | Trp | Ala | Ile | Glu | Asn | Leu | Ala | Asp | Lys | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Thr | Ile | Tyr | Ile | Ile | His | Thr | Leu | Pro | Leu | Ser | Gly | Asp | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asn | Ser | Leu | Trp | Phe | Lys | Ser | Gly | Ser | Pro | Leu | Ile | Pro | Leu | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Phe | Arg | Glu | Pro | Glu | Ile | Met | Glu | Lys | Tyr | Gly | Val | Lys | Thr | Asp |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ile | Ala | Cys | Leu | Asp | Met | Leu | Asp | Thr | Gly | Ser | Arg | Gln | Lys | Glu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Val | Val | Thr | Lys | Leu | Tyr | Trp | Gly | Asp | Ala | Arg | Glu | Lys | Leu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asp | Ala | Val | Lys | Asp | Leu | Lys | Leu | Asp | Ser | Ile | Val | Met | Gly | Ser | Arg |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Leu | Ser | Ala | Leu | Gln | Arg | Ile | Ile | Met | Gly | Ser | Val | Ser | Ser | Phe |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ile | Gln | His | Ala | Pro | Cys | Pro | Val | Thr | Val | Val | Lys | Asp | Asn | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..150
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570439
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

Met Asp Phe Ser Glu Ser Ser Lys Asn Ala Leu Lys Trp Ala Ile Glu  
1 5 10 15  
Asn Leu Ala Asp Lys Gly Asp Thr Ile Tyr Ile Ile His Thr Leu Pro  
20 25 30  
Leu Ser Gly Asp Glu Ser Arg Asn Ser Leu Trp Phe Lys Ser Gly Ser  
35 40 45  
Pro Leu Ile Pro Leu Ala Glu Phe Arg Glu Pro Glu Ile Met Glu Lys  
50 55 60  
Tyr Gly Val Lys Thr Asp Ile Ala Cys Leu Asp Met Leu Asp Thr Gly  
65 70 75 80  
Ser Arg Gln Lys Glu Val His Val Val Thr Lys Leu Tyr Trp Gly Asp  
85 90 95  
Ala Arg Glu Lys Leu Val Asp Ala Val Lys Asp Leu Lys Leu Asp Ser  
100 105 110  
Ile Val Met Gly Ser Arg Gly Leu Ser Ala Leu Gln Arg Ile Ile Met  
115 120 125  
Gly Ser Val Ser Ser Phe Val Ile Gln His Ala Pro Cys Pro Val Thr  
130 135 140  
Val Val Lys Asp Asn Glu  
145 150

- (2) INFORMATION FOR SEQ ID NO:1587:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 89 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..89
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1570440
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

Met Glu Lys Tyr Gly Val Lys Thr Asp Ile Ala Cys Leu Asp Met Leu  
1 5 10 15  
Asp Thr Gly Ser Arg Gln Lys Glu Val His Val Val Thr Lys Leu Tyr  
20 25 30  
Trp Gly Asp Ala Arg Glu Lys Leu Val Asp Ala Val Lys Asp Leu Lys  
35 40 45  
Leu Asp Ser Ile Val Met Gly Ser Arg Gly Leu Ser Ala Leu Gln Arg  
50 55 60  
Ile Ile Met Gly Ser Val Ser Ser Phe Val Ile Gln His Ala Pro Cys  
65 70 75 80  
Pro Val Thr Val Val Lys Asp Asn Glu  
85

- (2) INFORMATION FOR SEQ ID NO:1588:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 641 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -

(B) LOCATION: 1..641

(D) OTHER INFORMATION: / Ceres Seq. ID 1570446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aatattattg | tgtttggtcc  | tatttattac | tctctgctct | cttcctgaag  | cttcttcctc | 60  |
| tttttgtttg | acaagaagag  | gtagagaaga | agatgtctca | atcaatctcc  | tccagcacaa | 120 |
| aggcagaaga | agttgttagt  | gtagatgtga | gccaaagcaa | gactctcctc  | cagtctgggc | 180 |
| atcaatatct | tgacgttagg  | actcaggacg | agtttaggag | aggccattgt  | gaggcagcta | 240 |
| agatcgtcaa | cattccctac  | atgctcaaca | cacctcaagg | tagagtgaag  | aatcgagagt | 300 |
| totttgagca | agtatcttct  | cttctaaacc | cagctgatga | tatccttggtg | ggttgtcaga | 360 |
| gtggagccag | atccttaaaa  | gccacaactg | aacttggtgc | tgcaggttac  | aagaaagtga | 420 |
| gaaacgtggg | aggtggctac  | ttggcttggg | tagatcacag | ctttcccatc  | aacaaggagg | 480 |
| aggaggagcc | atctgctaata | taataatctt | aagattctct | tcttttstta  | atcaaatMat | 540 |
| ataactgcct | gtgtgatgta  | gtaatcattt | tcaatttaaa | attccagttt  | cttgtaatca | 600 |
| aaactttcgt | gtaccaaatt  | caataaaagc | tgtgtttctc | t           |            |     |

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1570447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Ser | Ile | Ser | Ser | Ser | Thr | Lys | Ala | Glu | Glu | Val | Val | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Asp | Val | Ser | Gln | Ala | Lys | Thr | Leu | Leu | Gln | Ser | Gly | His | Gln | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Val | Arg | Thr | Gln | Asp | Glu | Phe | Arg | Arg | Gly | His | Cys | Glu | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Ile | Val | Asn | Ile | Pro | Tyr | Met | Leu | Asn | Thr | Pro | Gln | Gly | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Asn | Arg | Glu | Phe | Leu | Glu | Gln | Val | Ser | Ser | Leu | Leu | Asn | Pro |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Asp | Asp | Ile | Leu | Val | Gly | Cys | Gln | Ser | Gly | Ala | Arg | Ser | Leu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Thr | Thr | Glu | Leu | Val | Ala | Ala | Gly | Tyr | Lys | Lys | Val | Arg | Asn | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Gly | Tyr | Leu | Ala | Trp | Val | Asp | His | Ser | Phe | Pro | Ile | Asn | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Glu | Glu | Glu | Pro | Ser | Ala | Asn |     |     |     |     |     |     |     |     |
| 130 |     |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1570448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Thr | Pro | Gln | Gly | Arg | Val | Lys | Asn | Arg | Glu | Phe | Leu | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Val | Ser | Ser | Leu | Leu | Asn | Pro | Ala | Asp | Asp | Ile | Leu | Val | Gly | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gln | Ser | Gly | Ala | Arg | Ser | Leu | Lys | Ala | Thr | Thr | Glu | Leu | Val | Ala | Ala |



(2) INFORMATION FOR SEO ID NO:1591:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α

```
(ix) FEATURE:
```

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1591:

caaacat cgaaccatc atgagggtta tctcaaaact gt

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| gaataaccgaa | atcgccgaag  | catttggatt  | cggcgaaag  | cgccacgtca | tcttcctcac | 120 |
| tcagcgacgt  | aaccaccggc  | tcaagcagcc  | ttcatagcag | tctctctctc | caaacgcttc | 180 |
| cttcagttcc  | ctctcttcag  | aaaataccat  | ccaccaccgt | caccgtctcN | tCactccggt | 240 |
| acctcctcgt  | ttaaactcog  | tgaacggagt  | cttcctgtaa | cttgctctcg | cgtcaacggt | 300 |
| ggctatctct  | tgcgcgtttc  | tggacacgaa  | Gtaagtatct | acgatcgcga | catgtgtgct | 360 |
| catctcgaca  | cattcaacgg  | ccaagatcct  | ttctcaggaa | ccgtgaagtc | cgtcggcttc | 420 |
| tccggtgaga  | aaatcttcac  | ggcgcaccaa  | gacggtaaaa | tccgagtttg | gaaactaacg | 480 |
| gcaaaaaagcg | gttataaaca  | gttaacgacg  | cttccaactt | taaacgaccg | tttacgacgt | 540 |
| tttgctcttc  | ctaaaaacta  | cgtttcaagta | cgcgcgcata | agaaacgtct | ctggatcgaa | 600 |
| catgCtgacg  | ccggttactgc | tctcgccggt  | aatgacggat | tcatttactc | tgtttcttg  | 660 |
| gataagacatt | tgaagatatg  | gagagcctcc  | gatcttcggt | gc         |            |     |

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1570450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..77  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Val | Ile | Ser | Lys | Leu | Phe | Asp | Ser | Asp | Arg | Arg | Arg | Ile | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Pro | Lys | His | Leu | Asp | Ser | Gly | Glu | Ser | Ala | Thr | Ser | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Ser | Asp | Val | Thr | Thr | Gly | Ser | Ser | Ser | Leu | His | Ser | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Leu | Gln | Thr | Leu | Pro | Ser | Val | Pro | Ser | Leu | Gln | Lys | Ile | Pro | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Thr | Val | Thr | Val | Xaa | Ser | Leu | Arg | Tyr | Leu | Leu | Val |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1594:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 117 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..117  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Ala | His | Leu | Asp | Thr | Phe | Asn | Gly | Gln | Asp | Pro | Phe | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Lys | Ser | Val | Gly | Phe | Ser | Gly | Glu | Lys | Ile | Phe | Thr | Ala | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Asp | Gly | Lys | Ile | Gly | Val | Trp | Lys | Leu | Thr | Ala | Lys | Ser | Gly | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gln | Leu | Thr | Thr | Leu | Pro | Thr | Leu | Asn | Asp | Arg | Leu | Arg | Arg | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Pro | Lys | Asn | Tyr | Val | Gln | Val | Arg | Arg | His | Lys | Lys | Arg | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Ile | Glu | His | Ala | Asp | Ala | Val | Thr | Ala | Leu | Ala | Val | Asn | Asp | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Ile | Tyr | Ser | Val | Ser | Trp | Asp | Lys | Thr | Leu | Lys | Ile | Trp | Arg | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Asp | Leu | Arg | Cys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1595:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 751 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..751  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atccaccaca  | tatttatggt | tgatccaaaa | gccaacacaa | gcaaagaaat | taaaagtgtt | 60  |
| cttggttgctg | tagaacacaa | acagaacaaa | caaaaaatca | attgaagagt | ctctcagtcg | 120 |
| ttaggggaag  | caaatagaga | aatggctagc | tttactgcct | ccgcttccac | cgtctccgcc | 180 |
| gctcgtccgg  | ctctccttct | caagcctacc | gtcgccatct | ctgctcctgt | tcttggtttg | 240 |
| cctccaatgg  | gtaagaagaa | gggaggagtg | agatgttcaa | tgagacaaa  | gcaaggaaac | 300 |

gtctcagtc tgggggctgg agtttcagct gcagcaacag ctgctttgac ggcgggtgatg 360  
agcaatcccg cgatggcttt ggttgatgag aggatgtcaa cagaaggaac aggattaccc 420  
tttgggtctaa gcaacaacct cttggggttg attctgtttg gagtctttgg tttgatctgg 480  
actttcttct tcgtctacac ttcattcttc gaggaggatg aagaatctgg tctttcactc 540  
tgaaggaaga atcaatcttt cgtcttctca tttccatttt catgtgagaa catgaatcaa 600  
gtgttcaccc ttctagtttc ttgtaattgt taagtaaaga ctaaaaacta ttttcatgtg 660  
tgtttacttt ccccccattct ctttatcttg tcataacatt gataaggagg agattatSgt 720  
gattattaaa tatcatgcat gacatgttca t

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1570475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

Met Ala Ser Phe Thr Ala Ser Ala Ser Thr Val Ser Ala Ala Arg Pro  
1 5 10 15  
Ala Leu Leu Leu Lys Pro Thr Val Ala Ile Ser Ala Pro Val Leu Gly  
20 25 30  
Leu Pro Pro Met Gly Lys Lys Lys Gly Gly Val Arg Cys Ser Met Glu  
35 40 45  
Thr Lys Gln Gly Asn Val Ser Val Met Gly Ala Gly Val Ser Ala Ala  
50 55 60  
Ala Thr Ala Ala Leu Thr Ala Val Met Ser Asn Pro Ala Met Ala Leu  
65 70 75 80  
Val Asp Glu Arg Met Ser Thr Glu Gly Thr Gly Leu Pro Phe Gly Leu  
85 90 95  
Ser Asn Asn Leu Leu Gly Trp Ile Leu Phe Gly Val Phe Gly Leu Ile  
100 105 110  
Trp Thr Phe Phe Phe Val Tyr Thr Ser Ser Leu Glu Glu Asp Glu Glu  
115 120 125  
Ser Gly Leu Ser Leu  
130

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1570476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

Met Gly Lys Lys Lys Gly Gly Val Arg Cys Ser Met Glu Thr Lys Gln  
1 5 10 15  
Gly Asn Val Ser Val Met Gly Ala Gly Val Ser Ala Ala Thr Ala  
20 25 30  
Ala Leu Thr Ala Val Met Ser Asn Pro Ala Met Ala Leu Val Asp Glu  
35 40 45  
Arg Met Ser Thr Glu Gly Thr Gly Leu Pro Phe Gly Leu Ser Asn Asn  
50 55 60  
Leu Leu Gly Trp Ile Leu Phe Gly Val Phe Gly Leu Ile Trp Thr Phe  
65 70 75 80  
Phe Phe Val Tyr Thr Ser Ser Leu Glu Glu Asp Glu Glu Ser Gly Leu

85 90 95  
Ser Leu

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

Met Glu Thr Lys Gln Gly Asn Val Ser Val Met Gly Ala Gly Val Ser  
1 5 10 15  
Ala Ala Ala Thr Ala Ala Leu Thr Ala Val Met Ser Asn Pro Ala Met  
20 25 30  
Ala Leu Val Asp Glu Arg Met Ser Thr Glu Gly Thr Gly Leu Pro Phe  
35 40 45  
Gly Leu Ser Asn Asn Leu Leu Gly Trp Ile Leu Phe Gly Val Phe Gly  
50 55 60  
Leu Ile Trp Thr Phe Phe Phe Val Tyr Thr Ser Ser Leu Glu Glu Asp  
65 70 75 80  
Glu Glu Ser Gly Leu Ser Leu  
85

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

taaaggaggc tactctagtc acattgttgt tcatgaaagg tactgctaca agatacctgt 60  
ggactatccc ttggaatcag ctgcaccatt actctgtgct ggaatcacgg tttatgcacc 120  
tatgatgcgt cacaatatga atcaacctgg taaatctctt ggggtgatcg ggctaggtgg 180  
tcttggacac atggcggtta agtttggcaa ggcttttggc cttagtgtta cggttttttag 240  
caccagcatt tccaagaaag aagaagcttt gaatctgcta ggagctgaga atttcgttat 300  
ctcatctgac catgaccaga tgaaggcact agagaaatct ctagactttc tagttgacac 360  
agcatctggt gatcacgcgt ttgataccta catgtctctc ttgaagattg ctggaactta 420  
tgtattgggt gggtttcccaa gtgaaattaa aatcagtcct gccaatctca atcttggtat 480  
gagaatgctc gctggaagcg taaccggggg gaccaaaata acacagcaaa tgtttagattt 540  
ctgtgcagct cataagattt atccaaacat agaggtgatt ccattcaaaa agataaacga 600  
agctctcgaa agagtagtga agaaggacat caagtaccgt ttcgtgattg acatcaagaa 660  
ctccctcaaa tagatgttgc tcaaaggaag gaataatgga gtctgtaata agagaataat 720  
actcactgct acaatcttta ttacgtattt tctcgTtttt bcattagtaa agcaaataaa 780  
tt

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1570479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Gly | Tyr | Ser | Ser | His | Ile | Val | Val | His | Glu | Arg | Tyr | Cys | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Ile | Pro | Val | Asp | Tyr | Pro | Leu | Glu | Ser | Ala | Ala | Pro | Leu | Leu | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Ile | Thr | Val | Tyr | Ala | Pro | Met | Met | Arg | His | Asn | Met | Asn | Gln |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Pro | Gly | Lys | Ser | Leu | Gly | Val | Ile | Gly | Leu | Gly | Gly | Leu | Gly | His | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Val | Lys | Phe | Gly | Lys | Ala | Phe | Gly | Leu | Ser | Val | Thr | Val | Phe | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ser | Ile | Ser | Lys | Lys | Glu | Glu | Ala | Leu | Asn | Leu | Leu | Gly | Ala | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Phe | Val | Ile | Ser | Ser | Asp | His | Asp | Gln | Met | Lys | Ala | Leu | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Leu | Asp | Phe | Leu | Val | Asp | Thr | Ala | Ser | Gly | Asp | His | Ala | Phe | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Tyr | Met | Ser | Leu | Leu | Lys | Ile | Ala | Gly | Thr | Tyr | Val | Leu | Val | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Phe | Pro | Ser | Glu | Ile | Lys | Ile | Ser | Pro | Ala | Asn | Leu | Asn | Leu | Gly | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Met | Leu | Ala | Gly | Ser | Val | Thr | Gly | Gly | Thr | Lys | Ile | Thr | Gln | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Leu | Asp | Phe | Cys | Ala | Ala | His | Lys | Ile | Tyr | Pro | Asn | Ile | Glu | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Pro | Ile | Gln | Lys | Ile | Asn | Glu | Ala | Leu | Glu | Arg | Val | Val | Lys | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Asp | Ile | Lys | Tyr | Arg | Phe | Val | Ile | Asp | Ile | Lys | Asn | Ser | Leu | Lys |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1570480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Arg | His | Asn | Met | Asn | Gln | Pro | Gly | Lys | Ser | Leu | Gly | Val | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Leu | Gly | Gly | Leu | Gly | His | Met | Ala | Val | Lys | Phe | Gly | Lys | Ala | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Ser | Val | Thr | Val | Phe | Ser | Thr | Ser | Ile | Ser | Lys | Lys | Glu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Asn | Leu | Leu | Gly | Ala | Glu | Asn | Phe | Val | Ile | Ser | Ser | Asp | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gln | Met | Lys | Ala | Leu | Glu | Lys | Ser | Leu | Asp | Phe | Leu | Val | Asp | Thr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Ser | Gly | Asp | His | Ala | Phe | Asp | Pro | Tyr | Met | Ser | Leu | Leu | Lys | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Gly | Thr | Tyr | Val | Leu | Val | Gly | Phe | Pro | Ser | Glu | Ile | Lys | Ile | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Ala | Asn | Leu | Asn | Leu | Gly | Met | Arg | Met | Leu | Ala | Gly | Ser | Val | Thr |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Thr | Lys | Ile | Thr | Gln | Gln | Met | Leu | Asp | Phe | Cys | Ala | Ala | His |

130 135 140  
Lys Ile Tyr Pro Asn Ile Glu Val Ile Pro Ile Gln Lys Ile Asn Glu  
145 150 155 160  
Ala Leu Glu Arg Val Lys Lys Asp Ile Lys Tyr Arg Phe Val Ile  
165 170 175  
Asp Ile Lys Asn Ser Leu Lys  
180

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1570481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

Met Arg His Asn Met Asn Gln Pro Gly Lys Ser Leu Gly Val Ile Gly  
1 5 10 15  
Leu Gly Gly Leu Gly His Met Ala Val Lys Phe Gly Lys Ala Phe Gly  
20 25 30  
Leu Ser Val Thr Val Phe Ser Thr Ser Ile Ser Lys Lys Glu Glu Ala  
35 40 45  
Leu Asn Leu Leu Gly Ala Glu Asn Phe Val Ile Ser Ser Asp His Asp  
50 55 60  
Gln Met Lys Ala Leu Glu Lys Ser Leu Asp Phe Leu Val Asp Thr Ala  
65 70 75 80  
Ser Gly Asp His Ala Phe Asp Pro Tyr Met Ser Leu Leu Lys Ile Ala  
85 90 95  
Gly Thr Tyr Val Leu Val Gly Phe Pro Ser Glu Ile Lys Ile Ser Pro  
100 105 110  
Ala Asn Leu Asn Leu Gly Met Arg Met Leu Ala Gly Ser Val Thr Gly  
115 120 125  
Gly Thr Lys Ile Thr Gln Gln Met Leu Asp Phe Cys Ala Ala His Lys  
130 135 140  
Ile Tyr Pro Asn Ile Glu Val Ile Pro Ile Gln Lys Ile Asn Glu Ala  
145 150 155 160  
Leu Glu Arg Val Val Lys Lys Asp Ile Lys Tyr Arg Phe Val Ile Asp  
165 170 175  
Ile Lys Asn Ser Leu Lys  
180

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 990 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..990

(D) OTHER INFORMATION: / Ceres Seq. ID 1570485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

agagtcttta accggcgaaa gaaaccaccc tctgactgtt aagaaaattc tcatcggcgt 60  
ttagatcaga aacttgggaa tcggagaagc tactgagaa caatggatat gagacgtgct 120  
tcgatgtgta tgatgttaat ttgogtctcc ttggttctcc ttctgggttt tggccagttt 180  
gtgatctgca gtgaagaaaa aggaacgtac aacgacaacg tCgtaaagat gaagcttggt 240  
ggatttagcg attccaagaa cgattggaac ggtggaaaag agatcgatga tattgcactc 300  
ttcgctgttc aagagcacaa cagacgagag aatgctgttc ttgagcttgc tagagtattg 360

aaggcaacag agcaggtggt tgctggcaag ctataccgtc ttactcttga agttattgaa 420  
gctggtgaga aaaagattta tgaagctaaa gtttgggtga agCcatggat gaactttaag 480  
cagcttcagg agttcaagaa tattatcccc tccttcacta tctctgacct tggcttcaaa 540  
ccagatggca atggatttga ctggagatca gtatcaacaa ataaccctga agtccaagaa 600  
gcagcgaagc acgcatgaa atcacttcaa cagaaatcaa actcactgtt cccctataaa 660  
ctcatagata taatcctagc caggggcaag gtgggttgaag agcgtgtgaa attcgaactg 720  
ctgctgaagc tagagagggg caacaaactg gagaagttca tggtagaagt gatgaaggat 780  
caaaccggca agtatgagta gaagttgcag atagcttttg ggttgtgtgc catgtgtgaa 840  
tggatccttt atagtatata gtatactaaa tactgctatg tagtgaaaat aaacatggtg 900  
attgtttggc tttaaacaag gtttcttgta aataaataca tgacttcaca tatgtaaaag 960  
ttacaaatat gatatgatta tgcgtgtttg

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

Met Asp Met Arg Arg Ala Ser Met Cys Met Met Leu Ile Cys Val Ser  
1 5 10 15  
Leu Val Leu Leu Ser Gly Phe Gly Gln Phe Val Ile Cys Ser Glu Glu  
20 25 30  
Lys Gly Thr Tyr Asn Asp Asn Val Val Lys Met Lys Leu Gly Gly Phe  
35 40 45  
Ser Asp Ser Lys Asn Asp Trp Asn Gly Gly Lys Glu Ile Asp Asp Ile  
50 55 60  
Ala Leu Phe Ala Val Gln Glu His Asn Arg Arg Glu Asn Ala Val Leu  
65 70 75 80  
Glu Leu Ala Arg Val Leu Lys Ala Thr Glu Gln Val Val Ala Gly Lys  
85 90 95  
Leu Tyr Arg Leu Thr Leu Glu Val Ile Glu Ala Gly Glu Lys Lys Ile  
100 105 110  
Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys Gln Leu  
115 120 125  
Gln Glu Phe Lys Asn Ile Ile Pro Ser Phe Thr Ile Ser Asp Leu Gly  
130 135 140  
Phe Lys Pro Asp Gly Asn Gly Phe Asp Trp Arg Ser Val Ser Thr Asn  
145 150 155 160  
Asn Pro Glu Val Gln Glu Ala Ala Lys His Ala Met Lys Ser Leu Gln  
165 170 175  
Gln Lys Ser Asn Ser Leu Phe Pro Tyr Lys Leu Ile Asp Ile Ile Leu  
180 185 190  
Ala Arg Ala Lys Val Val Glu Glu Arg Val Lys Phe Glu Leu Leu Leu  
195 200 205  
Lys Leu Glu Arg Gly Asn Lys Leu Glu Lys Phe Met Val Glu Val Met  
210 215 220  
Lys Asp Gln Thr Gly Lys Tyr Glu  
225 230

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1570487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

Met Arg Arg Ala Ser Met Cys Met Met Leu Ile Cys Val Ser Leu Val  
1 5 10 15  
Leu Leu Ser Gly Phe Gly Gln Phe Val Ile Cys Ser Glu Glu Lys Gly  
20 25 30  
Thr Tyr Asn Asp Asn Val Val Lys Met Lys Leu Gly Gly Phe Ser Asp  
35 40 45  
Ser Lys Asn Asp Trp Asn Gly Gly Lys Glu Ile Asp Asp Ile Ala Leu  
50 55 60  
Phe Ala Val Gln Glu His Asn Arg Arg Glu Asn Ala Val Leu Glu Leu  
65 70 75 80  
Ala Arg Val Leu Lys Ala Thr Glu Gln Val Val Ala Gly Lys Leu Tyr  
85 90 95  
Arg Leu Thr Leu Glu Val Ile Glu Ala Gly Glu Lys Lys Ile Tyr Glu  
100 105 110  
Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys Gln Leu Gln Glu  
115 120 125  
Phe Lys Asn Ile Ile Pro Ser Phe Thr Ile Ser Asp Leu Gly Phe Lys  
130 135 140  
Pro Asp Gly Asn Gly Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro  
145 150 155 160  
Glu Val Gln Glu Ala Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys  
165 170 175  
Ser Asn Ser Leu Phe Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg  
180 185 190  
Ala Lys Val Val Glu Glu Arg Val Lys Phe Glu Leu Leu Lys Leu  
195 200 205  
Glu Arg Gly Asn Lys Leu Glu Lys Phe Met Val Glu Val Met Lys Asp  
210 215 220  
Gln Thr Gly Lys Tyr Glu  
225 230

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1570488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

Met Cys Met Met Leu Ile Cys Val Ser Leu Val Leu Leu Ser Gly Phe  
1 5 10 15  
Gly Gln Phe Val Ile Cys Ser Glu Glu Lys Gly Thr Tyr Asn Asp Asn  
20 25 30  
Val Val Lys Met Lys Leu Gly Gly Phe Ser Asp Ser Lys Asn Asp Trp  
35 40 45  
Asn Gly Gly Lys Glu Ile Asp Asp Ile Ala Leu Phe Ala Val Gln Glu  
50 55 60  
His Asn Arg Arg Glu Asn Ala Val Leu Glu Leu Ala Arg Val Leu Lys  
65 70 75 80  
Ala Thr Glu Gln Val Val Ala Gly Lys Leu Tyr Arg Leu Thr Leu Glu  
85 90 95  
Val Ile Glu Ala Gly Glu Lys Lys Ile Tyr Glu Ala Lys Val Trp Val  
100 105 110  
Lys Pro Trp Met Asn Phe Lys Gln Leu Gln Glu Phe Lys Asn Ile Ile



115 120 125  
Pro Ser Phe Thr Ile Ser Asp Leu Gly Phe Lys Pro Asp Gly Asn Gly  
130 135 140  
Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro Glu Val Gln Glu Ala  
145 150 155 160  
Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys Ser Asn Ser Leu Phe  
165 170 175  
Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg Ala Lys Val Val Glu  
180 185 190  
Glu Arg Val Lys Phe Glu Leu Leu Leu Lys Leu Glu Arg Gly Asn Lys  
195 200 205  
Leu Glu Lys Phe Met Val Glu Val Met Lys Asp Gln Thr Gly Lys Tyr  
210 215 220  
Glu  
225

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..799
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| aagcatcact  | atgctcgaaa | atctctcttt | gttcgctttg  | tggggaacga  | actatggccg  | 60  |
| agagatggag  | gaacacggct | ctactcgtca | tgcacatgca  | gaacgatttc  | atagaggaag  | 120 |
| gtgctgtgac  | gcaagtga   | ggaggaaaat | ctatagttcc  | taatgttatc  | agagtcgtcg  | 180 |
| aactcgcgag  | gcagcgtggt | attctcgtaa | tttgggttgt  | tcgagaacat  | gatcgtcaag  | 240 |
| gaagagatgt  | tgaattattc | aggcgccata | actacagttc  | tgagaaagtc  | gggccagtta  | 300 |
| ttaaaggcac  | cgtagGagca | gaattgggtg | atggattgat  | gatcaacgaa  | gaagatgact  | 360 |
| ataagattgt  | gaaaactcgt | ttcagtgctt | tcttttagtac | taatcttcat  | tccttcttgc  | 420 |
| aaacttcagg  | ggttaccaag | ttagtgattg | ctggtgtgca  | aacgccgaac  | tgtatccggc  | 480 |
| aaacggtggt  | tgatgcagtg | gcgctggatt | atccCaatgt  | gactgttatt  | acagatgccca | 540 |
| cagctgctgc  | aacaccagag | atccatactg | cgaatattct  | tgacatgaag  | aatattggag  | 600 |
| tcaaaaactcc | tacattacac | gagtggtccg | aagaacttgc  | ttgacaaaaga | ccatcctaaa  | 660 |
| gcccttcggt  | tatctttttc | cttgtttgta | catgtaataa  | agaaaatggt  | aatcttgttg  | 720 |
| ttgtaagtta  | caaaatctcc | acctattggt | gtatactttt  | cttgtaatcc  | cgtccaaaaa  | 780 |
| aataaaaatgt | attacgttt  |            |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ala Ser Leu Cys Ser Lys Ile Ser Leu Cys Ser Leu Cys Gly Glu Arg |  |
| 1 5 10 15                                                       |  |
| Thr Met Ala Glu Arg Trp Arg Asn Thr Ala Leu Leu Val Ile Asp Met |  |
| 20 25 30                                                        |  |
| Gln Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly Gly |  |
| 35 40 45                                                        |  |
| Lys Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg Gln |  |
| 50 55 60                                                        |  |

Arg Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln Gly  
65 70 75 80  
Arg Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys Val  
85 90 95  
Gly Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly Leu  
100 105 110  
Met Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe Ser  
115 120 125  
Ala Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly Val  
130 135 140  
Thr Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg Gln  
145 150 155 160  
Thr Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val Ile  
165 170 175  
Thr Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn Ile  
180 185 190  
Leu Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu Trp  
195 200 205  
Ser Glu Glu Leu Ala  
210

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1570491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

Met Ala Glu Arg Trp Arg Asn Thr Ala Leu Leu Val Ile Asp Met Gln  
1 5 10 15  
Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly Gly Lys  
20 25 30  
Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg Gln Arg  
35 40 45  
Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln Gly Arg  
50 55 60  
Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys Val Gly  
65 70 75 80  
Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly Leu Met  
85 90 95  
Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe Ser Ala  
100 105 110  
Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly Val Thr  
115 120 125  
Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg Gln Thr  
130 135 140  
Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val Ile Thr  
145 150 155 160  
Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn Ile Leu  
165 170 175  
Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu Trp Ser  
180 185 190  
Glu Glu Leu Ala  
195

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..182  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

Met Gln Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly  
1 5 10 15  
Gly Lys Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg  
20 25 30  
Gln Arg Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln  
35 40 45  
Gly Arg Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys  
50 55 60  
Val Gly Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly  
65 70 75 80  
Leu Met Ile Asn Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe  
85 90 95  
Ser Ala Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly  
100 105 110  
Val Thr Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg  
115 120 125  
Gln Thr Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val  
130 135 140  
Ile Thr Asp Ala Thr Ala Ala Thr Pro Glu Ile His Thr Ala Asn  
145 150 155 160  
Ile Leu Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu  
165 170 175  
Trp Ser Glu Glu Leu Ala  
180

(2) INFORMATION FOR SEQ ID NO:1611:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 642 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..642  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

atcattcaca atggcatatg caactattct catgatcttc tcggtggtgg cactaatgtc 60  
cggcgagaga gctcatgcag cagtggactg ctcacgttg atactaaaca tggctgattg 120  
tttgtctttt gtgactagtg gtagtacagt tgtcaagccg gaaggaacat gttgttcagg 180  
gcttaagact gtggtttaga caggaccaga atgtctatgt gaggctttca agaacagtgg 240  
ttctcttggg ttaactcttg atctttctaa agctgcttct cttccttctg tttgtaaagt 300  
tgctgctcct ccttctgctc gttgtggcct ttctgtctct ggagatcctc ctgctactgc 360  
ccctggttta tctcCtacgg ccggagcagg agcaccgcg ttgtccagtg gtgcaaatgc 420  
ggcaactcca gtttcgtccc cgaggagttc cgatgcgtcc ttgctctctg tatcttttgc 480  
atttgtcatc ttcattggcac tcatttcttc tttctattga gtcttaaaat ttaattgctw 540  
cttggtttagt tatttttggg tgctatgtag ctgaagagtt tgggtgttact gatcatattt 600  
acctttcatg tgtcaatttt aatgagaaat ctccttttag tt

(2) INFORMATION FOR SEQ ID NO:1612:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 172 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..172  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570494  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Thr | Met | Ala | Tyr | Ala | Thr | Ile | Leu | Met | Ile | Phe | Ser | Val | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Met | Ser | Gly | Glu | Arg | Ala | His | Ala | Ala | Val | Asp | Cys | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Leu | Asn | Met | Ala | Asp | Cys | Leu | Ser | Phe | Val | Thr | Ser | Gly | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Val | Val | Lys | Pro | Glu | Gly | Thr | Cys | Cys | Ser | Gly | Leu | Lys | Thr | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Arg | Thr | Gly | Pro | Glu | Cys | Leu | Cys | Glu | Ala | Phe | Lys | Asn | Ser | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Leu | Gly | Leu | Thr | Leu | Asp | Leu | Ser | Lys | Ala | Ala | Ser | Leu | Pro | Ser |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Cys | Lys | Val | Ala | Ala | Pro | Pro | Ser | Ala | Arg | Cys | Gly | Leu | Ser | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly | Asp | Pro | Pro | Ala | Thr | Ala | Pro | Gly | Leu | Ser | Pro | Thr | Ala | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Gly | Ala | Pro | Ala | Leu | Ser | Ser | Gly | Ala | Asn | Ala | Ala | Thr | Pro | Val |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ser | Ser | Pro | Arg | Ser | Ser | Asp | Ala | Ser | Leu | Leu | Ser | Val | Ser | Phe | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Phe | Val | Ile | Phe | Met | Ala | Leu | Ile | Ser | Ser | Phe | Tyr |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1613:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 169 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..169  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570495  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Tyr | Ala | Thr | Ile | Leu | Met | Ile | Phe | Ser | Val | Val | Ala | Leu | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Glu | Arg | Ala | His | Ala | Ala | Val | Asp | Cys | Ser | Ser | Leu | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Met | Ala | Asp | Cys | Leu | Ser | Phe | Val | Thr | Ser | Gly | Ser | Thr | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Pro | Glu | Gly | Thr | Cys | Cys | Ser | Gly | Leu | Lys | Thr | Val | Val | Arg | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Pro | Glu | Cys | Leu | Cys | Glu | Ala | Phe | Lys | Asn | Ser | Gly | Ser | Leu | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Thr | Leu | Asp | Leu | Ser | Lys | Ala | Ala | Ser | Leu | Pro | Ser | Val | Cys | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ala | Ala | Pro | Pro | Ser | Ala | Arg | Cys | Gly | Leu | Ser | Val | Ser | Gly | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Ala | Thr | Ala | Pro | Gly | Leu | Ser | Pro | Thr | Ala | Gly | Ala | Gly | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Ala | Leu | Ser | Ser | Gly | Ala | Asn | Ala | Ala | Thr | Pro | Val | Ser | Ser | Pro |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Arg | Ser | Ser | Asp | Ala | Ser | Leu | Leu | Ser | Val | Ser | Phe | Ala | Phe | Val | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Phe Met Ala Leu Ile Ser Ser Phe Tyr  
165

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

Met Ile Phe Ser Val Val Ala Leu Met Ser Gly Glu Arg Ala His Ala  
1 5 10 15  
Ala Val Asp Cys Ser Ser Leu Ile Leu Asn Met Ala Asp Cys Leu Ser  
20 25 30  
Phe Val Thr Ser Gly Ser Thr Val Val Lys Pro Glu Gly Thr Cys Cys  
35 40 45  
Ser Gly Leu Lys Thr Val Val Arg Thr Gly Pro Glu Cys Leu Cys Glu  
50 55 60  
Ala Phe Lys Asn Ser Gly Ser Leu Gly Leu Thr Leu Asp Leu Ser Lys  
65 70 75 80  
Ala Ala Ser Leu Pro Ser Val Cys Lys Val Ala Ala Pro Pro Ser Ala  
85 90 95  
Arg Cys Gly Leu Ser Val Ser Gly Asp Pro Pro Ala Thr Ala Pro Gly  
100 105 110  
Leu Ser Pro Thr Ala Gly Ala Gly Ala Pro Ala Leu Ser Ser Gly Ala  
115 120 125  
Asn Ala Ala Thr Pro Val Ser Ser Pro Arg Ser Ser Asp Ala Ser Leu  
130 135 140  
Leu Ser Val Ser Phe Ala Phe Val Ile Phe Met Ala Leu Ile Ser Ser  
145 150 155 160  
Phe Tyr

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..863
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ttttggctgc  | acgatctcag | tttttcagat | caatgtttta | caatactcta | gcagagaaca | 60  |
| acagcgacgt  | aGtgatcagc | gatttggaa  | ctaaggtttt | caaggccttg | ttacacttca | 120 |
| tgtataaaga  | ttccctccca | ggagatgtgg | aaccattaac | ggctcattca | tttgacctat | 180 |
| taaggcogtc  | cgaaatagat | gatacactga | ttgtaaagct | tctggcagct | gcggaaatgt | 240 |
| acaatctgag  | taggctcaga | ttattgtgtg | aatctcacat | ctgcaaaggc | atatctatca | 300 |
| gctccgtgtc  | caagatctta | gctttatccg | acaaatataa | tgcatccgaa | ctaaaaagcg | 360 |
| tttccttaaa  | attcactgca | gaaaacctag | cagctgttct | gcagacaaaa | gcatatgaag | 420 |
| atctgaagga  | tgactgtcca | aacctccagt | ctgagctact | aaaggcggtc | gctggttatg | 480 |
| acgacacaag  | tagcagcgga | ggaggaaagt | ctcagagtgt | ttgggctcaa | ctctctaacg | 540 |
| gtggtgagac  | cagtagccga | agggtcaggc | agcgaaccac | ttagaagagc | ttcttcacat | 600 |
| gttggttaaca | aactactttt | gcttaccact | cgtaaacaga | ttaaccggtt | tatctagtat | 660 |
| gtaccgaatg  | aaagggaagc | ggagccagaa | atcttgtacc | acaagagaag | agctatgcgg | 720 |
| ctgtgcacta  | gtgattaacc | ggtgcttcac | ctttcagttc | cttcacgtct | ctgtggattt | 780 |

ttgtttgttga gtctttttttt caaattcttt tcccagcttc aaattactag aaacttatga 840  
tgatataata gaaagagtta act

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

Leu Ala Ala Arg Ser Gln Phe Phe Arg Ser Met Phe Tyr Asn Thr Leu  
1 5 10 15  
Ala Glu Asn Asn Ser Asp Val Val Ile Ser Asp Leu Glu Pro Lys Val  
20 25 30  
Phe Lys Ala Leu Leu His Phe Met Tyr Lys Asp Ser Leu Pro Gly Asp  
35 40 45  
Val Glu Pro Leu Thr Ala His Ser Phe Asp Leu Leu Arg Pro Ser Glu  
50 55 60  
Ile Asp Asp Thr Leu Ile Val Lys Leu Leu Ala Ala Ala Glu Met Tyr  
65 70 75 80  
Asn Leu Ser Arg Leu Arg Leu Leu Cys Glu Ser His Ile Cys Lys Gly  
85 90 95  
Ile Ser Ile Ser Ser Val Ser Lys Ile Leu Ala Leu Ser Asp Lys Tyr  
100 105 110  
Asn Ala Ser Glu Leu Lys Ser Val Ser Leu Lys Phe Thr Ala Glu Asn  
115 120 125  
Leu Ala Ala Val Leu Gln Thr Lys Ala Tyr Glu Asp Leu Lys Asp Asp  
130 135 140  
Cys Pro Asn Leu Gln Ser Glu Leu Leu Lys Ala Val Ala Gly Tyr Asp  
145 150 155 160  
Asp Thr Ser Ser Ser Gly Gly Gly Lys Ser Gln Ser Val Trp Ala Gln  
165 170 175  
Leu Ser Asn Gly Gly Glu Thr Ser Ser Arg Arg Val Arg Gln Arg Thr  
180 185 190  
Thr

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

Met Phe Tyr Asn Thr Leu Ala Glu Asn Asn Ser Asp Val Val Ile Ser  
1 5 10 15  
Asp Leu Glu Pro Lys Val Phe Lys Ala Leu Leu His Phe Met Tyr Lys  
20 25 30  
Asp Ser Leu Pro Gly Asp Val Glu Pro Leu Thr Ala His Ser Phe Asp  
35 40 45  
Leu Leu Arg Pro Ser Glu Ile Asp Asp Thr Leu Ile Val Lys Leu Leu  
50 55 60  
Ala Ala Ala Glu Met Tyr Asn Leu Ser Arg Leu Arg Leu Leu Cys Glu

60  
120

```
ggttaggttg ttcacggacc atggagctaa agtgggtcatc gtggacatac aagaagagct 180
tggccaaaac ctgcgcgttt cgatagggct agacaaagca agttttttacc gttgtaatgt 240
aaccgacgag acggatgtcg agaacgcgt taagttcacc gttgaaaaac acggaaagct 300
tgacgttctg tttagtaacg cgggggtctt ggaagcggtt ggaagcggtc ttgatttgga 360
tcttgaggcg tttgatcgaa cgatggcggt taacggttcgc ggtgcggtcg cgtttatcaa 420
acacgcggca cgttcgatgg tggctagtgg tactcgtggc tccattgtat gtacgacgag 480
tattgcggca gagataggtg gtccgggacc tcatagttac acgGcttcta agcacgcgct 540
tctcgggctg atccgatcag cgtgtgctgg actggggcag tacggtatta gagtcaacgg 600
tgttgaccog tatgggggtg cactggggat gactagcgcc tacaatgagg aagcggtgaa 660
gatgcttgaa gaatatggtg aagccctagg gaatctcaaa ggtgtggtgc ttaaagctcg 720
ccacatcgca gaagcagctt tgtttttggc ttctgatgat tcggtttata ttagcgggtca 780
gaatctggtg gttgatggtg gtttttagcgt cggttaagctc atgagcacgt gagaaacaac 840
taaaaaaatga gggcatagac tctcttgaca ctttcatttt atttcttgaa taaaaattga 900
atttataagt actttcgatc attgtgttgt atgttaggct cttgagttta tataaacctt 960
gagtttaata atttactttt tcttttagtt tctcaattct at
```

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1570502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

```
Phe Asn Phe Trp Trp Ser Phe Gln Lys Trp Lys Tyr Asn Lys Thr Met
1 5 10 15
Ser Gly Leu Arg Arg Leu Asp Gly Lys Ile Ala Ile Ile Thr Gly Gly
20 25 30
Ala Ser Gly Ile Gly Ala Glu Ala Val Arg Leu Phe Thr Asp His Gly
35 40 45
Ala Lys Val Val Ile Val Asp Ile Gln Glu Glu Leu Gly Gln Asn Leu
50 55 60
Ala Val Ser Ile Gly Leu Asp Lys Ala Ser Phe Tyr Arg Cys Asn Val
65 70 75 80
Thr Asp Glu Thr Asp Val Glu Asn Ala Val Lys Phe Thr Val Glu Lys
85 90 95
His Gly Lys Leu Asp Val Leu Phe Ser Asn Ala Gly Val Leu Glu Ala
100 105 110
Phe Gly Ser Val Leu Asp Leu Asp Leu Glu Ala Phe Asp Arg Thr Met
115 120 125
Ala Val Asn Val Arg Gly Ala Ala Ala Phe Ile Lys His Ala Ala Arg
130 135 140
Ser Met Val Ala Ser Gly Thr Arg Gly Ser Ile Val Cys Thr Thr Ser
145 150 155 160
Ile Ala Ala Glu Ile Gly Gly Pro Gly Pro His Ser Tyr Thr Ala Ser
165 170 175
Lys His Ala Leu Leu Gly Leu Ile Arg Ser Ala Cys Ala Gly Leu Gly
180 185 190
Gln Tyr Gly Ile Arg Val Asn Gly Val Ala Pro Tyr Gly Val Ala Thr
195 200 205
Gly Met Thr Ser Ala Tyr Asn Glu Glu Ala Val Lys Met Leu Glu Glu
210 215 220
Tyr Gly Glu Ala Leu Gly Asn Leu Lys Gly Val Val Leu Lys Ala Arg
225 230 235 240
His Ile Ala Glu Ala Ala Leu Phe Leu Ala Ser Asp Asp Ser Val Tyr
245 250 255
Ile Ser Gly Gln Asn Leu Val Val Asp Gly Gly Phe Ser Val Val Lys
260 265 270
```



Leu Met Ser Thr  
275

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

Met Ser Gly Leu Arg Arg Leu Asp Gly Lys Ile Ala Ile Ile Thr Gly  
1 5 10 15  
Gly Ala Ser Gly Ile Gly Ala Glu Ala Val Arg Leu Phe Thr Asp His  
20 25 30  
Gly Ala Lys Val Val Ile Val Asp Ile Gln Glu Glu Leu Gly Gln Asn  
35 40 45  
Leu Ala Val Ser Ile Gly Leu Asp Lys Ala Ser Phe Tyr Arg Cys Asn  
50 55 60  
Val Thr Asp Glu Thr Asp Val Glu Asn Ala Val Lys Phe Thr Val Glu  
65 70 75 80  
Lys His Gly Lys Leu Asp Val Leu Phe Ser Asn Ala Gly Val Leu Glu  
85 90 95  
Ala Phe Gly Ser Val Leu Asp Leu Asp Leu Glu Ala Phe Asp Arg Thr  
100 105 110  
Met Ala Val Asn Val Arg Gly Ala Ala Ala Phe Ile Lys His Ala Ala  
115 120 125  
Arg Ser Met Val Ala Ser Gly Thr Arg Gly Ser Ile Val Cys Thr Thr  
130 135 140  
Ser Ile Ala Ala Glu Ile Gly Gly Pro Gly Pro His Ser Tyr Thr Ala  
145 150 155 160  
Ser Lys His Ala Leu Leu Gly Leu Ile Arg Ser Ala Cys Ala Gly Leu  
165 170 175  
Gly Gln Tyr Gly Ile Arg Val Asn Gly Val Ala Pro Tyr Gly Val Ala  
180 185 190  
Thr Gly Met Thr Ser Ala Tyr Asn Glu Glu Ala Val Lys Met Leu Glu  
195 200 205  
Glu Tyr Gly Glu Ala Leu Gly Asn Leu Lys Gly Val Val Leu Lys Ala  
210 215 220  
Arg His Ile Ala Glu Ala Ala Leu Phe Leu Ala Ser Asp Asp Ser Val  
225 230 235 240  
Tyr Ile Ser Gly Gln Asn Leu Val Val Asp Gly Gly Phe Ser Val Val  
245 250 255  
Lys Leu Met Ser Thr  
260

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

Met Ala Val Asn Val Arg Gly Ala Ala Ala Phe Ile Lys His Ala Ala

1 5 10 15  
Arg Ser Met Val Ala Ser Gly Thr Arg Gly Ser Ile Val Cys Thr Thr  
20 25 30  
Ser Ile Ala Ala Glu Ile Gly Gly Pro Gly Pro His Ser Tyr Thr Ala  
35 40 45  
Ser Lys His Ala Leu Leu Gly Leu Ile Arg Ser Ala Cys Ala Gly Leu  
50 55 60  
Gly Gln Tyr Gly Ile Arg Val Asn Gly Val Ala Pro Tyr Gly Val Ala  
65 70 75 80  
Thr Gly Met Thr Ser Ala Tyr Asn Glu Glu Ala Val Lys Met Leu Glu  
85 90 95  
Glu Tyr Gly Glu Ala Leu Gly Asn Leu Lys Gly Val Val Leu Lys Ala  
100 105 110  
Arg His Ile Ala Glu Ala Ala Leu Phe Leu Ala Ser Asp Asp Ser Val  
115 120 125  
Tyr Ile Ser Gly Gln Asn Leu Val Val Asp Gly Gly Phe Ser Val Val  
130 135 140  
Lys Leu Met Ser Thr  
145

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..812
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aacaaaaaag ccctaaacgg agagaggcgg agaggagaag gaagacggcg tgaagcaatg  | 60  |
| gtgtcgctga agctccagaa gcggctcgcc gcatccgtaa tgaaatgcgg gaaaggaaaa  | 120 |
| gtttggctcg accccaatga atcgggcgat atctctatgg ccaattccag gcagaacatt  | 180 |
| aggaagcttg tgaaggatgg ttctattatc aggaagccta ctaagatcca ctcacgttct  | 240 |
| cgggctaggg ctttgaaagg ccaagcgaaa gggtcgtcac tctggatacg gtaagagaaa  | 300 |
| gggtacaaga gaggcaaggc taccaaccaa gattcttttg atgaggagaa tgagggtgtt  | 360 |
| gaggcgtttc ttgagcaagt accgtgagtc aaagaagatt gataggcaca tgtaccatga  | 420 |
| catgtacatg aaagtgaagg gtaatgtttt caagaacaag cgtgtgctta tggagagcat  | 480 |
| ccacaagatg aaggctgaga aggctagaga gaagaccctc gctgaccagt ttgaggccaa  | 540 |
| gcgtattaag aacaaggcta gcaggagagag aaagtttgcc agaagagagg agagattagc | 600 |
| tcagggacct ggagggtggag agacaacgac tcctgCtggc gcacctcaac aaccagaggt | 660 |
| aaccaagaag aagtcgaaga agtgatttgg tgttgaactt ttttgcaatt gaatctttga  | 720 |
| gtttacctgt agaagaagcg tctttttttt atcttttata tgattttgtc ggagattcct  | 780 |
| ttcttcaaaa atatttctta tgttatggat cc                                |     |

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

Asn Lys Lys Ala Leu Asn Gly Glu Arg Arg Arg Gly Glu Gly Arg Arg  
1 5 10 15  
Arg Glu Ala Met Val Ser Leu Lys Leu Gln Lys Arg Leu Ala Ala Ser  
20 25 30

Val Met Lys Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Ser  
35 40 45  
Gly Asp Ile Ser Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val  
50 55 60  
Lys Asp Gly Phe Ile Ile Arg Lys Pro Thr Lys Ile His Ser Arg Ser  
65 70 75 80  
Arg Ala Arg Ala Leu Lys Gly Gln Ala Lys Gly Ser Ser Leu Trp Ile  
85 90 95  
Arg

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1570507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

Met Arg Arg Met Arg Val Leu Arg Arg Phe Leu Ser Lys Tyr Arg Glu  
1 5 10 15  
Ser Lys Lys Ile Asp Arg His Met Tyr His Asp Met Tyr Met Lys Val  
20 25 30  
Lys Gly Asn Val Phe Lys Asn Lys Arg Val Leu Met Glu Ser Ile His  
35 40 45  
Lys Met Lys Ala Glu Lys Ala Arg Glu Lys Thr Leu Ala Asp Gln Phe  
50 55 60  
Glu Ala Lys Arg Ile Lys Asn Lys Ala Ser Arg Glu Arg Lys Phe Ala  
65 70 75 80  
Arg Arg Glu Glu Arg Leu Ala Gln Gly Pro Gly Gly Gly Glu Thr Thr  
85 90 95  
Thr Pro Ala Gly Ala Pro Gln Gln Pro Glu Val Thr Lys Lys Lys Ser  
100 105 110  
Lys Lys

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1570508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Arg Val Leu Arg Arg Phe Leu Ser Lys Tyr Arg Glu Ser Lys Lys  
1 5 10 15  
Ile Asp Arg His Met Tyr His Asp Met Tyr Met Lys Val Lys Gly Asn  
20 25 30  
Val Phe Lys Asn Lys Arg Val Leu Met Glu Ser Ile His Lys Met Lys  
35 40 45  
Ala Glu Lys Ala Arg Glu Lys Thr Leu Ala Asp Gln Phe Glu Ala Lys  
50 55 60  
Arg Ile Lys Asn Lys Ala Ser Arg Glu Arg Lys Phe Ala Arg Arg Glu  
65 70 75 80  
Glu Arg Leu Ala Gln Gly Pro Gly Gly Gly Glu Thr Thr Thr Pro Ala

85 90 95  
Gly Ala Pro Gln Gln Pro Glu Val Thr Lys Lys Lys Ser Lys Lys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..875  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

aaaatgatcg ctgcgacaGc gagtgtgtga cgttaaaccc taaatctggt gtctttgtgc 60  
aatcgcaaga ttcatctact cgacactaaa gatcgaaact tttgaattgc agaaattgcg 120  
acacttttagc ttccaagctc tccaaaggac gttcattgct tggagggtctt tgcaatgctt 180  
tctctggttt gatgaattcc tcttccaatg gaatgatgaa tgggaagcatc ctctctcagc 240  
aacaacatag gacattcatt caaatgggga cgattctcaa atgcgtggat aactcgtgtg 300  
ctaaagaggt gatgtgcatt caatccctga gaggtaaaga aggagcaaga cttggcgata 360  
tcattgttgg ttcaagtgaag gaagctaacc caattgttca aaaaaaagta aagaaagacg 420  
ctgtcccaaa aggtaaagtg aagaaaggga tggctgtgta cgggtgtggt gtgcgtgctg 480  
cgatgcctaa aggacgtgct gatggaagcc aagtcaagtt tgatgacaat gccattgtag 540  
ttgttggcat taaggaaaag aaagggcaga ataattcaca tgggtccaag aggaaaatgg 600  
agtacaacca accgactggt acccgagtgt ttggctcctgt cccgcacgag atgcgcctca 660  
ggaaacagct caagatcctt tctttggctc agcacattgt ttgagacaat acaccacact 720  
aaaacatcag ttatgatctc ctttatgtga ctctctttga tccattcatc acttgggttt 780  
ctgttgattc ttaaactatc caactcatta tttttgttaa ttctaatagaa ttatgaaacc 840  
ttaacgtacc aattatgatc tcttatttag gtttc

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..170  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

Met Asn Ser Ser Ser Asn Gly Met Met Asn Gly Ser Ile Leu Ser Gln  
1 5 10 15  
Gln Gln His Arg Thr Phe Ile Gln Met Gly Thr Ile Leu Lys Cys Val  
20 25 30  
Asp Asn Ser Cys Ala Lys Glu Val Met Cys Ile Gln Ser Leu Arg Gly  
35 40 45  
Lys Lys Gly Ala Arg Leu Gly Asp Ile Ile Val Gly Ser Val Lys Glu  
50 55 60  
Ala Asn Pro Ile Val Gln Lys Lys Val Lys Lys Asp Ala Val Pro Lys  
65 70 75 80  
Gly Lys Val Lys Lys Gly Met Val Val Tyr Gly Val Val Val Arg Ala  
85 90 95  
Ala Met Pro Lys Gly Arg Ala Asp Gly Ser Gln Val Lys Phe Asp Asp  
100 105 110  
Asn Ala Ile Val Val Val Gly Ile Lys Glu Lys Lys Gly Gln Asn Asn  
115 120 125  
Ser His Gly Ser Lys Arg Lys Met Glu Tyr Asn Gln Pro Thr Gly Thr  
130 135 140  
Arg Val Phe Gly Pro Val Pro His Glu Met Arg Leu Arg Lys Gln Leu

145                      150                      155                      160  
Lys Ile Leu Ser Leu Ala Gln His Ile Val  
                         165                      170

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

Met Met Asn Gly Ser Ile Leu Ser Gln Gln Gln His Arg Thr Phe Ile  
1                      5                      10                      15  
Gln Met Gly Thr Ile Leu Lys Cys Val Asp Asn Ser Cys Ala Lys Glu  
                         20                      25                      30  
Val Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly  
                         35                      40                      45  
Asp Ile Ile Val Gly Ser Val Lys Glu Ala Asn Pro Ile Val Gln Lys  
50                      55                      60  
Lys Val Lys Lys Asp Ala Val Pro Lys Gly Lys Val Lys Lys Gly Met  
65                      70                      75                      80  
Val Val Tyr Gly Val Val Val Arg Ala Ala Met Pro Lys Gly Arg Ala  
                         85                      90                      95  
Asp Gly Ser Gln Val Lys Phe Asp Asp Asn Ala Ile Val Val Val Gly  
                         100                      105                      110  
Ile Lys Glu Lys Lys Gly Gln Asn Ser His Gly Ser Lys Arg Lys  
115                      120                      125  
Met Glu Tyr Asn Gln Pro Thr Gly Thr Arg Val Phe Gly Pro Val Pro  
130                      135                      140  
His Glu Met Arg Leu Arg Lys Gln Leu Lys Ile Leu Ser Leu Ala Gln  
145                      150                      155                      160  
His Ile Val

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

Met Asn Gly Ser Ile Leu Ser Gln Gln Gln His Arg Thr Phe Ile Gln  
1                      5                      10                      15  
Met Gly Thr Ile Leu Lys Cys Val Asp Asn Ser Cys Ala Lys Glu Val  
                         20                      25                      30  
Met Cys Ile Gln Ser Leu Arg Gly Lys Lys Gly Ala Arg Leu Gly Asp  
35                      40                      45  
Ile Ile Val Gly Ser Val Lys Glu Ala Asn Pro Ile Val Gln Lys Lys  
50                      55                      60  
Val Lys Lys Asp Ala Val Pro Lys Gly Lys Val Lys Lys Gly Met Val  
65                      70                      75                      80  
Val Tyr Gly Val Val Val Arg Ala Ala Met Pro Lys Gly Arg Ala Asp  
                         85                      90                      95

Gly Ser Gln Val Lys Phe Asp Asp Asn Ala Ile Val Val Val Gly Ile  
100 105 110  
Lys Glu Lys Lys Gly Gln Asn Asn Ser His Gly Ser Lys Arg Lys Met  
115 120 125  
Glu Tyr Asn Gln Pro Thr Gly Thr Arg Val Phe Gly Pro Val Pro His  
130 135 140  
Glu Met Arg Leu Arg Lys Gln Leu Lys Ile Leu Ser Leu Ala Gln His  
145 150 155 160  
Ile Val

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1027
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

attcgtcttc tccaattttc tcgcgaagaa aactttccta ctttgtttca atccaaacga 60  
gtcaaaatgc ttatcaagac tgtttcttca tcttcttctt cagctctctc gctgggtgaat 120  
ttccatggcg tgaagaagga tgtgtctcct ttgttacctt ccatttcacg gaatcttcga 180  
gtttcttctg gaaaatctgg aaaattaact ttctctgttc gcgcacataa aagctcaacc 240  
accgacgcgc taagcggcgt tgtcttcgag ccgtttaagg aagtaaaaaa ggagctcgat 300  
ctcgtcccta ccagctctca tctctcactc gctcgacaaa agtactcaga cgagtgcgaa 360  
gccgccatta acgagcagat caatgtggVa tacaatgtct cgtatgtgta tcacgctatg 420  
tatgcttact ttgatcggga taacatcgcg ctcaaaggctc ttgccaagtt ctttaaggaa 480  
tcaagtcttg aagaaaagaga gcatgctgag aagttaatgg agtatcagaa caaacgtggt 540  
gggagggtta agttacagtc cattgtaatg cctctttcag agtttgaaca tgttgacaaa 600  
ggagatgctc tttatggcat ggagcttgct ctgtcactgg agaaactagt taatgagaag 660  
ctcttaaacc ttcacagtgt tgcttcgagg aacaatgatg tccacttggc agattttatt 720  
gagagcgagt ttctgacaga gcagggtggaa gcaatcaagt tgatctcaga atatgtggct 780  
caactgcgac gagttggcaa aggacacgga acatggcatt tcaatcagat gcttctggaa 840  
gggtaagcag cttcgaggga ctcttggtgc tactgtgttt ctatatgaag ctctcttagt 900  
gatatgtatg gaactacttt atgtttagtt ctttagcttt tacgattttg tgaggtagta 960  
gacttctttt tctgtaagag acaaaaagaca tgatcacata actttatatt ctggtataag 1020  
gttcacc

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

Ile Arg Leu Leu Gln Phe Ser Arg Glu Glu Asn Phe Pro Thr Leu Phe  
1 5 10 15  
Gln Ser Lys Arg Val Lys Met Leu Ile Lys Thr Val Ser Ser Ser  
20 25 30  
Ser Ser Ala Leu Ser Leu Val Asn Phe His Gly Val Lys Lys Asp Val  
35 40 45  
Ser Pro Leu Leu Pro Ser Ile Ser Ser Asn Leu Arg Val Ser Ser Gly  
50 55 60  
Lys Ser Gly Lys Leu Thr Phe Ser Val Arg Ala Ser Lys Ser Ser Thr

|                     |                 |                     |             |
|---------------------|-----------------|---------------------|-------------|
| 65                  | 70              | 75                  | 80          |
| Thr Asp Ala Leu Ser | Gly Val Val Phe | Glu Pro Phe Lys Glu | Val Lys     |
|                     | 85              | 90                  | 95          |
| Lys Glu Leu Asp Leu | Val Pro Thr Ser | His Leu Ser Leu     | Ala Arg     |
|                     | 100             | 105                 | 110         |
| Gln Lys Tyr Ser Asp | Glu Cys Glu Ala | Ala Ile Asn Glu     | Gln Ile Asn |
|                     | 115             | 120                 | 125         |
| Val Xaa Tyr Asn Val | Ser Tyr Val Tyr | His Ala Met Tyr     | Ala Tyr Phe |
|                     | 130             | 135                 | 140         |
| Asp Arg Asp Asn Ile | Ala Leu Lys Gly | Leu Ala Lys Phe     | Phe Lys Glu |
|                     | 145             | 150                 | 155         |
| Ser Ser Leu Glu Glu | Arg Glu His Ala | Glu Lys Leu Met     | Glu Tyr Gln |
|                     | 165             | 170                 | 175         |
| Asn Lys Arg Gly Gly | Arg Val Lys Leu | Gln Ser Ile Val     | Met Pro Leu |
|                     | 180             | 185                 | 190         |
| Ser Glu Phe Glu His | Val Asp Lys Gly | Asp Ala Leu Tyr     | Gly Met Glu |
|                     | 195             | 200                 | 205         |
| Leu Ala Leu Ser Leu | Glu Lys Leu Val | Asn Glu Lys Leu     | Leu Asn Leu |
|                     | 210             | 215                 | 220         |
| His Ser Val Ala Ser | Arg Asn Asn Asp | Val His Leu Ala     | Asp Phe Ile |
|                     | 225             | 230                 | 235         |
| Glu Ser Glu Phe Leu | Thr Glu Gln Val | Glu Ala Ile Lys     | Leu Ile Ser |
|                     | 245             | 250                 | 255         |
| Glu Tyr Val Ala Gln | Leu Arg Arg Val | Gly Lys Gly His     | Gly Thr Trp |
|                     | 260             | 265                 | 270         |
| His Phe Asn Gln Met | Leu Leu Glu Gly |                     |             |
|                     | 275             | 280                 |             |

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1570536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

|                     |                 |                 |             |
|---------------------|-----------------|-----------------|-------------|
| Met Leu Ile Lys Thr | Val Ser Ser Ser | Ser Ser Ser Ala | Leu Ser Leu |
| 1                   | 5               | 10              | 15          |
| Val Asn Phe His Gly | Val Lys Lys Asp | Val Ser Pro Leu | Leu Pro Ser |
|                     | 20              | 25              | 30          |
| Ile Ser Ser Asn Leu | Arg Val Ser Ser | Gly Lys Ser Gly | Lys Leu Thr |
|                     | 35              | 40              | 45          |
| Phe Ser Val Arg Ala | Ser Lys Ser Ser | Thr Thr Asp Ala | Leu Ser Gly |
|                     | 50              | 55              | 60          |
| Val Val Phe Glu Pro | Phe Lys Glu Val | Lys Lys Glu Leu | Asp Leu Val |
|                     | 65              | 70              | 75          |
| Pro Thr Ser Ser His | Leu Ser Leu Ala | Arg Gln Lys Tyr | Ser Asp Glu |
|                     | 85              | 90              | 95          |
| Cys Glu Ala Ala Ile | Asn Glu Gln Ile | Asn Val Xaa Tyr | Asn Val Ser |
|                     | 100             | 105             | 110         |
| Tyr Val Tyr His Ala | Met Tyr Ala Tyr | Phe Asp Arg Asp | Asn Ile Ala |
|                     | 115             | 120             | 125         |
| Leu Lys Gly Leu Ala | Lys Phe Lys Glu | Ser Ser Leu Glu | Glu Glu Arg |
|                     | 130             | 135             | 140         |
| Glu His Ala Glu Lys | Leu Met Glu Tyr | Gln Asn Lys Arg | Gly Gly Arg |
|                     | 145             | 150             | 155         |
| Val Lys Leu Gln Ser | Ile Val Met Pro | Leu Ser Glu Phe | Glu His Val |
|                     | 165             | 170             | 175         |

Asp Lys Gly Asp Ala Leu Tyr Gly Met Glu Leu Ala Leu Ser Leu Glu  
180 185 190  
Lys Leu Val Asn Glu Lys Leu Leu Asn Leu His Ser Val Ala Ser Arg  
195 200 205  
Asn Asn Asp Val His Leu Ala Asp Phe Ile Glu Ser Glu Phe Leu Thr  
210 215 220  
Glu Gln Val Glu Ala Ile Lys Leu Ile Ser Glu Tyr Val Ala Gln Leu  
225 230 235 240  
Arg Arg Val Gly Lys Gly His Gly Thr Trp His Phe Asn Gln Met Leu  
245 250 255  
Leu Glu Gly

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

Met Tyr Ala Tyr Phe Asp Arg Asp Asn Ile Ala Leu Lys Gly Leu Ala  
1 5 10 15  
Lys Phe Phe Lys Glu Ser Ser Leu Glu Glu Arg Glu His Ala Glu Lys  
20 25 30  
Leu Met Glu Tyr Gln Asn Lys Arg Gly Gly Arg Val Lys Leu Gln Ser  
35 40 45  
Ile Val Met Pro Leu Ser Glu Phe Glu His Val Asp Lys Gly Asp Ala  
50 55 60  
Leu Tyr Gly Met Glu Leu Ala Leu Ser Leu Glu Lys Leu Val Asn Glu  
65 70 75 80  
Lys Leu Leu Asn Leu His Ser Val Ala Ser Arg Asn Asn Asp Val His  
85 90 95  
Leu Ala Asp Phe Ile Glu Ser Glu Phe Leu Thr Glu Gln Val Glu Ala  
100 105 110  
Ile Lys Leu Ile Ser Glu Tyr Val Ala Gln Leu Arg Arg Val Gly Lys  
115 120 125  
Gly His Gly Thr Trp His Phe Asn Gln Met Leu Leu Glu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 basepairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| agattttcaaa | tccttggttta | caatctcttc | tctggctatc | ttagagggat | ttttgattga | 60  |
| gatttttaaaa | ttttctTgag  | ttggattagt | tggttggtta | agagatggat | ccggatacgg | 120 |
| tgaagtcgac  | cctctcgaat  | ctggcattcg | ggaatgtatt | ggcggcagct | gctagagatt | 180 |
| ataaaaagga  | agttcttgca  | aatgaaaagg | cacaaggatc | aagacctgGt | caacgaggaa | 240 |
| gttgatcttg  | acgaattgat  | ggatgatcca | gagctagaaa | agttgcacgc | agataggatt | 300 |
| gcagcactca  | ggagagaagt  | ggaaaagaga | gaagcattca | aaagacaagg | acatggtgaa | 360 |
| taccgagaag  | ttagcgaagg  | cgacttcttg | ggagaagtca | caaggagtga | aaaagttata | 420 |



|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tgtcacttct accacaagga gttctatcgc tgcaagataa tggacaagca tttgaagacc  | 480 |
| cttgtccta gacatgtgga cacaaagttc attaagatgg acgctgagaa cgctcccttc   | 540 |
| ttcgtcacca agcttgcaat caagactttg ccgtgtgtta tccttttttag caagggaatc | 600 |
| gcgatggata ggcttgtcgg gtttcaagat ctagggtgcca aggacgattt ctccacgacg | 660 |
| aagctggaga atcttctggg caagaaagga atgcttagtg aaaagagaaa agaggaagat  | 720 |
| gaggaagatt acgagtatca agaaagcata cgtcgggtccg ttaggtcttc agcgaatgtc | 780 |
| gactctgatt cagattgata tcgaagcttt tctcatagta gacctccgag cctttttgta  | 840 |
| ttttgttttc accgctgctc tgtttgaatt gtttgggtcta tgaatcttat gcttctataa | 900 |
| gtctttatag tgggaaatth cgttccacaa tgtttttggt tatttgaaaa ctgcaaatta  | 960 |
| tggtgtctaa ccatat                                                  |     |

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Tyr Trp Arg Gln Leu Leu Glu Ile Ile Lys Arg Lys Phe Leu Gln |  |
| 1 5 10 15                                                       |  |
| Met Lys Arg His Lys Asp Gln Asp Leu Val Asn Glu Glu Val Asp Leu |  |
| 20 25 30                                                        |  |
| Asp Glu Leu Met Asp Asp Pro Glu Leu Glu Lys Leu His Ala Asp Arg |  |
| 35 40 45                                                        |  |
| Ile Ala Ala Leu Arg Arg Glu Val Glu Lys Arg Glu Ala Phe Lys Arg |  |
| 50 55 60                                                        |  |
| Gln Gly His Gly Glu Tyr Arg Glu Val Ser Glu Gly Asp Phe Leu Gly |  |
| 65 70 75 80                                                     |  |
| Glu Val Thr Arg Ser Glu Lys Val Ile Cys His Phe Tyr His Lys Glu |  |
| 85 90 95                                                        |  |
| Phe Tyr Arg Cys Lys Ile Met Asp Lys His Leu Lys Thr Leu Ala Pro |  |
| 100 105 110                                                     |  |
| Arg His Val Asp Thr Lys Phe Ile Lys Met Asp Ala Glu Asn Ala Pro |  |
| 115 120 125                                                     |  |
| Phe Phe Val Thr Lys Leu Ala Ile Lys Thr Leu Pro Cys Val Ile Leu |  |
| 130 135 140                                                     |  |
| Phe Ser Lys Gly Ile Ala Met Asp Arg Leu Val Gly Phe Gln Asp Leu |  |
| 145 150 155 160                                                 |  |
| Gly Ala Lys Asp Asp Phe Ser Thr Thr Lys Leu Glu Asn Leu Leu Val |  |
| 165 170 175                                                     |  |
| Lys Lys Gly Met Leu Ser Glu Lys Arg Lys Glu Glu Asp Glu Glu Asp |  |
| 180 185 190                                                     |  |
| Tyr Glu Tyr Gln Glu Ser Ile Arg Arg Ser Val Arg Ser Ser Ala Asn |  |
| 195 200 205                                                     |  |
| Val Asp Ser Asp Ser Asp                                         |  |
| 210                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1570540

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | His | Lys | Asp | Gln | Asp | Leu | Val | Asn | Glu | Glu | Val | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Leu | Met | Asp | Asp | Pro | Glu | Leu | Glu | Lys | Leu | His | Ala | Asp | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Ala | Leu | Arg | Arg | Glu | Val | Glu | Lys | Arg | Glu | Ala | Phe | Lys | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gln | Gly | His | Gly | Glu | Tyr | Arg | Glu | Val | Ser | Glu | Gly | Asp | Phe | Leu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Val | Thr | Arg | Ser | Glu | Lys | Val | Ile | Cys | His | Phe | Tyr | His | Lys | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Tyr | Arg | Cys | Lys | Ile | Met | Asp | Lys | His | Leu | Lys | Thr | Leu | Ala | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | His | Val | Asp | Thr | Lys | Phe | Ile | Lys | Met | Asp | Ala | Glu | Asn | Ala | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Phe | Val | Thr | Lys | Leu | Ala | Ile | Lys | Thr | Leu | Pro | Cys | Val | Ile | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Ser | Lys | Gly | Ile | Ala | Met | Asp | Arg | Leu | Val | Gly | Phe | Gln | Asp | Leu |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gly | Ala | Lys | Asp | Asp | Phe | Ser | Thr | Thr | Lys | Leu | Glu | Asn | Leu | Leu | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Lys | Gly | Met | Leu | Ser | Glu | Lys | Arg | Lys | Glu | Glu | Asp | Glu | Glu | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Glu | Tyr | Gln | Glu | Ser | Ile | Arg | Arg | Ser | Val | Arg | Ser | Ser | Ala | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Asp | Ser | Asp | Ser | Asp |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Asp | Pro | Glu | Leu | Glu | Lys | Leu | His | Ala | Asp | Arg | Ile | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Arg | Glu | Val | Glu | Lys | Arg | Glu | Ala | Phe | Lys | Arg | Gln | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Glu | Tyr | Arg | Glu | Val | Ser | Glu | Gly | Asp | Phe | Leu | Gly | Glu | Val | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Ser | Glu | Lys | Val | Ile | Cys | His | Phe | Tyr | His | Lys | Glu | Phe | Tyr | Arg |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Cys | Lys | Ile | Met | Asp | Lys | His | Leu | Lys | Thr | Leu | Ala | Pro | Arg | His | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Thr | Lys | Phe | Ile | Lys | Met | Asp | Ala | Glu | Asn | Ala | Pro | Phe | Phe | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Lys | Leu | Ala | Ile | Lys | Thr | Leu | Pro | Cys | Val | Ile | Leu | Phe | Ser | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Ala | Met | Asp | Arg | Leu | Val | Gly | Phe | Gln | Asp | Leu | Gly | Ala | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asp | Asp | Phe | Ser | Thr | Thr | Lys | Leu | Glu | Asn | Leu | Leu | Val | Lys | Lys | Gly |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Met | Leu | Ser | Glu | Lys | Arg | Lys | Glu | Glu | Asp | Glu | Glu | Asp | Tyr | Glu | Tyr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Glu | Ser | Ile | Arg | Arg | Ser | Val | Arg | Ser | Ser | Ala | Asn | Val | Asp | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |

Asp Ser Asp

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1089
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

|            |            |            |             |             |            |      |
|------------|------------|------------|-------------|-------------|------------|------|
| acagagacaa | caaactaaag | ttggtggtga | tagagtgaga  | gagaaacatg  | gaaggcaaag | 60   |
| aagaagacgt | caatgttga  | gccacaagt  | tcccagagag  | acagccgac   | ggtacggcg  | 120  |
| ctcagacgga | gagcaaggac | tataaggaac | caccaccggc  | gccgtttttc  | gaaccggcg  | 180  |
| agctcaaatc | ttggtctttc | tacagagcag | ggatagctga  | gttcatagcc  | actttccttt | 240  |
| tcctctacgt | caccgttttg | acagtcattg | gtgttaagag  | agctcccaat  | atgtgtgcct | 300  |
| ctgttggaat | ccaaggcatc | gcttgggctt | ttggtggcat  | gactctttgct | cttgtttact | 360  |
| gtactgctgg | aatctcagga | ggacatatta | atccggcggt  | gacttttggg  | ttgttcttgg | 420  |
| cgaggaagct | atctttaacc | agagctctgt | tctacatagt  | aatgcagtc   | cttgagagta | 480  |
| tatgtggtgc | tggtgtggtt | aaagggtttc | aaccagggtc  | gtaccagacg  | aatggcggtg | 540  |
| gagctaattg | ggtggctcat | ggttacacaa | aggggttcagg | tcttggtgca  | gagattgttg | 600  |
| gaacttttgt | tctggtttac | actgttttct | cagctactga  | tgctaagaga  | agtgcagag  | 660  |
| actctcatgt | cgtatctttg | gctccgcttc | caattgggtt  | tgctgtcttc  | ttggtgcaat | 720  |
| tggctaccat | cccaattact | ggaactggca | ttaaccgggc  | caggagtctc  | ggagctgcca | 780  |
| tcactacaaa | caaggatcat | gcttgggatg | accattggat  | cttctgggtc  | ggtccattca | 840  |
| ttggtGctgc | gcttgcctgc | ctgtaccatc | agatagtcac  | cagagctatt  | cctttcaagt | 900  |
| ccaagacata | aagtttctta | catattctct | gatcatcatc  | aagctaagaa  | tatatcaatc | 960  |
| tttaattcta | tatgctttct | tcttggttcc | tatgtcatgt  | gtgatgatct  | ctatatgtac | 1020 |
| cactagagct | ttgatcttgt | aacagtgtaa | atgtgtaatc  | tattatgtat  | caatggcatt | 1080 |
| gtatcttgt  |            |            |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Lys | Glu | Asp | Val | Asn | Val | Gly | Ala | Asn | Lys | Phe | Pro |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Arg | Gln | Pro | Ile | Gly | Thr | Ala | Ala | Gln | Thr | Glu | Ser | Lys | Asp |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Pro | Pro | Pro | Ala | Pro | Phe | Phe | Glu | Pro | Gly | Glu | Leu | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Trp | Ser | Phe | Tyr | Arg | Ala | Gly | Ile | Ala | Glu | Phe | Ile | Ala | Thr | Phe |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Phe | Leu | Tyr | Val | Thr | Val | Leu | Thr | Val | Met | Gly | Val | Lys | Arg | Ala |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Asn | Met | Cys | Ala | Ser | Val | Gly | Ile | Gln | Gly | Ile | Ala | Trp | Ala | Phe |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Met | Ile | Phe | Ala | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly | Leu | Phe | Leu | Ala | Arg | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |

Ser Leu Thr Arg Ala Leu Phe Tyr Ile Val Met Gln Ser Leu Gly Ala  
130 135 140  
Ile Cys Gly Ala Gly Val Val Lys Gly Phe Gln Pro Gly Leu Tyr Gln  
145 150 155 160  
Thr Asn Gly Gly Gly Ala Asn Val Val Ala His Gly Tyr Thr Lys Gly  
165 170 175  
Ser Gly Leu Gly Ala Glu Ile Val Gly Thr Phe Val Leu Val Tyr Thr  
180 185 190  
Val Phe Ser Ala Thr Asp Ala Lys Arg Ser Ala Arg Asp Ser His Val  
195 200 205  
Arg Ile Leu Ala Pro Leu Pro Ile Gly Phe Ala Val Phe Leu Val His  
210 215 220  
Leu Ala Thr Ile Pro Ile Thr Gly Thr Gly Ile Asn Pro Ala Arg Ser  
225 230 235 240  
Leu Gly Ala Ala Ile Ile Tyr Asn Lys Asp His Ala Trp Asp Asp His  
245 250 255  
Trp Ile Phe Trp Val Gly Pro Phe Ile Gly Ala Ala Leu Ala Ala Leu  
260 265 270  
Tyr His Gln Ile Val Ile Arg Ala Ile Pro Phe Lys Ser Lys Thr  
275 280 285

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Gly Val Lys Arg Ala Pro Asn Met Cys Ala Ser Val Gly Ile Gln  
1 5 10 15  
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ala Leu Val Tyr Cys  
20 25 30  
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly  
35 40 45  
Leu Phe Leu Ala Arg Lys Leu Ser Leu Thr Arg Ala Leu Phe Tyr Ile  
50 55 60  
Val Met Gln Ser Leu Gly Ala Ile Cys Gly Ala Gly Val Val Lys Gly  
65 70 75 80  
Phe Gln Pro Gly Leu Tyr Gln Thr Asn Gly Gly Gly Ala Asn Val Val  
85 90 95  
Ala His Gly Tyr Thr Lys Gly Ser Gly Leu Gly Ala Glu Ile Val Gly  
100 105 110  
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Ala Lys Arg  
115 120 125  
Ser Ala Arg Asp Ser His Val Arg Ile Leu Ala Pro Leu Pro Ile Gly  
130 135 140  
Phe Ala Val Phe Leu Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr  
145 150 155 160  
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys  
165 170 175  
Asp His Ala Trp Asp Asp His Trp Ile Phe Trp Val Gly Pro Phe Ile  
180 185 190  
Gly Ala Ala Leu Ala Ala Leu Tyr His Gln Ile Val Ile Arg Ala Ile  
195 200 205  
Pro Phe Lys Ser Lys Thr  
210

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 206 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..206  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570564  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Cys | Ala | Ser | Val | Gly | Ile | Gln | Gly | Ile | Ala | Trp | Ala | Phe | Gly | Gly |  |  |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |  |  |
| Met | Ile | Phe | Ala | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly | Gly | His |  |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly | Leu | Phe | Leu | Ala | Arg | Lys | Leu | Ser |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |  |
| Leu | Thr | Arg | Ala | Leu | Phe | Tyr | Ile | Val | Met | Gln | Ser | Leu | Gly | Ala | Ile |  |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |  |
| Cys | Gly | Ala | Gly | Val | Val | Lys | Gly | Phe | Gln | Pro | Gly | Leu | Tyr | Gln | Thr |  |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Asn | Gly | Gly | Gly | Ala | Asn | Val | Val | Ala | His | Gly | Tyr | Thr | Lys | Gly | Ser |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Gly | Leu | Gly | Ala | Glu | Ile | Val | Gly | Thr | Phe | Val | Leu | Val | Tyr | Thr | Val |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Phe | Ser | Ala | Thr | Asp | Ala | Lys | Arg | Ser | Ala | Arg | Asp | Ser | His | Val | Arg |  |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ile | Leu | Ala | Pro | Leu | Pro | Ile | Gly | Phe | Ala | Val | Phe | Leu | Val | His | Leu |  |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |  |
| Ala | Thr | Ile | Pro | Ile | Thr | Gly | Thr | Gly | Ile | Asn | Pro | Ala | Arg | Ser | Leu |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Gly | Ala | Ala | Ile | Ile | Tyr | Asn | Lys | Asp | His | Ala | Trp | Asp | Asp | His | Trp |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Ile | Phe | Trp | Val | Gly | Pro | Phe | Ile | Gly | Ala | Ala | Leu | Ala | Ala | Leu | Tyr |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| His | Gln | Ile | Val | Ile | Arg | Ala | Ile | Pro | Phe | Lys | Ser | Lys | Thr |     |     |  |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:1643:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1122 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..1122  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| aaaaatcctg  | atttAytgag  | ctttaaaCcc | haRaccctc  | tcttctctct | tctccacgcc  | 60  |
| atttccagaa  | ttttcaggtg  | ttcgtgaaaa | gatgaatttt | aagaatgtca | aagttcccaa  | 120 |
| aggtcctggt  | ggtggtgtta  | tagctgcggt | ggttattggg | gggctcagtc | tttacggtgc  | 180 |
| tacgcacact  | ctctacaatg  | tcgatggagg | tcacgcagcc | attgtcttta | accggcttgt  | 240 |
| tggtatcaaa  | gacaaggtct  | accctgaggg | tactcacctt | atgattccat | ggttcgaaaag | 300 |
| gccaatcatc  | tatgacgttc  | gtgcaaaagc | ttatctagtt | gagagcacat | ctgggagccg  | 360 |
| tgatctccag  | atgggttaaga | ttgggcttcg | ggttctcacc | cgtcttatgg | ctgaccaatt  | 420 |
| accagaggta  | taccggtccc  | ttggtgagaa | ttaccgcgag | agagtcttgc | cttctatcat  | 480 |
| ccacgagacc  | ttgaaagctg  | tggttgctca | gtacaacgca | agccaactta | ttactcagag  | 540 |
| agagtcggtg  | agtagagaaa  | tcaggaaaat | cctaactcta | agagccgcaa | acttccacat  | 600 |
| tgcactggat  | gatgtgtcca  | tcacaggctt | gacattcgga | aaggagttca | cggcagccat  | 660 |
| agaaggaaaag | caggtcgctg  | ctcaagaggc | cgaacgggct | aagttcattg | tcgagaaaagc | 720 |

tgaacaggac aagagaagtg ctgttatccg cgccgaggga gaagccaaga gtgctcagct 780  
cattggtcaa gcaatcgcaa acaaccaagc gttcttaaca ctgaggaaga tcgaagcagc 840  
tagagagatc gcacagacca tctctaggtc ggcgaacaag gtttacttga gctctaacga 900  
tctgttgctt aacctacagg ctatggacct tgatgtgaag ccgaagaagt agagaatgat 960  
atgattaaac cacaccagag ctctttcttc ataatcgtat tttcaattca cggattctta 1020  
gaccaaagc tatgagttct atcttgtgaa tttcagacac tatcgtgcgt ttgtagtctt 1080  
tcttttgtga gatcaagaag aaaagaaaag atttatgttt tt

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Met Asn Phe Lys Asn Val Lys Val Pro Lys Gly Pro Gly Gly Val  
1 5 10 15  
Ile Ala Ala Val Val Ile Gly Gly Leu Ser Leu Tyr Gly Ala Thr His  
20 25 30  
Thr Leu Tyr Asn Val Asp Gly Gly His Arg Ala Ile Val Phe Asn Arg  
35 40 45  
Leu Val Gly Ile Lys Asp Lys Val Tyr Pro Glu Gly Thr His Leu Met  
50 55 60  
Ile Pro Trp Phe Glu Arg Pro Ile Ile Tyr Asp Val Arg Ala Lys Pro  
65 70 75 80  
Tyr Leu Val Glu Ser Thr Ser Gly Ser Arg Asp Leu Gln Met Val Lys  
85 90 95  
Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln Leu Pro Glu  
100 105 110  
Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val Leu Pro Ser  
115 120 125  
Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr Asn Ala Ser  
130 135 140  
Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile Arg Lys Ile  
145 150 155 160  
Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp Asp Val Ser  
165 170 175  
Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala Ile Glu Gly  
180 185 190  
Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe Ile Val Glu  
195 200 205  
Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala Glu Gly Glu  
210 215 220  
Ala Lys Ser Ala Gln Leu Ile Gly Gln Ala Ile Ala Asn Asn Gln Ala  
225 230 235 240  
Phe Leu Thr Leu Arg Lys Ile Glu Ala Ala Arg Glu Ile Ala Gln Thr  
245 250 255  
Ile Ser Arg Ser Ala Asn Lys Val Tyr Leu Ser Ser Asn Asp Leu Leu  
260 265 270  
Leu Asn Leu Gln Ala Met Asp Leu Asp Val Lys Pro Lys Lys  
275 280 285

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..223  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570567  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

Met Ile Pro Trp Phe Glu Arg Pro Ile Ile Tyr Asp Val Arg Ala Lys  
1                  5                  10                  15  
Pro Tyr Leu Val Glu Ser Thr Ser Gly Ser Arg Asp Leu Gln Met Val  
                  20                  25                  30  
Lys Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln Leu Pro  
                  35                  40                  45  
Glu Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val Leu Pro  
                  50                  55                  60  
Ser Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr Asn Ala  
65                  70                  75                  80  
Ser Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile Arg Lys  
                  85                  90                  95  
Ile Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp Asp Val  
                  100                 105                 110  
Ser Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala Ile Glu  
                 115                 120                 125  
Gly Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe Ile Val  
                 130                 135                 140  
Glu Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala Glu Gly  
145                 150                 155                 160  
Glu Ala Lys Ser Ala Gln Leu Ile Gly Gln Ala Ile Ala Asn Asn Gln  
                 165                 170                 175  
Ala Phe Leu Thr Leu Arg Lys Ile Glu Ala Ala Arg Glu Ile Ala Gln  
                 180                 185                 190  
Thr Ile Ser Arg Ser Ala Asn Lys Val Tyr Leu Ser Ser Asn Asp Leu  
                 195                 200                 205  
Leu Leu Asn Leu Gln Ala Met Asp Leu Asp Val Lys Pro Lys Lys  
210                 215                 220

(2) INFORMATION FOR SEQ ID NO:1646:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 193 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..193  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

Met Val Lys Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln  
1                  5                  10                  15  
Leu Pro Glu Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val  
                  20                  25                  30  
Leu Pro Ser Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr  
                  35                  40                  45  
Asn Ala Ser Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile  
                  50                  55                  60  
Arg Lys Ile Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp  
65                  70                  75                  80  
Asp Val Ser Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala  
                  85                  90                  95  
Ile Glu Gly Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe  
                 100                 105                 110  
Ile Val Glu Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 115 |     | 120 |     | 125 |     |     |     |     |     |     |     |     |     |     |
| Glu | Gly | Glu | Ala | Lys | Ser | Ala | Gln | Leu | Ile | Gly | Gln | Ala | Ile | Ala | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Gln | Ala | Phe | Leu | Thr | Leu | Arg | Lys | Ile | Glu | Ala | Ala | Arg | Glu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Gln | Thr | Ile | Ser | Arg | Ser | Ala | Asn | Lys | Val | Tyr | Leu | Ser | Ser | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Leu | Leu | Leu | Asn | Leu | Gln | Ala | Met | Asp | Leu | Asp | Val | Lys | Pro | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

Lys

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..903
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctctcaactc | cgcgcaGcta | aactttattg | gagaaaccct | aatcggcgac | aatgggtatt | 60  |
| tctcgtgact | ctatccacaa | gaggcgtgcc | actggaggca | agcagaagca | atggaggaag | 120 |
| aagcgaaagt | atgagatggg | aaggcagcca | gccaacacca | agctctcaag | caacaagacg | 180 |
| gtcagaagaa | taagagttcg | tgggtgaaat | gttaagtggc | gtgcgttgag | gctcgatact | 240 |
| ggtaactact | cgtggggaag | tgaagcaact | acccgcaaga | ccagagtcct | tgatgtggtc | 300 |
| tacaatgcct | ccaacaatga | gcttgtagct | actaagacac | ttgtcaagag | tgctattgtt | 360 |
| caggttgatg | ctgctccttt | caagcagtgg | tacctctcgc | actatgggtg | tgagcttggg | 420 |
| cgcaagaaga | agagtgtctc | ttccaccaag | aaggacggag | aggaaggtga | agaggcagct | 480 |
| gttgcaagtc | ctgaggaggt | caagaagagc | aaccacctcc | tgagaaagat | tgcaagccgt | 540 |
| caagagggtc | gcagtcttga | ttcacacatt | gaggaccaat | ttgcaagtgg | acgtttgttg | 600 |
| gcttgatatc | cttcaaggcc | tgggcagtgc | gggcgtgctg | atggatacat | cttgggaagg | 660 |
| aaagagttgg | agttctacat | gaagaagatc | cagaagaaga | agggcaaggg | tgctgcttag | 720 |
| agtctcttct | tatctgcctt | gagcttttgt | cttacaacat | gttttgagtt | ttcagtttca | 780 |
| attgtctgag | aaactatgtt | tttggttagg | cttgtgggat | ttctttaaaa | ctcccatcag | 840 |
| ttattatggt | acaatgtttt | tgtcttggat | tttctttata | attttaatcg | ataatttcac | 900 |
| tcc        |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ile | Ser | Arg | Asp | Ser | Ile | His | Lys | Arg | Arg | Ala | Thr | Gly | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Gln | Lys | Gln | Trp | Arg | Lys | Lys | Arg | Lys | Tyr | Glu | Met | Gly | Arg | Gln |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Pro | Ala | Asn | Thr | Lys | Leu | Ser | Ser | Asn | Lys | Thr | Val | Arg | Arg | Ile | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Gly | Gly | Asn | Val | Lys | Trp | Arg | Ala | Leu | Arg | Leu | Asp | Thr | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Tyr | Ser | Trp | Gly | Ser | Glu | Ala | Thr | Thr | Arg | Lys | Thr | Arg | Val | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |



Asp Val Val Tyr Asn Ala Ser Asn Asn Glu Leu Val Arg Thr Lys Thr  
85 90 95  
Leu Val Lys Ser Ala Ile Val Gln Val Asp Ala Ala Pro Phe Lys Gln  
100 105 110  
Trp Tyr Leu Ser His Tyr Gly Val Glu Leu Gly Arg Lys Lys Lys Ser  
115 120 125  
Ala Ser Ser Thr Lys Lys Asp Gly Glu Glu Gly Glu Glu Ala Ala Val  
130 135 140  
Ala Ala Pro Glu Glu Val Lys Lys Ser Asn His Leu Leu Arg Lys Ile  
145 150 155 160  
Ala Ser Arg Gln Glu Gly Arg Ser Leu Asp Ser His Ile Glu Asp Gln  
165 170 175  
Phe Ala Ser Gly Arg Leu Leu Ala Cys Ile Ser Ser Arg Pro Gly Gln  
180 185 190  
Cys Gly Arg Ala Asp Gly Tyr Ile Leu Glu Gly Lys Glu Leu Glu Phe  
195 200 205  
Tyr Met Lys Lys Ile Gln Lys Lys Lys Gly Lys Gly Ala Ala  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1570571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

Met Gly Arg Gln Pro Ala Asn Thr Lys Leu Ser Ser Asn Lys Thr Val  
1 5 10 15  
Arg Arg Ile Arg Val Arg Gly Gly Asn Val Lys Trp Arg Ala Leu Arg  
20 25 30  
Leu Asp Thr Gly Asn Tyr Ser Trp Gly Ser Glu Ala Thr Thr Arg Lys  
35 40 45  
Thr Arg Val Leu Asp Val Val Tyr Asn Ala Ser Asn Asn Glu Leu Val  
50 55 60  
Arg Thr Lys Thr Leu Val Lys Ser Ala Ile Val Gln Val Asp Ala Ala  
65 70 75 80  
Pro Phe Lys Gln Trp Tyr Leu Ser His Tyr Gly Val Glu Leu Gly Arg  
85 90 95  
Lys Lys Lys Ser Ala Ser Ser Thr Lys Lys Asp Gly Glu Glu Gly Glu  
100 105 110  
Glu Ala Ala Val Ala Ala Pro Glu Glu Val Lys Lys Ser Asn His Leu  
115 120 125  
Leu Arg Lys Ile Ala Ser Arg Gln Glu Gly Arg Ser Leu Asp Ser His  
130 135 140  
Ile Glu Asp Gln Phe Ala Ser Gly Arg Leu Leu Ala Cys Ile Ser Ser  
145 150 155 160  
Arg Pro Gly Gln Cys Gly Arg Ala Asp Gly Tyr Ile Leu Glu Gly Lys  
165 170 175  
Glu Leu Glu Phe Tyr Met Lys Lys Ile Gln Lys Lys Lys Gly Lys Gly  
180 185 190  
Ala Ala

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:

(2) INFORMATION FOR SEQ ID NO:1651:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

(2) INFORMATION FOR SEQ ID NO:1652:

```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..79
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570578
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:
```

Met Lys Ala Val Val Phe Leu Val Val Ala Asn Gly Ile Ala Ala Val  
1 5 10 15  
Tyr Ser Leu Leu Gln Ser Val Arg Cys Val Val Gly Thr Met Lys Gly  
20 25 30  
Lys Val Leu Phe Xaa Lys Pro Leu Ala Trp Ala Phe Phe Xaa Gly Asp  
35 40 45  
Gln Ala Met Ala Tyr Leu Asn Val Ala Ala Ile Ala Ala Thr Ala Glu  
50 55 60  
Ser Gly Xaa Xaa Leu Leu Gly Lys Glu Arg Lys Ile Cys Asn Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..736
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

|            |             |             |             |             |              |     |
|------------|-------------|-------------|-------------|-------------|--------------|-----|
| ctgaaccctt | cgatttttoga | ttcttctctcg | agccttcctt  | ccttccttcG  | ttMcttctcc   | 60  |
| aagaggattt | tgattgtctc  | cttaactctct | ccatgtcaag  | ttctggtgct  | ccttcacgca   | 120 |
| agactctgag | taagatcgcg  | actaatcgtc  | ttcagaaaga  | gcttgtggaa  | tggcagatga   | 180 |
| atccacctac | tggtttcaaa  | cacaaagtca  | ctgataatct  | ccaaagatgg  | ataattgaag   | 240 |
| ttattggagc | tccaggaact  | ctatatgcca  | acgatactta  | tcagcttcaa  | gttgattttc   | 300 |
| cagaacatta | tcctatggaa  | tgcgccacaag | tgatttttct  | tcattccagct | cctctgcatc   | 360 |
| ctcacattta | cagcaatggg  | catatttgtc  | tagatatattt | gtatgattcg  | tggtctccag   | 420 |
| ccatgacggt | gagttctatc  | tgcatttagca | tcctctccat  | gctctcaagc  | tcgactgaaa   | 480 |
| agcaacgacc | aaccgataat  | gacogatatg  | tgaagaattg  | taagaacgga  | agatctccaa   | 540 |
| aggagacccg | atggttggttc | cacgacgata  | aagtataaac  | ctcgatcaac  | caaaaaaaaaat | 600 |
| gtaaaatagt | ccaaaacagt  | ctttgagggtt | tgttgtctat  | ttttaattta  | attgggttta   | 660 |
| agctgtccca | aacccatttc  | caaaatccgt  | gatgtataaa  | aacaacacaa  | taaatttgac   | 720 |
| taattttgaa | tcttcc      |             |             |             |              |     |

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Glu Pro Phe Asp Phe Arg Phe Phe Leu Glu Pro Ser Phe Leu Pro Ser |  |
| 1 5 10 15                                                       |  |
| Xaa Leu Leu Gln Glu Asp Phe Asp Cys Leu Leu Thr Leu Ser Met Ser |  |
| 20 25 30                                                        |  |
| Ser Ser Gly Ala Pro Ser Arg Lys Thr Leu Ser Lys Ile Ala Thr Asn |  |
| 35 40 45                                                        |  |
| Arg Leu Gln Lys Glu Leu Val Glu Trp Gln Met Asn Pro Pro Thr Gly |  |
| 50 55 60                                                        |  |
| Phe Lys His Lys Val Thr Asp Asn Leu Gln Arg Trp Ile Ile Glu Val |  |
| 65 70 75 80                                                     |  |
| Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn Asp Thr Tyr Gln Leu Gln |  |
| 85 90 95                                                        |  |
| Val Asp Phe Pro Glu His Tyr Pro Met Glu Ser Pro Gln Val Ile Phe |  |
| 100 105 110                                                     |  |

Leu His Pro Ala Pro Leu His Pro His Ile Tyr Ser Asn Gly His Ile  
115 120 125  
Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser Pro Ala Met Thr Val Ser  
130 135 140  
Ser Ile Cys Ile Ser Ile Leu Ser Met Leu Ser Ser Ser Thr Glu Lys  
145 150 155 160  
Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val Lys Asn Cys Lys Asn Gly  
165 170 175  
Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe His Asp Asp Lys Val  
180 185 190

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1570585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Ser Ser Ser Gly Ala Pro Ser Arg Lys Thr Leu Ser Lys Ile Ala  
1 5 10 15  
Thr Asn Arg Leu Gln Lys Glu Leu Val Glu Trp Gln Met Asn Pro Pro  
20 25 30  
Thr Gly Phe Lys His Lys Val Thr Asp Asn Leu Gln Arg Trp Ile Ile  
35 40 45  
Glu Val Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn Asp Thr Tyr Gln  
50 55 60  
Leu Gln Val Asp Phe Pro Glu His Tyr Pro Met Glu Ser Pro Gln Val  
65 70 75 80  
Ile Phe Leu His Pro Ala Pro Leu His Pro His Ile Tyr Ser Asn Gly  
85 90 95  
His Ile Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser Pro Ala Met Thr  
100 105 110  
Val Ser Ser Ile Cys Ile Ser Ile Leu Ser Met Leu Ser Ser Ser Thr  
115 120 125  
Glu Lys Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val Lys Asn Cys Lys  
130 135 140  
Asn Gly Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe His Asp Asp Lys  
145 150 155 160  
Val

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1570586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Asn Pro Pro Thr Gly Phe Lys His Lys Val Thr Asp Asn Leu Gln  
1 5 10 15  
Arg Trp Ile Ile Glu Val Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn  
20 25 30  
Asp Thr Tyr Gln Leu Gln Val Asp Phe Pro Glu His Tyr Pro Met Glu

35 40 45  
Ser Pro Gln Val Ile Phe Leu His Pro Ala Pro Leu His Pro His Ile  
50 55 60  
Tyr Ser Asn Gly His Ile Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser  
65 70 75 80  
Pro Ala Met Thr Val Ser Ser Ile Cys Ile Ser Ile Leu Ser Met Leu  
85 90 95  
Ser Ser Ser Thr Glu Lys Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val  
100 105 110  
Lys Asn Cys Lys Asn Gly Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe  
115 120 125  
His Asp Asp Lys Val  
130

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..936
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ctagacgtcg aagatgaaGt tcaacGTbga gaatccaact actggatgcc agaagaagct   | 60  |
| cgagatcgac gatgaccaga aactacgtgc gttttacgac aagagaatct ctcaagaagt   | 120 |
| cagtggagat gctttgggagc aggagttcaa aggatacggt ttcaagatca aggggtggttg | 180 |
| cgataagcaa ggtttcccaa tgaagcaggg agttttgact ccaggccgtg ttcgcctttt   | 240 |
| gcttcaccga ggaactcctt gcttcagagg acatggaagg akaactggtg agaggagaag   | 300 |
| aaagtctgtt cgtggttgca ttgtgagccc tgatctctct gttctgaacc ttgtcattgt   | 360 |
| gaagaagggt gagaacgata ttctgtgggt taccgatact gagaagccaa gaatgagagg   | 420 |
| accaaagaga gcctccaaga tccgtaaact gtttaacctc aagaaggaag atgatgtcag   | 480 |
| gacctatgtc aacacttacc gccgcaagtt cacaacaag aagggaag aagttagcaa      | 540 |
| agcccctaag atccagaggc ttgtgacccc attgactctt cagaggaaga gagctagaat   | 600 |
| tgctgacaag aagaagaaaa ttgctaaggc taattctgat gctgctgatt accagaagct   | 660 |
| tctcgctctg aggttgaagg aacagcgtga caggaggagt gagagtttgg caaagaagag   | 720 |
| gtcgagactc tcttctgctg ctgccaaagg ctctgtcaca gcttaaaaaa gcttgagaat   | 780 |
| caaatacaag atgtcAcSSc tttctvgttt tgttctcttt tcttctccgg ctattaaaaa   | 840 |
| gttagttcga gttcatattc agctgttttt gttccaagac atgggtacac aatcgctttg   | 900 |
| ggcttgtttc atgatttatg cttttagttg aagacc                             |     |

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

Met Lys Phe Asn Xaa Glu Asn Pro Thr Thr Gly Cys Gln Lys Lys Leu  
1 5 10 15  
Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg Ile  
20 25 30  
Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr  
35 40 45  
Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys  
50 55 60

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly  
65 70 75 80  
Thr Pro Cys Phe Arg Gly His Gly Arg Xaa Thr Gly Glu Arg Arg Arg  
85 90 95  
Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn  
100 105 110  
Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp  
115 120 125  
Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg  
130 135 140  
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn  
145 150 155 160  
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys  
165 170 175  
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys  
180 185 190  
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser  
195 200 205  
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln  
210 215 220  
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser  
225 230 235 240  
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala  
245 250

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1570605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

Met Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His  
1 5 10 15  
Arg Gly Thr Pro Cys Phe Arg Gly His Gly Arg Xaa Thr Gly Glu Arg  
20 25 30  
Arg Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val  
35 40 45  
Leu Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu  
50 55 60  
Thr Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys  
65 70 75 80  
Ile Arg Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr  
85 90 95  
Val Asn Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val  
100 105 110  
Ser Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln  
115 120 125  
Arg Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala  
130 135 140  
Asn Ser Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys  
145 150 155 160  
Glu Gln Arg Asp Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg  
165 170 175  
Leu Ser Ser Ala Ala Ala Lys Pro Ser Val Thr Ala  
180 185

(2) INFORMATION FOR SEQ ID NO:1660:

| (xi)     | SEQUENCE DESCRIPTION: SEQ ID NO:1660: |             |             |            |            |  |  |     |
|----------|---------------------------------------|-------------|-------------|------------|------------|--|--|-----|
| cgctcgaa | gatgaagttc                            | aacgttgcgg  | agttcaaagg  | atacgttttc | aagatcaagg |  |  | 60  |
| gtttgcga | taagcaaggt                            | ttcccaatga  | agcagggagt  | tttgactcca | ggcgtgttc  |  |  | 120 |
| ctttgct  | tcacogagga                            | actccttgct  | tcagaggaca  | tggaaggaga | actggtgaga |  |  | 180 |
| gaagaaa  | gtctgttcgt                            | ggttgcatctg | tgagccctga  | tctctctgtt | ctgaaccttg |  |  | 240 |
| ctgtgaa  | gaagggtgag                            | aacgatcttc  | ctgggcttac  | cgatactgag | aagccaagaa |  |  | 300 |
| gaggacc  | aaagagagcc                            | tccaagatcc  | gtaaacctgtt | taacctcaag | aaggaagatg |  |  | 360 |
| tcaggac  | ctatgtcaac                            | acttacccgc  | gcaagttcac  | aaacaagaag | ggcaaggaag |  |  | 420 |
| gcaaaagc | ccctaagatc                            | cagaggcttg  | tgaccccatc  | gactcttcag | aggaagagag |  |  | 480 |
| gaattgc  | tgacaagaag                            | aagaaaattg  | ctaaggctaa  | ttctgatgct | gctgattacc |  |  | 540 |
| agcttct  | cgctcgagg                             | ttgaaggaac  | agcgtgacag  | gaggagtgag | agTttggcAa |  |  | 600 |
| agaggtc  | gagactctct                            | tctgctgctg  | ccaagccctc  | tgtcacagct | taaaaaagct |  |  | 660 |
| gaatcaa  | atcaaaagatg                           | tcacctttct  | agtCtttgtt  | ctctttttct | ctccggctat |  |  | 720 |
| aaagtta  | gttcaggttc                            | atattcagct  | gtttttgttc  | caagacatgg | gtacacaatc |  |  | 780 |
| ttggct   | tgtttcatga                            | tttatgcttt  | tagttgaaga  | ccattttaaa | ctc        |  |  |     |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1570607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Lys | Met | Lys | Phe | Asn | Val | Ala | Glu | Phe | Lys | Gly | Tyr | Val | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ile | Lys | Gly | Gly | Cys | Asp | Lys | Gln | Gly | Phe | Pro | Met | Lys | Gln | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Thr | Pro | Gly | Arg | Val | Arg | Leu | Leu | Leu | His | Arg | Gly | Thr | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Phe | Arg | Gly | His | Gly | Arg | Arg | Thr | Gly | Glu | Arg | Arg | Arg | Lys | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Arg | Gly | Cys | Ile | Val | Ser | Pro | Asp | Leu | Ser | Val | Leu | Asn | Leu | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Val | Lys | Lys | Gly | Glu | Asn | Asp | Leu | Pro | Gly | Leu | Thr | Asp | Thr | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Pro | Arg | Met | Arg | Gly | Pro | Lys | Arg | Ala | Ser | Lys | Ile | Arg | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Asn | Leu | Lys | Lys | Glu | Asp | Asp | Val | Arg | Thr | Tyr | Val | Asn | Thr | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Arg | Lys | Phe | Thr | Asn | Lys | Lys | Gly | Lys | Glu | Val | Ser | Lys | Ala | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ile | Gln | Arg | Leu | Val | Thr | Pro | Leu | Thr | Leu | Gln | Arg | Lys | Arg | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Ile | Ala | Asp | Lys | Lys | Lys | Lys | Ile | Ala | Lys | Ala | Asn | Ser | Asp | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Asp | Tyr | Gln | Lys | Leu | Leu | Ala | Ser | Arg | Leu | Lys | Glu | Gln | Arg | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser Ser Ala  
195 200 205  
Ala Ala Lys Pro Ser Val Thr Ala  
210 215

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

Met Lys Phe Asn Val Ala Glu Phe Lys Gly Tyr Val Phe Lys Ile Lys  
1 5 10 15  
Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys Gln Gly Val Leu Thr  
20 25 30  
Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro Cys Phe Arg  
35 40 45  
Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg Lys Ser Val Arg Gly  
50 55 60  
Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn Leu Val Ile Val Lys  
65 70 75 80  
Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu Lys Pro Arg  
85 90 95  
Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu Phe Asn Leu  
100 105 110  
Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr Tyr Arg Arg Lys  
115 120 125  
Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala Pro Lys Ile Gln  
130 135 140  
Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg Ala Arg Ile Ala  
145 150 155 160  
Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp Ala Ala Asp Tyr  
165 170 175  
Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg Asp Arg Arg Ser  
180 185 190  
Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser Ser Ala Ala Ala Lys  
195 200 205  
Pro Ser Val Thr Ala  
210

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

Met Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His  
1 5 10 15  
Arg Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg  
20 25 30  
Arg Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val

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35 40 45  
Leu Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu  
50 55 60  
Thr Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys  
65 70 75 80  
Ile Arg Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr  
85 90 95  
Val Asn Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val  
100 105 110  
Ser Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln  
115 120 125  
Arg Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala  
130 135 140  
Asn Ser Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys  
145 150 155 160  
Glu Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg  
165 170 175  
Leu Ser Ser Ala Ala Ala Lys Pro Ser Val Thr Ala  
180 185

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..721
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

agtttagatt ctttatccga ctactttggt catcggtttt gtttttcttt ttgtcttccg 60  
gaaggcgaat tacatgtcgg aagcagcaca gctcagaaga ggtctaaagc ctaaaggga 120  
gacttatggg ttgaccaatc agaagagacg agagatcaga gagatctttg atcttttcga 180  
catagacggg tcaggtagca tcgatgctag cgagctcaac gttgctatga ggtctcttgg 240  
atttgagatg aataatcagc aaataaacga attgatggca gaagtagata aaaaccaaaag 300  
tgagagccata gatttcgacg aatttgtgca tatgatgaca accaaattcg gagaacgaga 360  
ctccatagac gaattgtcta aggcgtttta gatcattgac cagacaata gtgggaagat 420  
ttcacctcgt gatataaaga tgatttgctaa agaattggga gaaaatttca cagataatga 480  
tatagaagaa atgatcgaag aagcagaccg tgacaaagat ggagaagtta acttggagga 540  
gttcatgaaS gatgatgaag agaacctctt tcggctaagt ataaatcaat tagtaatggt 600  
tgtgaataat atttggttaat caccttgatt tataataata aagaagtttg atttgggct 660  
tggtcgaata aaaatgtatt gttgtataaa aataataatg taattcacat ccattatattt 720

g

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

Met Ser Glu Ala Ala Gln Leu Arg Arg Gly Leu Lys Pro Lys Gly Lys  
1 5 10 15  
Thr Tyr Gly Leu Thr Asn Gln Lys Arg Arg Glu Ile Arg Glu Ile Phe  
20 25 30  
Asp Leu Phe Asp Ile Asp Gly Ser Gly Ser Ile Asp Ala Ser Glu Leu

35 40 45  
Asn Val Ala Met Arg Ser Leu Gly Phe Glu Met Asn Asn Gln Gln Ile  
50 55 60  
Asn Glu Leu Met Ala Glu Val Asp Lys Asn Gln Ser Gly Ala Ile Asp  
65 70 75 80  
Phe Asp Glu Phe Val His Met Met Thr Thr Lys Phe Gly Glu Arg Asp  
85 90 95  
Ser Ile Asp Glu Leu Ser Lys Ala Phe Lys Ile Ile Asp His Asp Asn  
100 105 110  
Ser Gly Lys Ile Ser Pro Arg Asp Ile Lys Met Ile Ala Lys Glu Leu  
115 120 125  
Gly Glu Asn Phe Thr Asp Asn Asp Ile Glu Glu Met Ile Glu Glu Ala  
130 135 140  
Asp Arg Asp Lys Asp Gly Glu Val Asn Leu Glu Glu Phe Met Xaa Asp  
145 150 155 160  
Asp Glu Glu Asn Leu Phe Arg Leu Ser Ile Asn Gln Leu Val Met Val  
165 170 175  
Val Asn Asn Ile Cys  
180

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1570612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

Met Arg Ser Leu Gly Phe Glu Met Asn Asn Gln Gln Ile Asn Glu Leu  
1 5 10 15  
Met Ala Glu Val Asp Lys Asn Gln Ser Gly Ala Ile Asp Phe Asp Glu  
20 25 30  
Phe Val His Met Met Thr Thr Lys Phe Gly Glu Arg Asp Ser Ile Asp  
35 40 45  
Glu Leu Ser Lys Ala Phe Lys Ile Ile Asp His Asp Asn Ser Gly Lys  
50 55 60  
Ile Ser Pro Arg Asp Ile Lys Met Ile Ala Lys Glu Leu Gly Glu Asn  
65 70 75 80  
Phe Thr Asp Asn Asp Ile Glu Glu Met Ile Glu Glu Ala Asp Arg Asp  
85 90 95  
Lys Asp Gly Glu Val Asn Leu Glu Glu Phe Met Xaa Asp Asp Glu Glu  
100 105 110  
Asn Leu Phe Arg Leu Ser Ile Asn Gln Leu Val Met Val Val Asn Asn  
115 120 125  
Ile Cys  
130

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1570613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

Met Asn Asn Gln Gln Ile Asn Glu Leu Met Ala Glu Val Asp Lys Asn  
1 5 10 15  
Gln Ser Gly Ala Ile Asp Phe Asp Glu Phe Val His Met Met Thr Thr  
20 25 30  
Lys Phe Gly Glu Arg Asp Ser Ile Asp Glu Leu Ser Lys Ala Phe Lys  
35 40 45  
Ile Ile Asp His Asp Asn Ser Gly Lys Ile Ser Pro Arg Asp Ile Lys  
50 55 60  
Met Ile Ala Lys Glu Leu Gly Glu Asn Phe Thr Asp Asn Asp Ile Glu  
65 70 75 80  
Glu Met Ile Glu Glu Ala Asp Arg Asp Lys Asp Gly Glu Val Asn Leu  
85 90 95  
Glu Glu Phe Met Xaa Asp Asp Glu Glu Asn Leu Phe Arg Leu Ser Ile  
100 105 110  
Asn Gln Leu Val Met Val Val Asn Asn Ile Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| actcagagac ttgttgtgaa gttgaaactc tctgaccgta gctttcttat ccttcattca | 60  |
| ggttcactac tatgtacagt ctcacattca aatgaatgag taccgggatc gtgttgatt  | 120 |
| gccatctgct tcaaagaaac agggacgacc aatttgact tgttgaaaa ttttgatat    | 180 |
| gtctgggtta aagctttcag ctttaagtca aattaagtta atgactgcta taacaacaat | 240 |
| agatgatttg aactatccag agaagacaga gacatactat gttgtcaatg tcccgtacat | 300 |
| attctctgct tgttgaaaa ccataaagcc tctgttgcaa gagagaacaa agaagaagat  | 360 |
| tcaagttctg aaaggttgcg ggaaagatga gttgctaaag ataatggact atgagtctct | 420 |
| cccacatttc tgtagaagag aagggtctgg atctggtagg catatctcaa atggaacagt | 480 |
| agacaattgt ttctctctgg atcactcttt ccaccaagac ctttatgatt atgtcaagca | 540 |
| gcaggctctg gttaaaggat caggtgcacc gatcagacat ggttcagtc acgttaagtt  | 600 |
| ccctgagcca gacaccgaag gcaacaagat cttcgatacc ttagaaaatg agttccagaa | 660 |
| gcttggaat gaccagaaga tctgagtgtat ctacaacct tataacacga attgccata   | 720 |
| agaaaccgga atttgtctct ggttgatgag cagtatttaa gataagaatc aatcaccttt | 780 |
| acttgattta ctagtttcgc ttgcatcagc tMcgatgcag gttttgytta aaaagaagat | 840 |
| ggaacacaat ttctctggaa tggatctttt gatctagtac cattatatat atagaactca | 900 |
| tttctattta tgtccttttg cc                                          |     |

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys Lys  
1 5 10 15  
Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser Gly  
20 25 30  
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile Thr

35 40 45  
Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr Glu Thr Tyr Tyr Val  
50 55 60  
Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp Lys Thr Ile Lys Pro  
65 70 75 80  
Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln Val Leu Lys Gly Cys  
85 90 95  
Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr Glu Ser Leu Pro His  
100 105 110  
Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg His Ile Ser Asn Gly  
115 120 125  
Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser Phe His Gln Asp Leu  
130 135 140  
Tyr Asp Tyr Val Lys Gln Ala Leu Val Lys Gly Ser Gly Ala Pro  
145 150 155 160  
Ile Arg His Gly Ser Val His Val Lys Phe Pro Glu Pro Asp Thr Glu  
165 170 175  
Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu Phe Gln Lys Leu Gly  
180 185 190  
Asn Asp Gln Lys Ile  
195

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

Met Ser Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr  
1 5 10 15  
Ala Ile Thr Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr Glu Thr  
20 25 30  
Tyr Tyr Val Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp Lys Thr  
35 40 45  
Ile Lys Pro Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln Val Leu  
50 55 60  
Lys Gly Cys Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr Glu Ser  
65 70 75 80  
Leu Pro His Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg His Ile  
85 90 95  
Ser Asn Gly Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser Phe His  
100 105 110  
Gln Asp Leu Tyr Asp Tyr Val Lys Gln Gln Ala Leu Val Lys Gly Ser  
115 120 125  
Gly Ala Pro Ile Arg His Gly Ser Val His Val Lys Phe Pro Glu Pro  
130 135 140  
Asp Thr Glu Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu Phe Gln  
145 150 155 160  
Lys Leu Gly Asn Asp Gln Lys Ile  
165

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..154  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570621  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

Met Thr Ala Ile Thr Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr  
1                  5                  10                  15  
Glu Thr Tyr Tyr Val Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp  
                  20                  25                  30  
Lys Thr Ile Lys Pro Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln  
                  35                  40                  45  
Val Leu Lys Gly Cys Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr  
                  50                  55                  60  
Glu Ser Leu Pro His Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg  
65                  70                  75                  80  
His Ile Ser Asn Gly Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser  
                  85                  90                  95  
Phe His Gln Asp Leu Tyr Asp Tyr Val Lys Gln Gln Ala Leu Val Lys  
                  100                 105                 110  
Gly Ser Gly Ala Pro Ile Arg His Gly Ser Val His Val Lys Phe Pro  
                 115                 120                 125  
Glu Pro Asp Thr Glu Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu  
130                 135                 140  
Phe Gln Lys Leu Gly Asn Asp Gln Lys Ile  
145                 150

(2) INFORMATION FOR SEQ ID NO:1672:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1082 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1082  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

gttttgtctc ctttctaagc cgcacactat cttttcctct cactcagact tcctcttcat 60  
ctcaagagaa atggctgaat ccaaggtagt gggtccagag tctgtgctaa agaagatcaa 120  
gaggcaagag gaatgggcat tggccaagaa agatgaagct gtagctgcta agaagaagag 180  
tggtgaggcc cgcaagctta ttttcaagag agctgagcag tatgccaaag aatacgctga 240  
gaaggataac gagttgatcc gattgaagcg ggaggctaag ttgaaaggag gtttctacgt 300  
tgacctgag gctaagttgc tttttatcat tcgtatccgt ggtatcaatg ccattgaccc 360  
aaaaaccaag aagattctgc agctcctgcg tttgagacag gtaggtttca cagtttgta 420  
ttttcatcca gctatattag cctaacatat gattattgat taatatttgt tatatgttca 480  
aactaatatg tgatagttgc ctgttcatca tttttaaaag agagtagaag actattgcgt 540  
tgtcaagaag tttactttcg tatacatttg tgcagatctt caatgggtgtg tttcttaagg 600  
tgaacaaggc aacagtaaac atGctgcgcc gagttgaacc atacgtgact tacggatacc 660  
caaacttgaa gagcgttaag gaactgatct acaaaagagg ttatggaaag ctgaaccacc 720  
agaggatagc acttactgac aactccattg tggatcaggc tctcgaaaag catgggatca 780  
tctgcgttga ggatctcatc cagcagatca tgactgttgg acctcacttc aaggaagcca 840  
acaacttcct gtggccattc caattgaagg caccactcgg tggccttaag aagaagagaa 900  
accactacgt cgaagggtgg gatgctggaa acagggagaa tttcatcaac gagcttgtca 960  
ggagaatgaa ttgatgaaag cttccttctt tatctttgca aatttcaaag attttgggac 1020  
cgagtttttt tttttttttg ttcaagttat cagagacttg tgatctttta tccgagatag 1080  
gc

(2) INFORMATION FOR SEQ ID NO:1673:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 147 amino acids  
    (B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..147  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570623  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

Phe Cys Pro Pro Ser Thr Pro His Thr Ile Phe Ser Ser His Ser Asp  
1                  5                  10                  15  
Phe Leu Phe Ile Ser Arg Glu Met Ala Glu Ser Lys Val Val Val Pro  
                  20                  25                  30  
Glu Ser Val Leu Lys Lys Ile Lys Arg Gln Glu Glu Trp Ala Leu Ala  
                  35                  40                  45  
Lys Lys Asp Glu Ala Val Ala Ala Lys Lys Lys Ser Val Glu Ala Arg  
                  50                  55                  60  
Lys Leu Ile Phe Lys Arg Ala Glu Gln Tyr Ala Lys Glu Tyr Ala Glu  
65                  70                  75                  80  
Lys Asp Asn Glu Leu Ile Arg Leu Lys Arg Glu Ala Lys Leu Lys Gly  
                  85                  90                  95  
Gly Phe Tyr Val Asp Pro Glu Ala Lys Leu Leu Phe Ile Ile Arg Ile  
                  100                  105                  110  
Arg Gly Ile Asn Ala Ile Asp Pro Lys Thr Lys Lys Ile Leu Gln Leu  
                  115                  120                  125  
Leu Arg Leu Arg Gln Val Gly Phe Thr Val Cys Tyr Phe His Pro Ala  
130                  135                  140  
Ile Leu Ala  
145

(2) INFORMATION FOR SEQ ID NO:1674:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 124 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..124  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570624  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

Met Ala Glu Ser Lys Val Val Val Pro Glu Ser Val Leu Lys Lys Ile  
1                  5                  10                  15  
Lys Arg Gln Glu Glu Trp Ala Leu Ala Lys Lys Asp Glu Ala Val Ala  
                  20                  25                  30  
Ala Lys Lys Lys Ser Val Glu Ala Arg Lys Leu Ile Phe Lys Arg Ala  
                  35                  40                  45  
Glu Gln Tyr Ala Lys Glu Tyr Ala Glu Lys Asp Asn Glu Leu Ile Arg  
50                  55                  60  
Leu Lys Arg Glu Ala Lys Leu Lys Gly Gly Phe Tyr Val Asp Pro Glu  
65                  70                  75                  80  
Ala Lys Leu Leu Phe Ile Ile Arg Ile Arg Gly Ile Asn Ala Ile Asp  
                  85                  90                  95  
Pro Lys Thr Lys Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln Val Gly  
                  100                  105                  110  
Phe Thr Val Cys Tyr Phe His Pro Ala Ile Leu Ala  
115                  120

(2) INFORMATION FOR SEQ ID NO:1675:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 117 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..117
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

Met Leu Arg Arg Val Glu Pro Tyr Val Thr Tyr Gly Tyr Pro Asn Leu  
1 5 10 15  
Lys Ser Val Lys Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn  
20 25 30  
His Gln Arg Ile Ala Leu Thr Asp Asn Ser Ile Val Asp Gln Ala Leu  
35 40 45  
Gly Lys His Gly Ile Ile Cys Val Glu Asp Leu Ile His Glu Ile Met  
50 55 60  
Thr Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe  
65 70 75 80  
Gln Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Lys Arg Asn His Tyr  
85 90 95  
Val Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Phe Ile Asn Glu Leu  
100 105 110  
Val Arg Arg Met Asn  
115

(2) INFORMATION FOR SEQ ID NO:1676:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 784 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..784
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

aatccaatca aaacacacag agagaagaaa aactcagaag aaaagccaaa gagtgaaaca 60  
aaaatggcgt cgacgactct ctcaatcgca acaacaatcc gttcctcatc ttatcctact 120  
ctcgtttcca tcaatcactt cccttcccga accaccacca tcgaattccc ctctcgcttc 180  
ggtggtggtt catcatccac attgaccac cgtgcaacc atctccgtcc aatcgccgcc 240  
gtcgaagctc cggagaaaat cgagaagatc ggatccgaaa tctcatccct aaccctcgaa 300  
gaagctcgta tctctcgta ctatctccaa gacaaattcg gtgtctcccc actctcttta 360  
gCccccgcag cagcggcggt tgctgtctca gccgacggtg gcgcggcggc tgtagtggaa 420  
gagcaaacag agttcgatgt gggttatcaat gaagttccca gcagttcccg tattgcagtg 480  
attaaagctg ttagggcttt aactagcttg gcgttgaagg aagctaagga gctaatacgaa 540  
ggattaccaa agaagtttaa agaaggtatc actaaagatg aagctgaaga aactaagaag 600  
actcttgaag aagctggtgc taaagtctcc attgcttaag gtttttatta aaaaaaaaaa 660  
agaagttggt atcttttctg gaatttgatt ggtcttttgt gttgtttagt atagtttgcg 720  
tctggaattg ttgagaaatt gttgtaattt gaatcacatt tggtttccca ttagctgatt 780  
tcgc

(2) INFORMATION FOR SEQ ID NO:1677:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 212 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..212
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

Asn Pro Ile Lys Thr His Arg Glu Lys Lys Asn Ser Glu Glu Lys Pro  
1 5 10 15  
Lys Ser Glu Thr Lys Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr  
20 25 30  
Ile Arg Ser Ser Ser Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro  
35 40 45  
Ser Arg Thr Thr Thr Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser  
50 55 60  
Ser Ser Thr Leu Thr His Arg Ala Thr His Leu Arg Pro Ile Ala Ala  
65 70 75 80  
Val Glu Ala Pro Glu Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser  
85 90 95  
Leu Thr Leu Glu Glu Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys  
100 105 110  
Phe Gly Val Ser Pro Leu Ser Leu Ala Pro Ala Ala Ala Val Ala  
115 120 125  
Ala Pro Ala Asp Gly Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu  
130 135 140  
Phe Asp Val Val Ile Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val  
145 150 155 160  
Ile Lys Ala Val Arg Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys  
165 170 175  
Glu Leu Ile Glu Gly Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys  
180 185 190  
Asp Glu Ala Glu Glu Thr Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys  
195 200 205  
Val Ser Ile Ala  
210

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1570638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser  
1 5 10 15  
Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro Ser Arg Thr Thr Thr  
20 25 30  
Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser Ser Ser Thr Leu Thr  
35 40 45  
His Arg Ala Thr His Leu Arg Pro Ile Ala Ala Val Glu Ala Pro Glu  
50 55 60  
Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu  
65 70 75 80  
Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro  
85 90 95  
Leu Ser Leu Ala Pro Ala Ala Ala Ala Val Ala Ala Pro Ala Asp Gly  
100 105 110  
Gly Ala Ala Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile  
115 120 125  
Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg  
130 135 140  
Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly  
145 150 155 160  
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu



(2) INFORMATION FOR SEO ID NO:1679:

(A) LENGTH: 1039 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1039

(D) OTHER INFORMATION: / Ceres Seq. ID 1570655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| atattacc    | ttgtagaaa  | gaagaaaaa  | agcaagaac  | acttgacgt   | ttctagatag | 60   |
| agatggaag   | gaaagaagag | gatgttcgag | tgggagctaa | caagttcccg  | gagaggcaac | 120  |
| cgataggtac  | atcggtctag | acggacaaag | actacaagga | gccaccacca  | gctccatttt | 180  |
| tcgagccagg  | cgagctgagt | togtggtcct | tctacagagc | cggaatcgcc  | gagttcatag | 240  |
| ccaccttcct  | gtttctatac | ataacagtat | tgacagtgat | gggagtgaag  | agagcaccaa | 300  |
| acatgtgtgc  | ctctgttgga | atccaaggca | ttgcttgggc | tttcgggtggc | atgatctttg | 360  |
| cccttgctta  | ctgtactgct | ggaatctctg | gtgggcacat | aaaccagcag  | gtgacatttg | 420  |
| gtctgtttct  | ggctcgtaag | ctgtcatttg | cgagagctgt | cttttaccatc | gtgatgcaat | 480  |
| gtctcggagc  | catctgcggc | gcggagtttg | tcaaagGctt | ccagccaaat  | ccttaccaaa | 540  |
| ctctcggcgg  | aggagccaac | acagtcgctc | acggctacac | taagggctct  | ggtttgggtg | 600  |
| ctgagataat  | cggaaccttc | gtccttgtct | acacggctct | ctccgccact  | gacgccaa   | 660  |
| gaagcgctcg  | tgactcccac | gttcggattt | tggcaccact | cccaatcggg  | ttcgtgtgt  | 720  |
| tcttggttca  | cttggcgacg | attccaatca | ccggaacagg | aattaacca   | gtcaggagtc | 780  |
| ttggagctgc  | aatcatctac | aacaaggacc | acgcttgga  | cgaccactgg  | atattctggg | 840  |
| tcggaccatt  | cattggagca | gctottgogg | ctctttacca | ccaacttgtc  | atcagagcca | 900  |
| ttccattcaa  | gtccagatcc | tgatttgatt | tctttcttta | taaaacttca  | ttgttgcatc | 960  |
| ttggtttgta  | attcagcttg | aaaatatttg | agagatctgg | atcatgtgtt  | tattttaatt | 1020 |
| aatggaacttg | tctttttct  |            |            |             |            |      |

(2) INFORMATION FOR SEO ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Lys | Glu | Glu | Asp | Val | Arg | Val | Gly | Ala | Asn | Lys | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Arg | Gln | Pro | Ile | Gly | Thr | Ser | Ala | Gln | Thr | Asp | Lys | Asp | Tyr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Pro | Pro | Pro | Ala | Pro | Phe | Phe | Glu | Pro | Gly | Glu | Leu | Ser | Ser | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Tyr | Arg | Ala | Gly | Ile | Ala | Glu | Phe | Ile | Ala | Thr | Phe | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Tyr | Ile | Thr | Val | Leu | Thr | Val | Met | Gly | Val | Lys | Arg | Ala | Pro | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Cys | Ala | Ser | Val | Gly | Ile | Gln | Gly | Ile | Ala | Trp | Ala | Phe | Gly | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Ile | Phe | Ala | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly | Gly | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly | Leu | Phe | Leu | Ala | Arg | Lys | Leu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Leu Thr Arg Ala Val Phe Tyr Ile Val Met Gln Cys Leu Gly Ala Ile  
130 135 140  
Cys Gly Ala Gly Val Val Lys Gly Phe Gln Pro Asn Pro Tyr Gln Thr  
145 150 155 160  
Leu Gly Gly Gly Ala Asn Thr Val Ala His Gly Tyr Thr Lys Gly Ser  
165 170 175  
Gly Leu Gly Ala Glu Ile Ile Gly Thr Phe Val Leu Val Tyr Thr Val  
180 185 190  
Phe Ser Ala Thr Asp Ala Lys Arg Ser Ala Arg Asp Ser His Val Pro  
195 200 205  
Ile Leu Ala Pro Leu Pro Ile Gly Phe Ala Val Phe Leu Val His Leu  
210 215 220  
Ala Thr Ile Pro Ile Thr Gly Thr Gly Ile Asn Pro Ala Arg Ser Leu  
225 230 235 240  
Gly Ala Ala Ile Ile Tyr Asn Lys Asp His Ala Trp Asp Asp His Trp  
245 250 255  
Ile Phe Trp Val Gly Pro Phe Ile Gly Ala Ala Leu Ala Ala Leu Tyr  
260 265 270  
His Gln Leu Val Ile Arg Ala Ile Pro Phe Lys Ser Arg Ser  
275 280 285

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

Met Gly Val Lys Arg Ala Pro Asn Met Cys Ala Ser Val Gly Ile Gln  
1 5 10 15  
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ala Leu Val Tyr Cys  
20 25 30  
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly  
35 40 45  
Leu Phe Leu Ala Arg Lys Leu Ser Leu Thr Arg Ala Val Phe Tyr Ile  
50 55 60  
Val Met Gln Cys Leu Gly Ala Ile Cys Gly Ala Gly Val Val Lys Gly  
65 70 75 80  
Phe Gln Pro Asn Pro Tyr Gln Thr Leu Gly Gly Gly Ala Asn Thr Val  
85 90 95  
Ala His Gly Tyr Thr Lys Gly Ser Gly Leu Gly Ala Glu Ile Ile Gly  
100 105 110  
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Ala Lys Arg  
115 120 125  
Ser Ala Arg Asp Ser His Val Pro Ile Leu Ala Pro Leu Pro Ile Gly  
130 135 140  
Phe Ala Val Phe Leu Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr  
145 150 155 160  
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys  
165 170 175  
Asp His Ala Trp Asp Asp His Trp Ile Phe Trp Val Gly Pro Phe Ile  
180 185 190  
Gly Ala Ala Leu Ala Ala Leu Tyr His Gln Leu Val Ile Arg Ala Ile  
195 200 205  
Pro Phe Lys Ser Arg Ser  
210

(2) INFORMATION FOR SEQ ID NO:1682:

SEQUENCE CHARACTERISTICS

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 206 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..206  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570658  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Ala | Ser | Val | Gly | Ile | Gln | Gly | Ile | Ala | Trp | Ala | Phe | Gly | Gly |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Met | Ile | Phe | Ala | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly | Gly | His |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly | Leu | Phe | Leu | Ala | Arg | Lys | Leu | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Leu | Thr | Arg | Ala | Val | Phe | Tyr | Ile | Val | Met | Gln | Cys | Leu | Gly | Ala | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Ala | Gly | Val | Val | Lys | Gly | Phe | Gln | Pro | Asn | Pro | Tyr | Gln | Thr |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Gly | Gly | Gly | Ala | Asn | Thr | Val | Ala | His | Gly | Tyr | Thr | Lys | Gly | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Leu | Gly | Ala | Glu | Ile | Ile | Gly | Thr | Phe | Val | Leu | Val | Tyr | Thr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Ala | Thr | Asp | Ala | Lys | Arg | Ser | Ala | Arg | Asp | Ser | His | Val | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu | Ala | Pro | Leu | Pro | Ile | Gly | Phe | Ala | Val | Phe | Leu | Val | His | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Ile | Pro | Ile | Thr | Gly | Thr | Gly | Ile | Asn | Pro | Ala | Arg | Ser | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Ala | Ala | Ile | Ile | Tyr | Asn | Lys | Asp | His | Ala | Trp | Asp | Asp | His | Trp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Phe | Trp | Val | Gly | Pro | Phe | Ile | Gly | Ala | Ala | Leu | Ala | Ala | Leu | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Gln | Leu | Val | Ile | Arg | Ala | Ile | Pro | Phe | Lys | Ser | Arg | Ser |     |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1142 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1142  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570669  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| aagcacttca  | ctctctaatt | tccttctctc | tatctctcac  | catattcgcg  | attaaaaact | 60  |
| ctcaactttt  | ctctcaaatt | tctgatacct | taatccaaca  | gttagaagaa  | gattcatctg | 120 |
| atcatggccc  | tcgaagcgat | gaacactcca | acttcttctt  | tcaccagaat  | cgaaacgaaa | 180 |
| gaagatttga  | tgaacgacgc | cgttttcatt | gagccgtggc  | ttaaacgcaa  | acgctccaaa | 240 |
| cgtcagcggt  | ctcacagccc | ttcttogtct | tcttctctac  | cgctctgata  | tcgacccaaa | 300 |
| tcccagaatc  | aagatcttac | ggaagaagag | tatctcgctc  | tttgtctcct  | catgctcgct | 360 |
| aaagatcaac  | cgtcgcaaac | gcgatttcat | caacagtogc  | aatcgttaac  | gccgccgcca | 420 |
| gaatcaaaga  | accttccgta | caagtgtaac | gtctgtgaaa  | aagcgtttcc  | ttcctatcag | 480 |
| gcttttaggcg | gtcacaaagc | aagtcaccga | atcaaaccac  | caaccgtaat  | ctcaacaact | 540 |
| gccgatgatt  | caacagctcc | gaccatctcc | atcgctcgccg | gagaaaaaca  | tccgattgct | 600 |
| gcctccggaa  | agatCcacga | gtgttcaatc | tgtcataaag  | tgtttccgac  | gggtcaagct | 660 |
| ttaggcggtc  | acaaacgttg | tcactacgaa | ggcaacctcg  | gcggcgaggag | aggaggagga | 720 |

```
agcaaatcaa tcagtcacag tggaagcgtg tcgagcacgg tatcggaaga aaggagccac 780
cgtggattca tcgatctaaa cctaccggcg ttacctgaac tcagccttca tcacaatcca 840
atcgtcgacg aagagatctt gagtccgttg accggtaaaa aaccgctttt gttgaccgat 900
cacgaccaag tcatcaagaa agaagattta tctttaaaaa tctaatactc gactattaat 960
tcttggtgtt tcatcttcat ttttttagtt acaaattttt aattgttctg atttggttg 1020
aatattggta tattgttagg gattgataca aaaatttgat gattgattaa gtcagaattt 1080
ctttttaatt atggttaacta atctcttgat cagtccactc tgtataaata ttgcgtggca 1140
tt
```

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1570670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

```
Met Ala Leu Glu Ala Met Asn Thr Pro Thr Ser Ser Phe Thr Arg Ile
1 5 10 15
Glu Thr Lys Glu Asp Leu Met Asn Asp Ala Val Phe Ile Glu Pro Trp
20 25 30
Leu Lys Arg Lys Arg Ser Lys Arg Gln Arg Ser His Ser Pro Ser Ser
35 40 45
Ser Ser Ser Ser Pro Pro Arg Ser Arg Pro Lys Ser Gln Asn Gln Asp
50 55 60
Leu Thr Glu Glu Glu Tyr Leu Ala Leu Cys Leu Met Leu Ala Lys
65 70 75 80
Asp Gln Pro Ser Gln Thr Arg Phe His Gln Gln Ser Gln Ser Leu Thr
85 90 95
Pro Pro Pro Glu Ser Lys Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu
100 105 110
Lys Ala Phe Pro Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His
115 120 125
Arg Ile Lys Pro Pro Thr Val Ile Ser Thr Thr Ala Asp Asp Ser Thr
130 135 140
Ala Pro Thr Ile Ser Ile Val Ala Gly Glu Lys His Pro Ile Ala Ala
145 150 155 160
Ser Gly Lys Ile His Glu Cys Ser Ile Cys His Lys Val Phe Pro Thr
165 170 175
Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Asn Leu
180 185 190
Gly Gly Gly Gly Gly Gly Ser Lys Ser Ile Ser His Ser Gly Ser
195 200 205
Val Ser Ser Thr Val Ser Glu Arg Ser His Arg Gly Phe Ile Asp
210 215 220
Leu Asn Leu Pro Ala Leu Pro Glu Leu Ser Leu His His Asn Pro Ile
225 230 235 240
Val Asp Glu Glu Ile Leu Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu
245 250 255
Leu Thr Asp His Asp Gln Val Ile Lys Lys Glu Asp Leu Ser Leu Lys
260 265 270
Ile
```

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..268  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570671  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

Met Asn Thr Pro Thr Ser Ser Phe Thr Arg Ile Glu Thr Lys Glu Asp  
1                  5                  10                  15  
Leu Met Asn Asp Ala Val Phe Ile Glu Pro Trp Leu Lys Arg Lys Arg  
          20                  25                  30  
Ser Lys Arg Gln Arg Ser His Ser Pro Ser Ser Ser Ser Ser Pro  
          35                  40                  45  
Pro Arg Ser Arg Pro Lys Ser Gln Asn Gln Asp Leu Thr Glu Glu Glu  
          50                  55                  60  
Tyr Leu Ala Leu Cys Leu Leu Met Leu Ala Lys Asp Gln Pro Ser Gln  
65                  70                  75                  80  
Thr Arg Phe His Gln Gln Ser Gln Ser Leu Thr Pro Pro Pro Glu Ser  
          85                  90                  95  
Lys Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu Lys Ala Phe Pro Ser  
          100                 105                 110  
Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Ile Lys Pro Pro  
          115                 120                 125  
Thr Val Ile Ser Thr Thr Ala Asp Asp Ser Thr Ala Pro Thr Ile Ser  
130                 135                 140  
Ile Val Ala Gly Glu Lys His Pro Ile Ala Ala Ser Gly Lys Ile His  
145                 150                 155                 160  
Glu Cys Ser Ile Cys His Lys Val Phe Pro Thr Gly Gln Ala Leu Gly  
          165                 170                 175  
Gly His Lys Arg Cys His Tyr Glu Gly Asn Leu Gly Gly Gly Gly Gly  
          180                 185                 190  
Gly Gly Ser Lys Ser Ile Ser His Ser Gly Ser Val Ser Ser Thr Val  
195                 200                 205  
Ser Glu Glu Arg Ser His Arg Gly Phe Ile Asp Leu Asn Leu Pro Ala  
210                 215                 220  
Leu Pro Glu Leu Ser Leu His His Asn Pro Ile Val Asp Glu Glu Ile  
225                 230                 235                 240  
Leu Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu Leu Thr Asp His Asp  
          245                 250                 255  
Gln Val Ile Lys Lys Glu Asp Leu Ser Leu Lys Ile  
          260                 265

(2) INFORMATION FOR SEQ ID NO:1686:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 251 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..251  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570672  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

Met Asn Asp Ala Val Phe Ile Glu Pro Trp Leu Lys Arg Lys Arg Ser  
1                  5                  10                  15  
Lys Arg Gln Arg Ser His Ser Pro Ser Ser Ser Ser Ser Pro Pro  
          20                  25                  30  
Arg Ser Arg Pro Lys Ser Gln Asn Gln Asp Leu Thr Glu Glu Glu Tyr  
          35                  40                  45  
Leu Ala Leu Cys Leu Leu Met Leu Ala Lys Asp Gln Pro Ser Gln Thr  
50                  55                  60

Arg Phe His Gln Gln Ser Gln Ser Leu Thr Pro Pro Pro Glu Ser Lys  
65 70 75 80  
Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu Lys Ala Phe Pro Ser Tyr  
85 90 95  
Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Ile Lys Pro Pro Thr  
100 105 110  
Val Ile Ser Thr Thr Ala Asp Asp Ser Thr Ala Pro Thr Ile Ser Ile  
115 120 125  
Val Ala Gly Glu Lys His Pro Ile Ala Ala Ser Gly Lys Ile His Glu  
130 135 140  
Cys Ser Ile Cys His Lys Val Phe Pro Thr Gly Gln Ala Leu Gly Gly  
145 150 155 160  
His Lys Arg Cys His Tyr Glu Gly Asn Leu Gly Gly Gly Gly Gly  
165 170 175  
Gly Ser Lys Ser Ile Ser His Ser Gly Ser Val Ser Ser Thr Val Ser  
180 185 190  
Glu Glu Arg Ser His Arg Gly Phe Ile Asp Leu Asn Leu Pro Ala Leu  
195 200 205  
Pro Glu Leu Ser Leu His His Asn Pro Ile Val Asp Glu Glu Ile Leu  
210 215 220  
Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu Leu Thr Asp His Asp Gln  
225 230 235 240  
Val Ile Lys Lys Glu Asp Leu Ser Leu Lys Ile  
245 250

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1083
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ttttttacga tctggtgctg gataagcctt ttgcttcatt ctcaacttct tctcatcca   | 60   |
| aaaaagctcc tccatttcaa tggcgacaGc atcagctctc tcatcactct cttcactctc  | 120  |
| actccacacc cgaacctctt ctctcatctc ctcttcctcc acaaaatcca tcgtctcttt  | 180  |
| ctctctcttc ctcaaccgcc gcttctcatc tctcactctc gtcaaagcct catcgaccga  | 240  |
| taccgaaacc atcttcttcg aagacgaaac accagaaata accgcaaag tcgtcttcga   | 300  |
| cccaccaatt gctcccgaag attcgtctct cctccgtatt tcgacgaagg aagcgacgag  | 360  |
| acagaggaag agatcgctac cgcttttgaa gagctctatg gacctgcgta tagtggtgag  | 420  |
| agtatgcttg ggaaagatat ttatgtgatg gactcaaagc ataagaagag ttcagggtatt | 480  |
| ggtgggaagc caaagaaaga taagattaga gatgggtttg aagagagagt tgtgcaagtt  | 540  |
| aggagagtga ctaaggttgt taaaggaggg aagcaattga agtttagagc tatcgttggt  | 600  |
| gttggtgata aacaaggga tgttggtggt ggttggtgcta aggctaaaga agttggtgct  | 660  |
| gctgttcaga aatctgctat tgatgctagg agaaacattg ttcaagttcc tatgactaag  | 720  |
| tattctactt tccctcacag atcagaggtt gattatggag cagccaaggt gatgcttaga  | 780  |
| cctgcttcac caggtaactg tgtgattgct ggaggagcgg ttaggattgt gctagagatg  | 840  |
| gcaggagtcg agaatgcatt ggggaaacag cttggaagca acaatgctct caacaatgcg  | 900  |
| agagccactc ttgcagcagt acaacagatg agacagttcc gcgatgttgc acaagagcgt  | 960  |
| ggaatcccca tggaagaact ctggaagtga aaactcatct tcgctttaac attttcatcc  | 1020 |
| tcttttggtg agatttcttg taatgatgta attcatgaga aaatatgttt attttgaaat  | 1080 |

agc

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..329  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570682  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

Phe Phe Thr Ile Trp Cys Trp Ile Ser Leu Leu Leu His Ser His Phe  
1                    5                    10                    15  
Leu Pro His Pro Lys Lys Leu Leu His Phe Asn Gly Asp Ser Ile Ser  
                    20                    25                    30  
Ser Leu Ile Thr Leu Phe Thr Leu Thr Pro His Pro Asn Leu Phe Ser  
                    35                    40                    45  
His Leu Leu Phe Leu His Lys Ile His Arg Leu Phe Leu Leu Leu Pro  
50                    55                    60  
Gln Pro Pro Leu Leu Ile Ser His Ser Arg Gln Ser Leu Ile Asp Arg  
65                    70                    75                    80  
Tyr Arg Asn His Leu Leu Arg Arg Arg Asn Thr Arg Asn Asn Arg Lys  
                    85                    90                    95  
Cys Arg Leu Arg Pro Thr Asn Cys Ser Arg Arg Phe Val Ser Pro Pro  
100                    105                    110  
Tyr Phe Asp Glu Gly Ser Asp Glu Thr Glu Glu Glu Ile Ala Thr Ala  
115                    120                    125  
Phe Glu Glu Leu Tyr Gly Pro Ala Tyr Ser Gly Glu Ser Met Leu Gly  
130                    135                    140  
Lys Asp Ile Tyr Val Met Asp Ser Lys His Lys Lys Ser Ser Gly Ile  
145                    150                    155                    160  
Gly Gly Lys Pro Lys Lys Asp Lys Ile Arg Asp Gly Phe Glu Glu Arg  
                    165                    170                    175  
Val Val Gln Val Arg Arg Val Thr Lys Val Val Lys Gly Gly Lys Gln  
180                    185                    190  
Leu Lys Phe Arg Ala Ile Val Val Val Gly Asp Lys Gln Gly Asn Val  
195                    200                    205  
Gly Val Gly Cys Ala Lys Ala Lys Glu Val Val Ala Ala Val Gln Lys  
210                    215                    220  
Ser Ala Ile Asp Ala Arg Arg Asn Ile Val Gln Val Pro Met Thr Lys  
225                    230                    235                    240  
Tyr Ser Thr Phe Pro His Arg Ser Glu Gly Asp Tyr Gly Ala Ala Lys  
                    245                    250                    255  
Val Met Leu Arg Pro Ala Ser Pro Gly Thr Gly Val Ile Ala Gly Gly  
260                    265                    270  
Ala Val Arg Ile Val Leu Glu Met Ala Gly Val Glu Asn Ala Leu Gly  
275                    280                    285  
Lys Gln Leu Gly Ser Asn Asn Ala Leu Asn Asn Ala Arg Ala Thr Leu  
290                    295                    300  
Ala Ala Val Gln Gln Met Arg Gln Phe Arg Asp Val Ala Gln Glu Arg  
305                    310                    315                    320  
Gly Ile Pro Met Glu Glu Leu Trp Lys  
                    325

(2) INFORMATION FOR SEQ ID NO:1689:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 188 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..188  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570683  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

Met Leu Gly Lys Asp Ile Tyr Val Met Asp Ser Lys His Lys Lys Ser

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1 5 10 15  
Ser Gly Ile Gly Gly Lys Pro Lys Lys Asp Lys Ile Arg Asp Gly Phe  
20 25 30  
Glu Glu Arg Val Val Gln Val Arg Arg Val Thr Lys Val Val Lys Gly  
35 40 45  
Gly Lys Gln Leu Lys Phe Arg Ala Ile Val Val Val Gly Asp Lys Gln  
50 55 60  
Gly Asn Val Gly Val Gly Cys Ala Lys Ala Lys Glu Val Val Ala Ala  
65 70 75 80  
Val Gln Lys Ser Ala Ile Asp Ala Arg Arg Asn Ile Val Gln Val Pro  
85 90 95  
Met Thr Lys Tyr Ser Thr Phe Pro His Arg Ser Glu Gly Asp Tyr Gly  
100 105 110  
Ala Ala Lys Val Met Leu Arg Pro Ala Ser Pro Gly Thr Gly Val Ile  
115 120 125  
Ala Gly Gly Ala Val Arg Ile Val Leu Glu Met Ala Gly Val Glu Asn  
130 135 140  
Ala Leu Gly Lys Gln Leu Gly Ser Asn Asn Ala Leu Asn Asn Ala Arg  
145 150 155 160  
Ala Thr Leu Ala Ala Val Gln Gln Met Arg Gln Phe Arg Asp Val Ala  
165 170 175  
Gln Glu Arg Gly Ile Pro Met Glu Glu Leu Trp Lys  
180 185

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1570684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

Met Asp Ser Lys His Lys Lys Ser Ser Gly Ile Gly Gly Lys Pro Lys  
1 5 10 15  
Lys Asp Lys Ile Arg Asp Gly Phe Glu Arg Val Val Gln Val Arg  
20 25 30  
Arg Val Thr Lys Val Val Lys Gly Gly Lys Gln Leu Lys Phe Arg Ala  
35 40 45  
Ile Val Val Val Gly Asp Lys Gln Gly Asn Val Gly Val Gly Cys Ala  
50 55 60  
Lys Ala Lys Glu Val Val Ala Ala Val Gln Lys Ser Ala Ile Asp Ala  
65 70 75 80  
Arg Arg Asn Ile Val Gln Val Pro Met Thr Lys Tyr Ser Thr Phe Pro  
85 90 95  
His Arg Ser Glu Gly Asp Tyr Gly Ala Ala Lys Val Met Leu Arg Pro  
100 105 110  
Ala Ser Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Val Arg Ile Val  
115 120 125  
Leu Glu Met Ala Gly Val Glu Asn Ala Leu Gly Lys Gln Leu Gly Ser  
130 135 140  
Asn Asn Ala Leu Asn Asn Ala Arg Ala Thr Leu Ala Ala Val Gln Gln  
145 150 155 160  
Met Arg Gln Phe Arg Asp Val Ala Gln Glu Arg Gly Ile Pro Met Glu  
165 170 175  
Glu Leu Trp Lys  
180

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 1547 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1547  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570692  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

```
actctctttc tttctcatgt tctttttcggc cagaacaaaa ctccctaata caaatgtcaa 60
ttccttttggc ctctctctga ataactcatc ctcttcaaac cctattcaat ttttaactatc 120
gatcttcggc taagtctcca atggcgggcgg cggttgccctc tcttcccaca tttagtgtcg 180
tcaattcctc cagattttccc agaagaagaa tcggtttttc ttgctccaaa aagcccctcg 240
aagttcggtg ttcttccggc aatactcggt acactaagca gagaggggca tttacatcat 300
tgaagaatg tgcgatttca ttagctttat cgggttggtt aatggtttca gtaccttcga 360
ttgctttgcc tcccaatgct cagcgaGtGg cgaatccagt gattccagat gtttcagtgt 420
tgatctccgg tctctcgatt aaagatccgg aagctttact aagatatgca ttgcctattg 480
acaacaaagc catcagggaa gtgcagaagc ctcttgagga tatcactgat agcctcaaga 540
ttgctggcgt taaggctcta gattctgttg aacggaatgt gaggcaggca agtagaacat 600
tgcagcaagg gaaaagtata attgtggcag gttttgctga atcgaagaag gatcatggta 660
atgaaatgat tgaaaagtgt gaagctggga tgcaagatat gcttaagata gtggaagatc 720
gaaaaagaga cgcagttgct ccaaaacaga aagaaattct caaatatggt ggcggaatag 780
aagaggatat gggttgatggc ttcccatatg aagtgcgga agagtatcgg aacatgcctc 840
tctcaagggt aagagctagt gtggacatga aggtcaagat caaggacaat cccaacatcg 900
aggactgtgt gttccgcatt gttcttgatg gttataacgc ccctgttacc gccggaaact 960
ttgtggactt ggtagagagg catttctacg atggcatgga gatccagaga tctgatggat 1020
ttgtggtaca aacgggagat ccagaggggtc ctgcggaagg atttatcgat ccaagcacag 1080
agaaaacgag gacggttcct ctagagatta tgggtgactgg agagaaaacg ccttttttacg 1140
gctcaactct tgaagaactt ggtctttaca aggtcaggt tgtgattcct ttcaacgctt 1200
ttgggacaat ggcaatggca agagaagagt ttgagaatga ctcaggatca agccaagtgt 1260
tttggtgctt aaaagagagt gagctgacac caagcaattc caacatcttg gatggtcgtt 1320
acgctgtctt tggttacggt actgataacg aagattttct agctgatctt aaagtgtgtg 1380
atgttatcga atccattcaa gttgtctccg gtttagagaa cctcgctaac ccgagttaca 1440
aaatcgccgg ttaactcctc ttatcttttt ccttttcttg gttcgtaatt aatactctgt 1500
ttattttaat tttgtgagag tatattaaag gtgcattgct ttttccc
```

(2) INFORMATION FOR SEQ ID NO:1692:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 437 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..437  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

```
Met Ala Ala Ala Phe Ala Ser Leu Pro Thr Phe Ser Val Val Asn Ser
1 5 10 15
Ser Arg Phe Pro Arg Arg Arg Ile Gly Phe Ser Cys Ser Lys Lys Pro
 20 25 30
Leu Glu Val Arg Cys Ser Ser Gly Asn Thr Arg Tyr Thr Lys Gln Arg
 35 40 45
Gly Ala Phe Thr Ser Leu Lys Glu Cys Ala Ile Ser Leu Ala Leu Ser
 50 55 60
Val Gly Leu Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala
 65 70 75 80
His Ala Val Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser
 85 90 95
Gly Pro Pro Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro
```

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
|                                                                 | 100 |     | 105 |     | 110 |
| Ile Asp Asn Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile |     |     |     |     |     |
| 115                                                             |     | 120 |     | 125 |     |
| Thr Asp Ser Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu |     |     |     |     |     |
| 130                                                             |     | 135 |     | 140 |     |
| Arg Asn Val Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile |     |     |     |     |     |
| 145                                                             |     | 150 |     | 155 | 160 |
| Ile Val Ala Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met |     |     |     |     |     |
|                                                                 | 165 |     | 170 |     | 175 |
| Ile Glu Lys Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu |     |     |     |     |     |
|                                                                 | 180 |     | 185 |     | 190 |
| Asp Arg Lys Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys |     |     |     |     |     |
|                                                                 | 195 |     | 200 |     | 205 |
| Tyr Val Gly Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu |     |     |     |     |     |
|                                                                 | 210 |     | 215 |     | 220 |
| Val Pro Glu Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala Ser |     |     |     |     |     |
| 225                                                             |     | 230 |     | 235 | 240 |
| Val Asp Met Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp Cys |     |     |     |     |     |
|                                                                 | 245 |     | 250 |     | 255 |
| Val Phe Arg Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala Gly |     |     |     |     |     |
|                                                                 | 260 |     | 265 |     | 270 |
| Asn Phe Val Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu Ile |     |     |     |     |     |
|                                                                 | 275 |     | 280 |     | 285 |
| Gln Arg Ser Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly Pro |     |     |     |     |     |
|                                                                 | 290 |     | 295 |     | 300 |
| Ala Glu Gly Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val Pro |     |     |     |     |     |
| 305                                                             |     | 310 |     | 315 | 320 |
| Leu Glu Ile Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser Thr |     |     |     |     |     |
|                                                                 | 325 |     | 330 |     | 335 |
| Leu Glu Glu Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe Asn |     |     |     |     |     |
|                                                                 | 340 |     | 345 |     | 350 |
| Ala Phe Gly Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp Ser |     |     |     |     |     |
|                                                                 | 355 |     | 360 |     | 365 |
| Gly Ser Ser Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr Pro |     |     |     |     |     |
|                                                                 | 370 |     | 375 |     | 380 |
| Ser Asn Ser Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr Val |     |     |     |     |     |
| 385                                                             |     | 390 |     | 395 | 400 |
| Thr Asp Asn Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val Ile |     |     |     |     |     |
|                                                                 | 405 |     | 410 |     | 415 |
| Glu Ser Ile Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro Ser |     |     |     |     |     |
|                                                                 | 420 |     | 425 |     | 430 |
| Tyr Lys Ile Ala Gly                                             |     |     |     |     |     |
| 435                                                             |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..370

(D) OTHER INFORMATION: / Ceres Seq. ID 1570694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala His Ala Val |    |    |
| 1                                                               | 5  | 10 |
| Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser Gly Pro Pro |    |    |
|                                                                 | 20 | 30 |
| Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro Ile Asp Asn |    |    |
| 35                                                              | 40 | 45 |

Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile Thr Asp Ser  
50 55 60  
Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu Arg Asn Val  
65 70 75 80  
Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile Ile Val Ala  
85 90 95  
Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met Ile Glu Lys  
100 105 110  
Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu Asp Arg Lys  
115 120 125  
Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys Tyr Val Gly  
130 135 140  
Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu Val Pro Glu  
145 150 155 160  
Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala Ser Val Asp Met  
165 170 175  
Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp Cys Val Phe Arg  
180 185 190  
Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala Gly Asn Phe Val  
195 200 205  
Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu Ile Gln Arg Ser  
210 215 220  
Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly Pro Ala Glu Gly  
225 230 235 240  
Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val Pro Leu Glu Ile  
245 250 255  
Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser Thr Leu Glu Glu  
260 265 270  
Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe Asn Ala Phe Gly  
275 280 285  
Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp Ser Gly Ser Ser  
290 295 300  
Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr Pro Ser Asn Ser  
305 310 315 320  
Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr Val Thr Asp Asn  
325 330 335  
Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val Ile Glu Ser Ile  
340 345 350  
Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro Ser Tyr Lys Ile  
355 360 365  
Ala Gly  
370

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1570695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

Met Ile Glu Lys Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val  
1 5 10 15  
Glu Asp Arg Lys Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu  
20 25 30  
Lys Tyr Val Gly Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr  
35 40 45  
Glu Val Pro Glu Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala

50 55 60  
Ser Val Asp Met Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp  
65 70 75 80  
Cys Val Phe Arg Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala  
85 90 95  
Gly Asn Phe Val Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu  
100 105 110  
Ile Gln Arg Ser Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly  
115 120 125  
Pro Ala Glu Gly Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val  
130 135 140  
Pro Leu Glu Ile Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser  
145 150 155 160  
Thr Leu Glu Glu Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe  
165 170 175  
Asn Ala Phe Gly Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp  
180 185 190  
Ser Gly Ser Ser Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr  
195 200 205  
Pro Ser Asn Ser Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr  
210 215 220  
Val Thr Asp Asn Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val  
225 230 235 240  
Ile Glu Ser Ile Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro  
245 250 255  
Ser Tyr Lys Ile Ala Gly  
260

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

atcgattagg gtttaggaac cttgtcatcg gaaatcattt cttgtctttg tttgtttattc 60  
gaagcttctc ctgcttattt gatacatatt ctctcttcca gttactctac atggaaccat 120  
tcgttggttaa ggagaacatc gtcgcacccg cttcttcgcc gatgaagaag cgacggatcg 180  
atcacactga gtcagctgat gggtctgcga ttaacgcttc taactctagt agcatcggtg 240  
gtaacgatac ggtgatgaac atggcggagt ttggtaacga caactccaac aatcaggagt 300  
ctcaacaagt ttgcactttc ttcaagaagc caacgaaaag taaaaacata aggaaaagaa 360  
ccattgacgc tgatgaagaa gacggagatt cgaaaagcga aagctctatt ttacaaaatc 420  
taaagaaagt tgcaaaaccc gatagcaact tgtacttttc ttctggacca tctactagaa 480  
cgagtggagc tcctgagaga ccggtttttc actacgattc atccaaggaa atccaggttc 540  
agaacgacag tggagcaaca gcgacccttg aaactgaaac cgacttcaat caagacgctc 600  
gagctatccg tgaaagagtt cttaaaaaag cagaccatgc attgaagggg aataagaaaa 660  
aggcttcaga tgagaagctg tacaaaggaa ttcattggata tacagatcac aaagctgggt 720  
ttagaagaga acaaacaatc tcgagcgaga aagctggagg ctcacacggg cctttaagag 780  
cttctgctca catcagagta tcggctagat tcgattacca gccagacatt tgcaaggatt 840  
acaaggaaac cggtactgtt ggatatggag attcgtgtaa gttcttgcac gaccgtgggg 900  
attacaagcc Gggatggcag atagagaaag agtggaaga ggcagagaaa gtttaggaaga 960  
gaaataaagc tatgggagtt gaggatgacg atgatgagg tgacaaggat agcgacgaag 1020  
acgaaaatgc attgcccttt gcttgcttca tttgcaggga gccttttctt gatccagttg 1080  
tcaccaaagt caagcattac ttctgtgagc attgtgcttt aaagcatcac acgaagaaca 1140  
agaaatgctt tgtgtgtaac caaccaacaa tggggatttt caatgcagca catgagatca 1200  
agaagaggat ggctgaagaa cggagtaaaag ctgaacaagg attgtgaagt ccttctttca 1260  
caggacaaaa aggcaaaaac tatacatttg attatttgct tgaggaaaagc tttttgtttt 1320

gttgactca ctggcctata tactgtatat tcggatgacg atggttgttt caaactgatt 1380  
aacttttaaa ttt

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..414
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Gly | Phe | Arg | Asn | Leu | Val | Ile | Gly | Asn | His | Phe | Leu | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Val | Ile | Arg | Ser | Phe | Ser | Cys | Leu | Phe | Asp | Thr | Tyr | Ser | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Leu | Tyr | Met | Glu | Pro | Phe | Val | Val | Lys | Glu | Asn | Ile | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Ser | Ser | Pro | Met | Lys | Lys | Arg | Arg | Ile | Asp | His | Thr | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Asp | Gly | Ser | Ala | Ile | Asn | Ala | Ser | Asn | Ser | Ser | Ser | Ile | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Asp | Thr | Val | Met | Asn | Met | Ala | Glu | Phe | Gly | Asn | Asp | Asn | Ser | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gln | Glu | Ser | Gln | Gln | Val | Cys | Thr | Phe | Phe | Lys | Lys | Pro | Thr | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Lys | Asn | Ile | Arg | Lys | Arg | Thr | Ile | Asp | Ala | Asp | Glu | Glu | Asp | Gly |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ser | Lys | Ser | Glu | Ser | Ser | Ile | Leu | Gln | Asn | Leu | Lys | Lys | Val | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Pro | Asp | Ser | Asn | Leu | Tyr | Phe | Ser | Ser | Gly | Pro | Ser | Thr | Arg | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gly | Ala | Pro | Glu | Arg | Pro | Val | Phe | His | Tyr | Asp | Ser | Ser | Lys | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Gln | Val | Gln | Asn | Asp | Ser | Gly | Ala | Thr | Ala | Thr | Leu | Glu | Thr | Glu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Asp | Phe | Asn | Gln | Asp | Ala | Arg | Ala | Ile | Arg | Glu | Arg | Val | Leu | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Ala | Asp | His | Ala | Leu | Lys | Gly | Asn | Lys | Lys | Lys | Ala | Ser | Asp | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Leu | Tyr | Lys | Gly | Ile | His | Gly | Tyr | Thr | Asp | His | Lys | Ala | Gly | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Arg | Glu | Gln | Thr | Ile | Ser | Ser | Glu | Lys | Ala | Gly | Gly | Ser | His | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Leu | Arg | Ala | Ser | Ala | His | Ile | Arg | Val | Ser | Ala | Arg | Phe | Asp | Tyr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Pro | Asp | Ile | Cys | Lys | Asp | Tyr | Lys | Glu | Thr | Gly | Tyr | Cys | Gly | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Asp | Ser | Cys | Lys | Phe | Leu | His | Asp | Arg | Gly | Asp | Tyr | Lys | Pro | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Trp | Gln | Ile | Glu | Lys | Glu | Trp | Glu | Glu | Ala | Glu | Lys | Val | Arg | Lys | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Asn | Lys | Ala | Met | Gly | Val | Glu | Asp | Asp | Asp | Asp | Glu | Ala | Asp | Lys | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Asp | Glu | Asp | Glu | Asn | Ala | Leu | Pro | Phe | Ala | Cys | Phe | Ile | Cys | Arg |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Pro | Phe | Leu | Asp | Pro | Val | Val | Thr | Lys | Cys | Lys | His | Tyr | Phe | Cys |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Glu | His | Cys | Ala | Leu | Lys | His | His | Thr | Lys | Asn | Lys | Lys | Cys | Phe | Val |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 370                                                             | 375 | 380 |
| Cys Asn Gln Pro Thr Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys |     |     |
| 385                                                             | 390 | 395 |
| Lys Arg Met Ala Glu Arg Ser Lys Ala Glu Gln Gly Leu             |     | 400 |
| 405                                                             | 410 |     |

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1570698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Pro | Phe | Val | Val | Lys | Glu | Asn | Ile | Val | Ala | Ser | Ala | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Met | Lys | Lys | Arg | Arg | Ile | Asp | His | Thr | Glu | Ser | Ala | Asp | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Asn | Ala | Ser | Asn | Ser | Ser | Ser | Ile | Gly | Gly | Asn | Asp | Thr | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Met | Ala | Glu | Phe | Gly | Asn | Asp | Asn | Ser | Asn | Asn | Gln | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Gln | Val | Cys | Thr | Phe | Phe | Lys | Lys | Pro | Thr | Lys | Ser | Lys | Asn | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Lys | Arg | Thr | Ile | Asp | Ala | Asp | Glu | Glu | Asp | Gly | Asp | Ser | Lys | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Ser | Ser | Ile | Leu | Gln | Asn | Leu | Lys | Lys | Val | Ala | Lys | Pro | Asp | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Tyr | Phe | Ser | Ser | Gly | Pro | Ser | Thr | Arg | Thr | Ser | Gly | Ala | Pro |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Glu | Arg | Pro | Val | Phe | His | Tyr | Asp | Ser | Ser | Lys | Glu | Ile | Gln | Val | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asn | Asp | Ser | Gly | Ala | Thr | Ala | Thr | Leu | Glu | Thr | Glu | Thr | Asp | Phe | Asn |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Asp | Ala | Arg | Ala | Ile | Arg | Glu | Arg | Val | Leu | Lys | Lys | Ala | Asp | His |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Lys | Gly | Asn | Lys | Lys | Lys | Ala | Ser | Asp | Glu | Lys | Leu | Tyr | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ile | His | Gly | Tyr | Thr | Asp | His | Lys | Ala | Gly | Phe | Arg | Arg | Glu | Gln |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Thr | Ile | Ser | Ser | Glu | Lys | Ala | Gly | Gly | Ser | His | Gly | Pro | Leu | Arg | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ala | His | Ile | Arg | Val | Ser | Ala | Arg | Phe | Asp | Tyr | Gln | Pro | Asp | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Cys | Lys | Asp | Tyr | Lys | Glu | Thr | Gly | Tyr | Cys | Gly | Tyr | Gly | Asp | Ser | Cys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Lys | Phe | Leu | His | Asp | Arg | Gly | Asp | Tyr | Lys | Pro | Gly | Trp | Gln | Ile | Glu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Glu | Trp | Glu | Glu | Ala | Glu | Lys | Val | Arg | Lys | Arg | Asn | Lys | Ala | Met |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Val | Glu | Asp | Asp | Asp | Asp | Glu | Ala | Asp | Lys | Asp | Ser | Asp | Glu | Asp |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Asn | Ala | Leu | Pro | Phe | Ala | Cys | Phe | Ile | Cys | Arg | Glu | Pro | Phe | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Asp | Pro | Val | Val | Thr | Lys | Cys | Lys | His | Tyr | Phe | Cys | Glu | His | Cys | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Lys | His | His | Thr | Lys | Asn | Lys | Lys | Cys | Phe | Val | Cys | Asn | Gln | Pro |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |

Thr Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys Lys Arg Met Ala  
355 360 365  
Glu Glu Arg Ser Lys Ala Glu Gln Gly Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1570699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

Met Lys Lys Arg Arg Ile Asp His Thr Glu Ser Ala Asp Gly Ser Ala  
1 5 10 15  
Ile Asn Ala Ser Asn Ser Ser Ser Ile Gly Gly Asn Asp Thr Val Met  
20 25 30  
Asn Met Ala Glu Phe Gly Asn Asp Asn Ser Asn Asn Gln Glu Ser Gln  
35 40 45  
Gln Val Cys Thr Phe Phe Lys Lys Pro Thr Lys Ser Lys Asn Ile Arg  
50 55 60  
Lys Arg Thr Ile Asp Ala Asp Glu Glu Asp Gly Asp Ser Lys Ser Glu  
65 70 75 80  
Ser Ser Ile Leu Gln Asn Leu Lys Lys Val Ala Lys Pro Asp Ser Asn  
85 90 95  
Leu Tyr Phe Ser Ser Gly Pro Ser Thr Arg Thr Ser Gly Ala Pro Glu  
100 105 110  
Arg Pro Val Phe His Tyr Asp Ser Ser Lys Glu Ile Gln Val Gln Asn  
115 120 125  
Asp Ser Gly Ala Thr Ala Thr Leu Glu Thr Glu Thr Asp Phe Asn Gln  
130 135 140  
Asp Ala Arg Ala Ile Arg Glu Arg Val Leu Lys Lys Ala Asp His Ala  
145 150 155 160  
Leu Lys Gly Asn Lys Lys Lys Ala Ser Asp Glu Lys Leu Tyr Lys Gly  
165 170 175  
Ile His Gly Tyr Thr Asp His Lys Ala Gly Phe Arg Arg Glu Gln Thr  
180 185 190  
Ile Ser Ser Glu Lys Ala Gly Gly Ser His Gly Pro Leu Arg Ala Ser  
195 200 205  
Ala His Ile Arg Val Ser Ala Arg Phe Asp Tyr Gln Pro Asp Ile Cys  
210 215 220  
Lys Asp Tyr Lys Glu Thr Gly Tyr Cys Gly Tyr Gly Asp Ser Cys Lys  
225 230 235 240  
Phe Leu His Asp Arg Gly Asp Tyr Lys Pro Gly Trp Gln Ile Glu Lys  
245 250 255  
Glu Trp Glu Glu Ala Glu Lys Val Arg Lys Arg Asn Lys Ala Met Gly  
260 265 270  
Val Glu Asp Asp Asp Asp Glu Ala Asp Lys Asp Ser Asp Glu Asp Glu  
275 280 285  
Asn Ala Leu Pro Phe Ala Cys Phe Ile Cys Arg Glu Pro Phe Leu Asp  
290 295 300  
Pro Val Val Thr Lys Cys Lys His Tyr Phe Cys Glu His Cys Ala Leu  
305 310 315 320  
Lys His His Thr Lys Asn Lys Lys Cys Phe Val Cys Asn Gln Pro Thr  
325 330 335  
Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys Lys Arg Met Ala Glu  
340 345 350  
Glu Arg Ser Lys Lys Ala Glu Gln Gly Leu

SEQUENCE LISTING

355 360

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..609

(D) OTHER INFORMATION: / Ceres Seq. ID 1570716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| gaaaaatggt | gaaaaaagcg | tattagcaga | Gggacaaacg | cttttttaggg | tttttagattt | 60  |
| cctctgagag | agaattttcg | aaagcttcag | agagatttcc | aactacgtta  | gccatggcga  | 120 |
| gcaccaaagt | tcaaaggatt | atgacccaac | ctatcaactt | gatttttagg  | tttcttcaaa  | 180 |
| gtaaagctag | gatccagatt | tggtctattg | agcagaaaga | tttgaggatt  | gaaggaagaa  | 240 |
| tcactgggtt | tgacgaatac | atgaatctag | ttttggatga | ggctgaagaa  | gtgagcatca  | 300 |
| agaagaacac | caggaaacca | cttgaagga  | ttttactcaa | aggagacaac  | ataactctga  | 360 |
| tgatgaacac | gggaaagtga | tgtctgtctc | aaacaactct | cttcgatgac  | cttcaagctt  | 420 |
| atgttaaata | tctgttgagt | tcttcctcag | cttaattggg | acttgacgat  | accttctttt  | 480 |
| cttcaatgtc | gtataatata | ttgcaatgta | gtgagtgaca | aaggagcttg  | atcgaatcta  | 540 |
| gtggattggg | tggttaaaac | ttcaaaaaag | agatttggtc | ccttttggtt  | aaatctagtg  | 600 |
| taatttggc  |            |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1570717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Thr | Lys | Val | Gln | Arg | Ile | Met | Thr | Gln | Pro | Ile | Asn | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Phe | Arg | Phe | Leu | Gln | Ser | Lys | Ala | Arg | Ile | Gln | Ile | Trp | Leu | Phe |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gln | Lys | Asp | Leu | Arg | Ile | Glu | Gly | Arg | Ile | Thr | Gly | Phe | Asp | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Tyr | Met | Asn | Leu | Val | Leu | Asp | Glu | Ala | Glu | Glu | Val | Ser | Ile | Lys | Lys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Asn | Thr | Arg | Lys | Pro | Leu | Gly | Arg | Ile | Leu | Leu | Lys | Gly | Asp | Asn | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Leu | Met | Met | Asn | Thr | Gly | Lys |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1570718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Gln | Pro | Ile | Asn | Leu | Ile | Phe | Arg | Phe | Leu | Gln | Ser | Lys | Ala |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



1 5 10 15  
Arg Ile Gln Ile Trp Leu Phe Glu Gln Lys Asp Leu Arg Ile Glu Gly  
20 25 30  
Arg Ile Thr Gly Phe Asp Glu Tyr Met Asn Leu Val Leu Asp Glu Ala  
35 40 45  
Glu Glu Val Ser Ile Lys Lys Asn Thr Arg Lys Pro Leu Gly Arg Ile  
50 55 60  
Leu Leu Lys Gly Asp Asn Ile Thr Leu Met Met Asn Thr Gly Lys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atcacacaac | tcacaattac | aaaagctaaa  | cagttctcta | aaatcaaadc | aagttttttt | 60  |
| cgaagagaag | attagaaaat | gtctaacWaa  | cagtcagagc | atgagcttca | acgcaggcca | 120 |
| agctaaaggc | caaactcagg | agaaggcaag  | caacttgatg | gacaaggcct | ccaatgctgc | 180 |
| ccaatctgct | aaggaatcta | tccaagaggg  | tggacagcag | ctgaagcaga | aggcacaagg | 240 |
| tgcgagttag | accattaagg | aaaagaccgg  | catcagcaaa | tgagaagcac | gttctaataa | 300 |
| taatttatgt | tttctgtttt | cgttttttatt | ctaccagaaa | taataattag | atagatatgt | 360 |
| ctatctaaat | ccaagactat | ggattttcgat | cgaagccatt | taggcgatta | cttttgcttt | 420 |
| tctatgtttt | ttttatatat | ctatatatct  | aagagttttt | gactcttgtc | tattgataat | 480 |
| ttgtagccat | gcagttattt | ctataatatt  | taaataaatg | acatgwttac | atg        |     |

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

Ser His Asn Ser Gln Leu Gln Lys Leu Asn Ser Ser Leu Lys Ser Asn  
1 5 10 15  
Gln Val Phe Phe Glu Glu Lys Ile Arg Lys Cys Leu Xaa Asn Ser Gln  
20 25 30  
Ser Met Ser Phe Asn Ala Gly Gln Ala Lys Gly Gln Thr Gln Glu Lys  
35 40 45  
Ala Ser Asn Leu Met Asp Lys Ala Ser Asn Ala Ala Gln Ser Ala Lys  
50 55 60  
Glu Ser Ile Gln Glu Gly Gly Gln Gln Leu Lys Gln Lys Ala Gln Gly  
65 70 75 80  
Ala Ser Glu Thr Ile Lys Glu Lys Thr Gly Ile Ser Lys  
85 90

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1570721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

```
Met Ser Phe Asn Ala Gly Gln Ala Lys Gly Gln Thr Gln Glu Lys Ala
1 5 10 15
Ser Asn Leu Met Asp Lys Ala Ser Asn Ala Ala Gln Ser Ala Lys Glu
 20 25 30
Ser Ile Gln Glu Gly Gly Gln Gln Leu Lys Gln Lys Ala Gln Gly Ala
 35 40 45
Ser Glu Thr Ile Lys Glu Lys Thr Gly Ile Ser Lys
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1062

(D) OTHER INFORMATION: / Ceres Seq. ID 1570735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

```
aatgatctga tctgatctcc caaaaattcc caaatccaaa tctacgaatc tccgtctcct 60
ccgtcgcatc ttccgaggta gagagagaga tcaaaccaaa gagacacaga gagagtatcc 120
accgatggaa tccgcagcaa cggctgttgt acctccggca gccgccgcca ccaccgccac 180
cgccaccgat gataatctcc aatcaagcga ctcatcatct cccgccgacg ccgttaaccg 240
attgatccac gcccttttcgc agcgacaaca acatcttctc gacaaaacgg ttcttcacgt 300
tctctatcga tggatcgcat gtctctgtgt tgtattgata tacatcggtc gtgtttactt 360
tgtggaaggc ttctacatca tcaattacgc catcggcatc taccttttga atctcatcat 420
tgctttttcta tctcctcaag aagatcccgga agcttctctc acttccggtg gttctcttcc 480
tactcggaga tccgatgagt atcgctcctt cgttcgccgt ctccctgagt tcaaattctg 540
gttatcgatc ataagggcct tcatcatcgg atttatgatg acgttcttcg aggtgtttga 600
tgtacctgta ttctggccaa tactttctct ctactgggtg atgttgtttt tccttacgat 660
gaggaaacag atacagcata tgatcaaata cagatatgtc ctttctctt ttgggaaaaa 720
gcagtatgga aagaaaccgg ctccaacaga gagcagtga tgatcaatca aaactgttca 780
ggtcagcaat tttacagtct tttgagagaa gtagcatttg aaaaggtcgg tcttttggtc 840
tcttttgatg gcctatatct ttgttaggga tgaagtagag atagacatat tttgctcttt 900
tatcatcctg actattttac tggtttcacc tgaactcaat gtacaatctt atttttttac 960
atcctttttt cagtgaagaa ataatgttGt catacttgac ctttttgtaa tcatcatggt 1020
ggaaaactaa agactaatca gtaactactg tccggttcta tc
```

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1570736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

```
Met Glu Ser Ala Ala Thr Ala Val Val Pro Pro Ala Ala Ala Ala Thr
1 5 10 15
Thr Ala Thr Ala Thr Asp Asp Asn Leu Gln Ser Ser Asp Ser Ser Ser
 20 25 30
Pro Ala Asp Ala Val Asn Arg Leu Ile His Ala Phe Ser Gln Arg Gln
 35 40 45
```

Gln His Leu Leu Asp Lys Thr Val Pro His Val Leu Tyr Arg Trp Ile  
50 55 60  
Ala Cys Leu Cys Val Val Leu Ile Tyr Ile Val Arg Val Tyr Phe Val  
65 70 75 80  
Glu Gly Phe Tyr Ile Ile Thr Tyr Ala Ile Gly Ile Tyr Leu Leu Asn  
85 90 95  
Leu Ile Ile Ala Phe Leu Ser Pro Gln Glu Asp Pro Glu Ala Ser Leu  
100 105 110  
Thr Ser Gly Gly Ser Leu Pro Thr Arg Arg Ser Asp Glu Tyr Arg Pro  
115 120 125  
Phe Val Arg Arg Leu Pro Glu Phe Lys Phe Trp Leu Ser Ile Ile Arg  
130 135 140  
Ala Phe Ile Ile Gly Phe Met Met Thr Phe Phe Glu Val Phe Asp Val  
145 150 155 160  
Pro Val Phe Trp Pro Ile Leu Leu Phe Tyr Trp Val Met Leu Phe Phe  
165 170 175  
Leu Thr Met Arg Lys Gln Ile Gln His Met Ile Lys Tyr Arg Tyr Val  
180 185 190  
Pro Phe Ser Phe Gly Lys Lys Gln Tyr Gly Lys Lys Pro Ala Pro Thr  
195 200 205  
Glu Ser Ser Glu  
210

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..562
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atttcatttt | cgttttcact | ttctcogaac | atccaaaagc | ttgtagcttg | ctcctcaa   | 60  |
| cttcttgaaa | aatgaagggt | gcogetgctt | tcctcctcgc | cgttttgggc | ggaaacgcta | 120 |
| atccttcagc | cgagaatatc | aaagatatca | tcggagctgt | tggtgctgat | gttgatggag | 180 |
| agagcattga | gcttctattg | aaagaagtga | gtggtaagga | cattgctgag | ctgattgctt | 240 |
| ctggtagggg | gaaattagcg | tctgtgccat | ctggtgggtg | tgtggctgtt | tcagctgctc | 300 |
| catcaagcgg | tggtgggtgt | gctgctgctg | ctgcccCtgc | ggagaagaaa | gaagccaaga | 360 |
| aggaagagaa | agaagagtct | gatgatgaca | tgggattcag | tctcttcgag | taaggttttt | 420 |
| gtccccacgg | aaaggagtcg | agatttgatt | ttttgttctc | ttagtggttc | tggbytttgc | 480 |
| tcctctttgt | agttcgggtg | tattaaagat | tcttgatta  | cgaattttac | tcgtagata  | 540 |
| atgaagcaag | aagagttttt | tc         |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Val Ala Ala Ala Phe Leu Leu Ala Val Leu Gly Gly Asn Ala |  |
| 1 5 10 15                                                       |  |
| Asn Pro Ser Ala Glu Asn Ile Lys Asp Ile Ile Gly Ala Val Gly Ala |  |
| 20 25 30                                                        |  |
| Asp Val Asp Gly Glu Ser Ile Glu Leu Leu Leu Lys Glu Val Ser Gly |  |

35 40 45  
Lys Asp Ile Ala Glu Leu Ile Ala Ser Gly Arg Glu Lys Leu Ala Ser  
50 55 60  
Val Pro Ser Gly Gly Gly Val Ala Val Ser Ala Ala Pro Ser Ser Gly  
65 70 75 80  
Gly Gly Gly Ala Ala Ala Ala Ala Pro Ala Glu Lys Lys Glu Ala Lys  
85 90 95  
Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser Leu Phe  
100 105 110  
Glu

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| agagatatat  | tgaaatcaag | gagacaaaaa | cttaagaaaa | aaaacccaaa | aaaaaaagag  | 60  |
| agaggtgaaa  | ttgattttct | gctcgcgatc | gtcatttcaa | tttctaatta | gctttcctgg  | 120 |
| tgttttcttct | ccggcgtaat | catgacaacc | tcaaaaagac | tagcagacag | gaagattgag  | 180 |
| aaattogaca  | aaaacatttt | aaagagagga | tttgttcctg | agaccaccac | caagaagggc  | 240 |
| aaggattatc  | ccgttggtcc | catccttctt | ggcttctttg | tctttgttgt | cattgggatca | 300 |
| tctctctttc  | agatcattag | gactgcaact | agcggaggca | tggcataaac | caaaacacag  | 360 |
| tcaagctaga  | agaagcagtt | ttcaaaatgt | agaatcttct | tctgtctcct | ttctttttct  | 420 |
| ctccttatac  | tgtagaatgt | gtcaactttc | tgttactat  | atcatgtaat | gaagattatt  | 480 |
| tgagtttttt  | ataatccaag | tatccaacgc | ttaagtatgK | tDcttc     |             |     |

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

Arg Asp Ile Leu Lys Ser Arg Arg Gln Lys Leu Lys Lys Lys Asn Pro  
1 5 10 15  
Lys Lys Lys Glu Arg Gly Glu Ile Asp Phe Leu Leu Ala Ile Val Ile  
20 25 30  
Ser Ile Ser Asn  
35

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

```
Met Thr Thr Ser Lys Arg Leu Ala Asp Arg Lys Ile Glu Lys Phe Asp
1 5 10 15
Lys Asn Ile Leu Lys Arg Gly Phe Val Pro Glu Thr Thr Thr Lys Lys
 20 25 30
Gly Lys Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val Phe
 35 40 45
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser
 50 55 60
Gly Gly Met Ala
65
```

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..664
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

```
tcacctatct ctgcagcgga gcttcttctt cttctagggc ttccacgcga ctacgcctgc 60
caaaatcatt ctacaggaag catgaagcca gtcttctgtg ggaactttga gtatgatgcg 120
cgcgaaagtg acctggaacg actattcagg aaatacggca aggttgagag ggttgatatg 180
aaagctgggt ttgcttttgt atacatggaa gatgaaaggg atgcggaaga tgccatccga 240
gcacttgacc gctttgaatt tgggcgtaag ggacgcagac ttcgtgttga atggacaaag 300
agtgaacgtg gaggtgataa aagatctggt ggtggttcaa ggagatcctc atccagcatg 360
agaccttcca agactctctt tgtgattaac tttgatgcgg ataatactag gacccgggat 420
ctagagaaac actttgagcc gtatggaaag atcgtaaacg ttaggatcag gaggaatttt 480
gcatttatcc agtacgaggc acaagaggat gccaccagag cattggatgc ttcaaataac 540
agtaagctga tggataaggt gatctcggtg gagtatgctg tgAaggatga tgatgctaga 600
atcatataaa cctcaactta taattataga cactttttatc tttaaatacag ctacgttttg 660
tggc
```

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

```
Ser Pro Ile Ser Arg Glu Leu Leu Leu Leu Gly Leu Pro Arg
1 5 10 15
Asp Tyr Ala Cys Gln Asn His Ser Thr Gly Ser Met Lys Pro Val Phe
 20 25 30
Cys Gly Asn Phe Glu Tyr Asp Ala Arg Glu Gly Asp Leu Glu Arg Leu
 35 40 45
Phe Arg Lys Tyr Gly Lys Val Glu Arg Val Asp Met Lys Ala Gly Phe
 50 55 60
Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala Glu Asp Ala Ile Arg
 65 70 75 80
Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly Arg Arg Leu Arg Val
 85 90 95
Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys Arg Ser Gly Gly Gly
 100 105 110
```

Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser Lys Thr Leu Phe Val  
115 120 125  
Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg Asp Leu Glu Lys His  
130 135 140  
Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg Ile Arg Arg Asn Phe  
145 150 155 160  
Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala Thr Arg Ala Leu Asp  
165 170 175  
Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val Ile Ser Val Glu Tyr  
180 185 190  
Ala Val Lys Asp Asp Asp Ala Arg Ile Ile  
195 200

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

Met Lys Pro Val Phe Cys Gly Asn Phe Glu Tyr Asp Ala Arg Glu Gly  
1 5 10 15  
Asp Leu Glu Arg Leu Phe Arg Lys Tyr Gly Lys Val Glu Arg Val Asp  
20 25 30  
Met Lys Ala Gly Phe Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala  
35 40 45  
Glu Asp Ala Ile Arg Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly  
50 55 60  
Arg Arg Leu Arg Val Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys  
65 70 75 80  
Arg Ser Gly Gly Gly Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser  
85 90 95  
Lys Thr Leu Phe Val Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg  
100 105 110  
Asp Leu Glu Lys His Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg  
115 120 125  
Ile Arg Arg Asn Phe Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala  
130 135 140  
Thr Arg Ala Leu Asp Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val  
145 150 155 160  
Ile Ser Val Glu Tyr Ala Val Lys Asp Asp Ala Arg Ile Ile  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

Met Lys Ala Gly Phe Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala  
1 5 10 15  
Glu Asp Ala Ile Arg Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly

20 25 30  
Arg Arg Leu Arg Val Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys  
35 40 45  
Arg Ser Gly Gly Gly Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser  
50 55 60  
Lys Thr Leu Phe Val Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg  
65 70 75 80  
Asp Leu Glu Lys His Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg  
85 90 95  
Ile Arg Arg Asn Phe Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala  
100 105 110  
Thr Arg Ala Leu Asp Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val  
115 120 125  
Ile Ser Val Glu Tyr Ala Val Lys Asp Asp Asp Ala Arg Ile Ile  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..537  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

atgctacata actcaaagta acaaacatac acatataaca tatagaaaga tcgRaaMaca 60  
aaagatcggg atgagtatgg ctccaaagac ctcaactaca cttgctttat tccttgtgac 120  
caatattctc ttcttcaacc tcattaccct gagttgcgca gacaatactt gcccaagaga 180  
cgttctcaaa ctttcgacat gctogaatgt tctcaacctc atcaacttga agctcggggc 240  
accagctatg aggccttgtt gctctattct ctttgggtcta attgatctcg atgttgcggt 300  
ttgcctttgc accgcgctca agctcagcct tcttggcatc accatcgaca ctctatttca 360  
ccttaacttg gctcttaacg cctgtggagg tacccttctt gatggattcc gttgccaac 420  
atagctacaa tatattcata ttttctatct atgttcttga attggtttTg tctaacatcc 480  
aaattcaaac cttaaattcat gtataagcaa ataacaagta aaattaagac ttttatg

(2) INFORMATION FOR SEQ ID NO:1717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..140  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

Cys Tyr Ile Thr Gln Ser Asn Lys His Thr His Ile Thr Tyr Arg Lys  
1 5 10 15  
Ile Xaa Xaa Gln Lys Ile Gly Met Ser Met Ala Pro Lys Thr Ser Thr  
20 25 30  
Thr Leu Ala Leu Phe Leu Val Thr Asn Ile Leu Phe Leu Asn Leu Ile  
35 40 45  
Thr Leu Ser Cys Ala Asp Asn Thr Cys Pro Arg Asp Val Leu Lys Leu  
50 55 60  
Ser Thr Cys Ser Asn Val Leu Asn Leu Ile Asn Leu Lys Leu Gly Ala  
65 70 75 80  
Pro Ala Met Arg Pro Cys Cys Ser Ile Leu Phe Gly Leu Ile Asp Leu  
85 90 95  
Asp Val Ala Val Cys Leu Cys Thr Ala Leu Lys Leu Ser Leu Leu Gly

100 105 110  
Ile Thr Ile Asp Thr Pro Ile His Leu Asn Leu Ala Leu Asn Ala Cys  
115 120 125  
Gly Gly Thr Leu Pro Asp Gly Phe Arg Cys Pro Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

Met Ser Met Ala Pro Lys Thr Ser Thr Thr Leu Ala Leu Phe Leu Val  
1 5 10 15  
Thr Asn Ile Leu Phe Leu Asn Leu Ile Thr Leu Ser Cys Ala Asp Asn  
20 25 30  
Thr Cys Pro Arg Asp Val Leu Lys Leu Ser Thr Cys Ser Asn Val Leu  
35 40 45  
Asn Leu Ile Asn Leu Lys Leu Gly Ala Pro Ala Met Arg Pro Cys Cys  
50 55 60  
Ser Ile Leu Phe Gly Leu Ile Asp Leu Asp Val Ala Val Cys Leu Cys  
65 70 75 80  
Thr Ala Leu Lys Leu Ser Leu Leu Gly Ile Thr Ile Asp Thr Pro Ile  
85 90 95  
His Leu Asn Leu Ala Leu Asn Ala Cys Gly Gly Thr Leu Pro Asp Gly  
100 105 110  
Phe Arg Cys Pro Thr  
115

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

Met Ala Pro Lys Thr Ser Thr Thr Leu Ala Leu Phe Leu Val Thr Asn  
1 5 10 15  
Ile Leu Phe Leu Asn Leu Ile Thr Leu Ser Cys Ala Asp Asn Thr Cys  
20 25 30  
Pro Arg Asp Val Leu Lys Leu Ser Thr Cys Ser Asn Val Leu Asn Leu  
35 40 45  
Ile Asn Leu Lys Leu Gly Ala Pro Ala Met Arg Pro Cys Cys Ser Ile  
50 55 60  
Leu Phe Gly Leu Ile Asp Leu Asp Val Ala Val Cys Leu Cys Thr Ala  
65 70 75 80  
Leu Lys Leu Ser Leu Leu Gly Ile Thr Ile Asp Thr Pro Ile His Leu  
85 90 95  
Asn Leu Ala Leu Asn Ala Cys Gly Gly Thr Leu Pro Asp Gly Phe Arg  
100 105 110  
Cys Pro Thr  
115



(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..644
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atcgaaaagt ctacgaattt aggGtttaat ttgtgttaat gagccaccgt gtttcgattc | 60  |
| tatcatctca tttctcacct gcctccgccg tcatggcttc cgagaaagaa gctgctctcg | 120 |
| ccgccactcc ttccgattct cccaccatat ttgacaagat catcagcaaa gagattccat | 180 |
| ccaccgtggg ttttgaggat gacaagggtc tagcttttag ggacataacg ccccagggtc | 240 |
| ctgttcacat cctccttatt ccaaaagtga gggatggcct aactggcctc tctaaggctg | 300 |
| aggaaaggca catcgacatc ttggggccgc ttctctacac tgccaagctt gtagcaaaac | 360 |
| aagaaggcct agcagagggt ttcagaattg ttatcaatga tggtcctcaa ggctgtcaat | 420 |
| cgggtgatca cattcatgtt catctcattg gaggacgcca aatgaactgg cctcctgggt | 480 |
| aaagatcatc ttgaagtgga ttgttttctt gatgataaga gggacgctta gagtttgctc | 540 |
| tcgtctacta atgtctctat aaataaaaaa acgtgggaca tgacttttat gattgttatg | 600 |
| caaaacctta ttttatgtta tgaaaaggat atttactgt tttc                   |     |

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser His Arg Val Ser Ile Leu Ser Ser His Phe Ser Pro Ala Ser |  |
| 1 5 10 15                                                       |  |
| Ala Val Met Ala Ser Glu Lys Glu Ala Ala Leu Ala Ala Thr Pro Ser |  |
| 20 25 30                                                        |  |
| Asp Ser Pro Thr Ile Phe Asp Lys Ile Ile Ser Lys Glu Ile Pro Ser |  |
| 35 40 45                                                        |  |
| Thr Val Val Phe Glu Asp Asp Lys Val Leu Ala Phe Arg Asp Ile Thr |  |
| 50 55 60                                                        |  |
| Pro Gln Gly Pro Val His Ile Leu Leu Ile Pro Lys Val Arg Asp Gly |  |
| 65 70 75 80                                                     |  |
| Leu Thr Gly Leu Ser Lys Ala Glu Glu Arg His Ile Asp Ile Leu Gly |  |
| 85 90 95                                                        |  |
| Arg Leu Leu Tyr Thr Ala Lys Leu Val Ala Lys Gln Glu Gly Leu Ala |  |
| 100 105 110                                                     |  |
| Glu Gly Phe Arg Ile Val Ile Asn Asp Gly Pro Gln Gly Cys Gln Ser |  |
| 115 120 125                                                     |  |
| Val Tyr His Ile His Val His Leu Ile Gly Gly Arg Gln Met Asn Trp |  |
| 130 135 140                                                     |  |
| Pro Pro Gly                                                     |  |
| 145                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..129  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570781  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:  
Met Ala Ser Glu Lys Glu Ala Ala Leu Ala Ala Thr Pro Ser Asp Ser  
1                  5                  10                  15  
Pro Thr Ile Phe Asp Lys Ile Ile Ser Lys Glu Ile Pro Ser Thr Val  
                  20                  25                  30  
Val Phe Glu Asp Asp Lys Val Leu Ala Phe Arg Asp Ile Thr Pro Gln  
                  35                  40                  45  
Gly Pro Val His Ile Leu Leu Ile Pro Lys Val Arg Asp Gly Leu Thr  
                  50                  55                  60  
Gly Leu Ser Lys Ala Glu Glu Arg His Ile Asp Ile Leu Gly Arg Leu  
65                  70                  75                  80  
Leu Tyr Thr Ala Lys Leu Val Ala Lys Gln Glu Gly Leu Ala Glu Gly  
                  85                  90                  95  
Phe Arg Ile Val Ile Asn Asp Gly Pro Gln Gly Cys Gln Ser Val Tyr  
                  100                 105                 110  
His Ile His Val His Leu Ile Gly Gly Arg Gln Met Asn Trp Pro Pro  
                 115                 120                 125  
Gly

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..521
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

```
acttaaaccg aacagatttg tcacgaagah gaaatcagtg tagcaaacac catccatccc 60
tgagcaaaga tagaagaaaa gctatgactg atttgcaaat ggaggtagag gtagatacca 120
attcttcttt gcaggagtct ctcccgaagc cgcaagtcac gtacagatgt aagaaatgta 180
gaaggatagt tgctattgag gaaaacatag tcccgcacga accaggaaaag ggtgaagaat 240
gctttgcttg gaaaaagaga agtggaaact ctgaacaagt gcaatgctct tccatctttg 300
tcgagcctat gaaatggatg cagacaatac atgatggagt ggtggaagag aagcttctat 360
gttttgatg taacgggaga ttaggttatt tcaactgggc tgggatgcaa ttagctgtg 420
gtgcatgggt taatccggct ttccagctta ataaaagccg aatagacgag tgtaaaccg 480
agccaaaccc gaacctgaat atggaaactt gatgaaaaAg g
```

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

Leu Asn Arg Thr Asp Leu Ser Arg Arg Xaa Asn Gln Cys Ser Lys His  
1                  5                  10                  15  
His Pro Ser Leu Ser Lys Asp Arg Arg Lys Ala Met Thr Asp Leu Gln  
                  20                  25                  30

Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu Gln Glu Ser Leu Pro  
35 40 45  
Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys Arg Arg Ile Val Ala  
50 55 60  
Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly Lys Gly Glu Glu Cys  
65 70 75 80  
Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu Gln Val Gln Cys Ser  
85 90 95  
Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln Thr Ile His Asp Gly  
100 105 110  
Val Val Glu Lys Leu Leu Cys Phe Gly Cys Asn Gly Arg Leu Gly  
115 120 125  
Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys Gly Ala Trp Val Asn  
130 135 140  
Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp Glu Cys Lys Ser Glu  
145 150 155 160  
Pro Asn Pro Asn Leu Asn Met Glu Thr  
165

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1570784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

Met Thr Asp Leu Gln Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu  
1 5 10 15  
Gln Glu Ser Leu Pro Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys  
20 25 30  
Arg Arg Ile Val Ala Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly  
35 40 45  
Lys Gly Glu Glu Cys Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu  
50 55 60  
Gln Val Gln Cys Ser Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln  
65 70 75 80  
Thr Ile His Asp Gly Val Val Glu Glu Lys Leu Leu Cys Phe Gly Cys  
85 90 95  
Asn Gly Arg Leu Gly Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys  
100 105 110  
Gly Ala Trp Val Asn Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp  
115 120 125  
Glu Cys Lys Ser Glu Pro Asn Pro Asn Leu Asn Met Glu Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1570785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu Gln Glu Ser Leu Pro

1 5 10 15  
Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys Arg Arg Ile Val Ala  
20 25 30  
Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly Lys Gly Glu Glu Cys  
35 40 45  
Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu Gln Val Gln Cys Ser  
50 55 60  
Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln Thr Ile His Asp Gly  
65 70 75 80  
Val Val Glu Glu Lys Leu Leu Cys Phe Gly Cys Asn Gly Arg Leu Gly  
85 90 95  
Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys Gly Ala Trp Val Asn  
100 105 110  
Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp Glu Cys Lys Ser Glu  
115 120 125  
Pro Asn Pro Asn Leu Asn Met Glu Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..744
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ttcactcacc aaagcatcac ataacactca cacacacact ttctcttctc ttattttctc  | 60  |
| agttcttttta actcttttct ctacctatat tcaaattgcc accgtcgagg ttgaacaagt | 120 |
| gactccagta gcagctgaga acatcgaggt gccaccacca aaggctgtgg agtcggagga  | 180 |
| agtcaccacc gtctccgagt ctcttccagc tccggttaaca gaatctcaag cgcctgtcga | 240 |
| agtaacaact aaagatttgg tcgtggaaga gacagagaaa ccaatcgaag aaacagagga  | 300 |
| agctcaagtt gaaactccgg aggttgtgga gatcaagaaa gatgaagaag ctccggttga  | 360 |
| aactccggtg gttgtggagg atgagagcaa aacagaggaa gttgtagagg cgaagaaaga  | 420 |
| ggaagaagta gaagaaaaga agacagagga agctccagtg gttgtggagg aagagaagaa  | 480 |
| gccagaggga gaggaggaga aAcccgccgt ggaagcctcc gtgacagctc cagtggagaa  | 540 |
| ggctgatgag taaatgtgaa gaaaaaaact gtcttttgaa agacaaaaga agaagaaaat  | 600 |
| gtagcaagt aattttattg ctactttaag tactttgtgt cttgttatgt ttttgagtct   | 660 |
| atgactcttc ttgcttttgg ttttttaatc ttcttaagta ctattttcaa tggttatcat  | 720 |
| ttttaataag atatacatta tttt                                         |     |

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

Ser Leu Thr Lys Ala Ser His Asn Thr His Thr His Thr Phe Ser Ser  
1 5 10 15  
Leu Ile Phe Ser Val Leu Leu Thr Leu Phe Ser Thr Tyr Ile Gln Met  
20 25 30  
Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn Ile  
35 40 45  
Glu Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr Val

(2) INFORMATION FOR SEQ ID NO:1729:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1570788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 458 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..458

(D) OTHER INFORMATION: / Ceres Seq. ID 1570793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

catttttcgac cgctacaacg attcctatct cagacgaatc ggatccaatg ttttgtctta 60  
cgtgaacatg gtctgtgctg gcCtgcggaa ttcaatcccc aagtccatcg tatactgcca 120  
agtccgagaa gcgaagcgCa Ngtctcctcg accatttctt tgcggagCtc ggtaccatgg 180  
atatgaagag gctctcgctg ctattgaacg aagatccagc aatcatggag agacgcagtg 240  
ccatctcaaaa cgggctagaa ttgtatcgag cagcccaatc cgagatcgat gctgttgctt 300  
gggtccaagtg ataccggcat gtcatgtcca ctgttttgct cggttctggt cggtgtgggt 360  
cagactcgga gcagagattt aggggtctgta atttgataaa gatgatcttc ccgataccat 420  
gcagtatcgt tttatataac atccacattg tttgtccc

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

Ile Phe Asp Arg Tyr Asn Asp Ser Tyr Leu Arg Arg Ile Gly Ser Asn  
1 5 10 15  
Val Leu Ser Tyr Val Asn Met Val Cys Ala Gly Leu Arg Asn Ser Ile  
20 25 30  
Pro Lys Ser Ile Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Xaa Ser  
35 40 45  
Pro Arg Pro Phe Leu Cys Gly Ala Arg Tyr His Gly Tyr Glu Glu Ala  
50 55 60  
Leu Val Ala Ile Glu Arg Arg Ser Ser Asn His Gly Glu Thr Gln Cys  
65 70 75 80  
His Leu Lys Ala Ala Arg Ile Val Ser Ser Pro Ile Arg Asp Arg  
85 90 95  
Cys Cys Cys Leu Val Gln Val Ile Pro Ala Cys His Val His Cys Phe  
100 105 110  
Ala Arg Phe Trp Ser Val Trp Leu Arg Leu Gly Ala Glu Ile  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1570795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

Met Val Cys Ala Gly Leu Arg Asn Ser Ile Pro Lys Ser Ile Val Tyr  
1 5 10 15  
Cys Gln Val Arg Glu Ala Lys Arg Xaa Ser Pro Arg Pro Phe Leu Cys  
20 25 30  
Gly Ala Arg Tyr His Gly Tyr Glu Glu Ala Leu Val Ala Ile Glu Arg  
35 40 45  
Arg Ser Ser Asn His Gly Glu Thr Gln Cys His Leu Lys Ala Ala Arg  
50 55 60  
Ile Val Ser Ser Ser Pro Ile Arg Asp Arg Cys Cys Cys Leu Val Gln  
65 70 75 80  
Val Ile Pro Ala Cys His Val His Cys Phe Ala Arg Phe Trp Ser Val  
85 90 95  
Trp Leu Arg Leu Gly Ala Glu Ile

100

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..527
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aattttgctt tgagacgacg aaacgaagdG agaaagagac aagccctaaa aatcgctttg  | 60  |
| agacgataaa ttcttaaaat cttcgattcg ttcaagatga tcgtccctgt tcgttggttt  | 120 |
| acttggtggaa aggtgattgg gaacaaatgg gacacatata ttgaacttct ccaggctgat | 180 |
| tacgctgaag gggatgctct tgacgcgctt ggattagtcc gttactgctg caggcgatg   | 240 |
| cttatgactc atgtcgatct aatcgaaaag cttctaaact acaacactat ggagaaatcc  | 300 |
| gaccccaatt aaagaagat gctataatga ataacaaatc atcaagagct aaagtgtagg   | 360 |
| agtgaggcat ctcatcatg tgaaagtctt aataaaacca caatgtttca gaaattttgt   | 420 |
| tgaatttaga aactaggaat gttgatattt caatgttttc tgatgttctt gttcgggttt  | 480 |
| agaagacaac ttttcgagct acaaataaag ctcaagcttg tagagcc                |     |

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ile Val Pro Val Arg Cys Phe Thr Cys Gly Lys Val Ile Gly Asn |  |
| 1 5 10 15                                                       |  |
| Lys Trp Asp Thr Tyr Leu Glu Leu Leu Gln Ala Asp Tyr Ala Glu Gly |  |
| 20 25 30                                                        |  |
| Asp Ala Leu Asp Ala Leu Gly Leu Val Arg Tyr Cys Cys Arg Arg Met |  |
| 35 40 45                                                        |  |
| Leu Met Thr His Val Asp Leu Ile Glu Lys Leu Leu Asn Tyr Asn Thr |  |
| 50 55 60                                                        |  |
| Met Glu Lys Ser Asp Pro Asn                                     |  |
| 65 70                                                           |  |

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..605
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaataaaaa cttttactta tcttctttct tctcacttct cagacctcaa tttccaagca | 60  |
| gagatgacgg tgaagataag gCtcgcgcgt cttggttgta aacaccgacc cttctatcgt | 120 |
| gtagttgtcg ccgatgaaaa atcgcgagg gacggtaaac aaatcgaggt gttaggcttt  | 180 |
| tatgatccac tccaaggcaa agaagatgcg gatagagtga gcctcaaatt cgacagaatc | 240 |
| aagtactggt tatctgttgg agctcaacca acagacacag tggaaagcat gcttttcagg | 300 |

gccggtttga taccacaaaa gcctatggta gtggtcgggt caaaaaatgg gcagaagtct 360  
acgagccaac atgtttcacc cattacaggt gaaatcttga actaagagtg ttgatgcgtt 420  
gagcaagaaa gagccttttg tgtctgtgtg aaaggagttt atgtaatgtt gtttaagact 480  
tttctgttta tgtgaaagga gttaatgtaa tgttgtttaa gacttttgc tttctatgtga 540  
aagcagttta atgttatgtt ggtaagact tttctgcaac agagtttggg gaatttttaw 600  
tcytt

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1570799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

Lys Ile Lys Thr Phe Thr Tyr Leu Leu Ser Ser His Phe Ser Asp Leu  
1 5 10 15  
Asn Phe Gln Ala Glu Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly  
20 25 30  
Cys Lys His Arg Pro Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser  
35 40 45  
Arg Arg Asp Gly Lys Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu  
50 55 60  
Gln Gly Lys Glu Asp Ala Asp Arg Val Ser Leu Lys Phe Asp Arg Ile  
65 70 75 80  
Lys Tyr Trp Leu Ser Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser  
85 90 95  
Met Leu Phe Arg Ala Gly Leu Ile Pro Pro Lys Pro Met Val Val Val  
100 105 110  
Gly Ser Lys Asn Gly Gln Lys Ser Thr Ser Gln His Val Ser Pro Ile  
115 120 125  
Thr Gly Glu Ile Leu Asn  
130

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1570800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly Cys Lys His Arg Pro  
1 5 10 15  
Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser Arg Arg Asp Gly Lys  
20 25 30  
Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu Gln Gly Lys Glu Asp  
35 40 45  
Ala Asp Arg Val Ser Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser  
50 55 60  
Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser Met Leu Phe Arg Ala  
65 70 75 80  
Gly Leu Ile Pro Pro Lys Pro Met Val Val Val Gly Ser Lys Asn Gly  
85 90 95  
Gln Lys Ser Thr Ser Gln His Val Ser Pro Ile Thr Gly Glu Ile Leu



Asn 100 105 110

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atttgaacga gattgtatta agaagtaatc tatatggaNa cgCgcaacgc gCttatttgt   | 60  |
| gtccaagggtc ctggatatat aactgctcga gacattatct taccgccctc tgtggaaatc  | 120 |
| attgataata cacagcatat agctacctta acagaaccaa tagatttgtg tattgaatta   | 180 |
| aaaattgaga ggaatcgcgg atatatgtcta aaaatgtcaa ataactttga agacagaagt  | 240 |
| tatcctatcg atgctgtatt catgacctgtt gaaaatgccca atcatagtat tcattcttat | 300 |
| gggaatggga atgaaaaaca agagattctt tttctagaaa tatggacaaa tggaagttaa   | 360 |
| actoctaaag aagcacttca tcaagcctcc cggaatttga ttaattttatt tattcctttt  | 420 |
| ctacatgtag aagaagaaac gttctattta gagaacaatc aacatcaagt tactttaccc   | 480 |
| ttttttcctt ttcataatcg attagttaac c                                  |     |

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Xaa Thr Arg Asn Ala Leu Ile Cys Val Gln Gly Pro Gly Tyr Ile |  |
| 1 5 10 15                                                       |  |
| Thr Ala Arg Asp Ile Ile Leu Pro Pro Ser Val Glu Ile Ile Asp Asn |  |
| 20 25 30                                                        |  |
| Thr Gln His Ile Ala Thr Leu Thr Glu Pro Ile Asp Leu Cys Ile Glu |  |
| 35 40 45                                                        |  |
| Leu Lys Ile Glu Arg Asn Arg Gly Tyr Ser Leu Lys Met Ser Asn Asn |  |
| 50 55 60                                                        |  |
| Phe Glu Asp Arg Ser Tyr Pro Ile Asp Ala Val Phe Met Pro Val Glu |  |
| 65 70 75 80                                                     |  |
| Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly Asn Glu Lys Gln |  |
| 85 90 95                                                        |  |
| Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser Leu Thr Pro Lys |  |
| 100 105 110                                                     |  |
| Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn Leu Phe Ile Pro |  |
| 115 120 125                                                     |  |
| Phe Leu His Val Glu Glu Glu Thr Phe Tyr Leu Glu Asn Asn Gln His |  |
| 130 135 140                                                     |  |
| Gln Val Thr Leu Pro Phe Pro Phe His Asn Arg Leu Val Asn         |  |
| 145 150 155                                                     |  |

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..99  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570807  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

Met Ser Asn Asn Phe Glu Asp Arg Ser Tyr Pro Ile Asp Ala Val Phe  
1                  5                  10                  15  
Met Pro Val Glu Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly  
                  20                  25                  30  
Asn Glu Lys Gln Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser  
                  35                  40                  45  
Leu Thr Pro Lys Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn  
                  50                  55                  60  
Leu Phe Ile Pro Phe Leu His Val Glu Glu Glu Thr Phe Tyr Leu Glu  
65                  70                  75                  80  
Asn Asn Gln His Gln Val Thr Leu Pro Phe Phe Pro Phe His Asn Arg  
                  85                  90                  95  
Leu Val Asn

- (2) INFORMATION FOR SEQ ID NO:1741:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 83 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..83  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570808  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

Met Pro Val Glu Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly  
1                  5                  10                  15  
Asn Glu Lys Gln Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser  
                  20                  25                  30  
Leu Thr Pro Lys Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn  
                  35                  40                  45  
Leu Phe Ile Pro Phe Leu His Val Glu Glu Glu Thr Phe Tyr Leu Glu  
50                  55                  60  
Asn Asn Gln His Gln Val Thr Leu Pro Phe Phe Pro Phe His Asn Arg  
65                  70                  75                  80  
Leu Val Asn

- (2) INFORMATION FOR SEQ ID NO:1742:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 475 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..475  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570816  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

gttgatcgga aaggaaaagt aaaaaagaga gatctgagaa atgggaaatg agacgaagac 60  
caacggtggt cctgcaagta tggccggagg Cggaggattc agagctaaaa tggaacatta 120  
cgtttacagt ggtgaaaaga agcacgtcct ggtcgggatc ggaatcgta ccatcatctt 180  
cggagttcct tggtatttga tgactcaagg gtcaaagcat caatctcacc aagattacat 240

ggacaaggcc gataaagctc gaaaagcacg cctctcatcg tcttcatcag ctaacaagta 300  
gtctgtctga aggattgagt catttgcaca ctgttatctc atactcattt tcccacacaa 360  
gttaaaactt agtcaaaatc tgagtctttt ttgtgattta gattcaaaat cattctcatt 420  
ttcatgcacc atgttttggtt atccgttttt taataaaaag atcaaagatt ctatc

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

Met Gly Asn Glu Thr Lys Thr Asn Gly Gly Pro Ala Ser Met Ala Gly  
1 5 10 15  
Gly Gly Gly Phe Arg Ala Lys Met Glu His Tyr Val Tyr Ser Gly Glu  
20 25 30  
Lys Lys His Val Leu Val Gly Ile Gly Ile Val Thr Ile Ile Phe Gly  
35 40 45  
Val Pro Trp Tyr Leu Met Thr Gln Gly Ser Lys His Gln Ser His Gln  
50 55 60  
Asp Tyr Met Asp Lys Ala Asp Lys Ala Arg Lys Ala Arg Leu Ser Ser  
65 70 75 80  
Ser Ser Ser Ala Asn Lys  
85

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

Met Ala Gly Gly Gly Gly Phe Arg Ala Lys Met Glu His Tyr Val Tyr  
1 5 10 15  
Ser Gly Glu Lys Lys His Val Leu Val Gly Ile Gly Ile Val Thr Ile  
20 25 30  
Ile Phe Gly Val Pro Trp Tyr Leu Met Thr Gln Gly Ser Lys His Gln  
35 40 45  
Ser His Gln Asp Tyr Met Asp Lys Ala Asp Lys Ala Arg Lys Ala Arg  
50 55 60  
Leu Ser Ser Ser Ser Ser Ala Asn Lys  
65 70

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

Met Glu His Tyr Val Tyr Ser Gly Glu Lys Lys His Val Leu Val Gly  
1 5 10 15  
Ile Gly Ile Val Thr Ile Ile Phe Gly Val Pro Trp Tyr Leu Met Thr  
20 25 30  
Gln Gly Ser Lys His Gln Ser His Gln Asp Tyr Met Asp Lys Ala Asp  
35 40 45  
Lys Ala Arg Lys Ala Arg Leu Ser Ser Ser Ser Ser Ala Asn Lys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..805
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

aaagtaaccc caaaagaaaa aaagcaaaga gagaggaaaa gaaaaaaaaat gacgaagacg 60  
atgatgatct tcgcggcgac gatgacggcg atggccttgc tttcagttcc tgcgattgaa 120  
gcacaaactg agtgcgtgag Caagctagtc ccttgcttca acgacctgaa caccgacaaca 180  
acgccggtga aagaatggtg cgactcgata aaagaagcgg tggagaagga acttacatgt 240  
ctctgtacaa tctacaccag tccaggtttg ctcgctcagt tcaacgtcac cactgagaaa 300  
gctctcggtc ttagccgctg ttgcaacgtc accactgac tctccgcttg taccgctaaa 360  
ggagctccat cgccaaaagc ttctttacct cctccagctc cagcagggaa taccaaaaaa 420  
gacgccggag ctgggaacaa gctgcgccgt tatggagtca ccaccgtgat cttgtctttg 480  
atctcatcca tcttcttctg aattccttta cccggtttta ttattattag ctcaataaat 540  
tctsgagatt tgyttgcttt ttggcttaac ttatttaata tttaaagaaa aacaaaGaag 600  
tattttttgt tcacatgtta tgtattatca ttgattcatc attgagtcac atgttagtat 660  
atttaccggt ttcaatcgga ctctatcatt tgcatactcg ttttgagtgt ggatgtgtgt 720  
tgttttatgt aactctctac tctatgggac ttaattattc tactgtgtga ctggatttaa 780  
ttgatgtaaa aactgtCgtt ggttt

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

Lys Val Thr Pro Lys Glu Lys Lys Gln Arg Glu Arg Lys Arg Lys Lys  
1 5 10 15  
Met Thr Lys Thr Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala  
20 25 30  
Leu Leu Ser Val Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys  
35 40 45  
Leu Val Pro Cys Phe Asn Asp Leu Asn Thr Thr Thr Pro Val Lys  
50 55 60  
Glu Cys Cys Asp Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys  
65 70 75 80  
Leu Cys Thr Ile Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val  
85 90 95  
Thr Thr Glu Lys Ala Leu Gly Leu Ser Arg Arg Cys Asn Val Thr Thr  
100 105 110

Asp Leu Ser Ala Cys Thr Ala Lys Gly Ala Pro Ser Pro Lys Ala Ser  
115 120 125  
Leu Pro Pro Pro Ala Pro Ala Gly Asn Thr Lys Lys Asp Ala Gly Ala  
130 135 140  
Gly Asn Lys Leu Ala Gly Tyr Gly Val Thr Thr Val Ile Leu Ser Leu  
145 150 155 160  
Ile Ser Ser Ile Phe Phe  
165

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1570825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

Met Thr Lys Thr Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala  
1 5 10 15  
Leu Leu Ser Val Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys  
20 25 30  
Leu Val Pro Cys Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys  
35 40 45  
Glu Cys Cys Asp Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys  
50 55 60  
Leu Cys Thr Ile Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val  
65 70 75 80  
Thr Thr Glu Lys Ala Leu Gly Leu Ser Arg Arg Cys Asn Val Thr Thr  
85 90 95  
Asp Leu Ser Ala Cys Thr Ala Lys Gly Ala Pro Ser Pro Lys Ala Ser  
100 105 110  
Leu Pro Pro Pro Ala Pro Ala Gly Asn Thr Lys Lys Asp Ala Gly Ala  
115 120 125  
Gly Asn Lys Leu Ala Gly Tyr Gly Val Thr Thr Val Ile Leu Ser Leu  
130 135 140  
Ile Ser Ser Ile Phe Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1570826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala Leu Leu Ser Val  
1 5 10 15  
Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys Leu Val Pro Cys  
20 25 30  
Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys Glu Cys Cys Asp  
35 40 45  
Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys Leu Cys Thr Ile  
50 55 60  
Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val Thr Thr Glu Lys

(2) INFORMATION FOR SEQ ID NO:1750:

(A) LENGTH: 659 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..659

(D) OTHER INFORMATION: / Ceres Seq. ID 1570827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| aaaaaacacac | gcgctagagt | tttctaagaa  | caacagtgac | gaaaaggttt  | ttagggtttc | 60  |
| tttaccaatc  | agaatctccg | ccaagtaacg  | attttcagat | tccgaagcag  | caaagttcaa | 120 |
| ataatttccg  | aactgtaaca | tggcggcaac  | tactggactt | gagaccctcg  | tcgatcagat | 180 |
| tatttcggtg  | attacaaatg | acggacgcaa  | cattgtggga | gttcttaaag  | gttttgacca | 240 |
| ggctacaaat  | ataatccttg | atgaatctca  | tgaacgtgtg | ttttccacaa  | aggaaggagt | 300 |
| acaacaacat  | gtgttggtt  | tgtacatcat  | cagaggggac | aacatagggtg | ttatcgggga | 360 |
| gctggacgag  | gagcttgatg | ctagttctgga | tttttcgaag | ctgagagccc  | atcggttgaa | 420 |
| accgtagtg   | cattgattga | atatagttat  | ggtgagaaaa | tctaattctc  | tcattcaaag | 480 |
| cctaaaaaca  | aagagagat  | ttgattgtaa  | acaatttggg | tagttttgtt  | tgatgtctgg | 540 |
| agttgtctta  | tttgtgtatc | ctaaggacaa  | aagctatatg | atattttatg  | tcttaaacgt | 600 |
| tttggtcggg  | aaCcttaaat | cataCCcaat  | CcttttggAa | cggAacctag  | gtttgcTct  |     |

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1570828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1752:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 543 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..543  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1570829  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ataaaatcga ttttctctca caaatcttat tctctttcga cttcagtggc ggcgcattca   | 60  |
| gagattcaaa ctcagagaaa atggtggcga caggcttatt cgtggggcta aacaaaggac   | 120 |
| acgttggttac caaacgcgag caacctcctc gccctaacaa cagaaaaggc aaaacaagca  | 180 |
| aaaggactat ttttatcagg aatctcatca aggaagtgtc gggtaagct ccctatgaga    | 240 |
| agaggatcac tgagcttttg aaggttggtta aagacaagag agctcttaaa gttgccaagc  | 300 |
| gaaagttggg aactcacaag agagctaaac gaaagagaga ggagatgtct agtgttctcc   | 360 |
| gcaagatgag gtctgggtggt gctgggtgcat ccgagaagaa gaagtgatgc gctgactctg | 420 |
| gttcagcgct ctgtttcttc taaaccagtt ttctgttttt tgaatttttt gGcagtacct   | 480 |
| tgtgtttcct ttggatattt tgtagcagag ataattaaat gttaaaacga aaccattatg   | 540 |

acg

- (2) INFORMATION FOR SEQ ID NO:1753:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 134 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..134  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1570830  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Asp | Phe | Leu | Ser | Gln | Ile | Leu | Phe | Ser | Phe | Asp | Phe | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Ala | Phe | Arg | Asp | Ser | Asn | Ser | Glu | Lys | Met | Val | Ala | Thr | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Val | Gly | Leu | Asn | Lys | Gly | His | Val | Val | Thr | Lys | Arg | Glu | Gln | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Pro | Arg | Pro | Asn | Asn | Arg | Lys | Gly | Lys | Thr | Ser | Lys | Arg | Thr | Ile | Phe |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Arg | Asn | Leu | Ile | Lys | Glu | Val | Ala | Gly | Gln | Ala | Pro | Tyr | Glu | Lys |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Ile | Thr | Glu | Leu | Leu | Lys | Val | Gly | Lys | Asp | Lys | Arg | Ala | Leu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Ala | Lys | Arg | Lys | Leu | Gly | Thr | His | Lys | Arg | Ala | Lys | Arg | Lys | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Glu | Met | Ser | Ser | Val | Leu | Arg | Lys | Met | Arg | Ser | Gly | Gly | Ala | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Ser | Glu | Lys | Lys | Lys |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

- (2) INFORMATION FOR SEQ ID NO:1754:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 108 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1570831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

```
Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val
1 5 10 15
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr
20 25 30
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly
35 40 45
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys Val Gly Lys
50 55 60
Asp Lys Arg Ala Leu Lys Val Ala Lys Arg Lys Leu Gly Thr His Lys
65 70 75 80
Arg Ala Lys Arg Lys Arg Glu Glu Met Ser Ser Val Leu Arg Lys Met
85 90 95
Arg Ser Gly Gly Ala Gly Ala Ser Glu Lys Lys Lys
100 105
```

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..552

(D) OTHER INFORMATION: / Ceres Seq. ID 1570836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

```
agatcagtgga ttgttcgatg aacgaagagg agccagacaa agaacacgtg gcggattcta 60
ctatgtcggc ggcggcgatt gatggtgtgg cggctctgag atcgggtgtt cagcgggtaa 120
accaggcggc ggagaaagcg ggtcgtgggt cggatcagat acgggtcgta gcggtgagta 180
agaagaaacc agtttctctg attcgccaag tatacgacgc tggtcagagg tcttttgag 240
agaattatgt gcaagagatc attgagaagg cacctcagct tccagaagat atagagtggc 300
atttcattgg gaatttgcag agcaacaaag tgaagccttt gctatgtaaa ttgactttgc 360
tatttcaaag tcttcatctt tagttttttt gtattgagtt actaaattgg gtgtaaaact 420
ccacacttga gttctattct taattctttg gtttgatcag ctgggtgttc taaccttggt 480
accgtggaaa gtgttgatga tgaaaaggta aaagtttctc ttttgtatat ttaaagagRa 540
aattggtttg tt
```

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

```
Ile Ser Asp Cys Ser Met Asn Glu Glu Glu Pro Asp Lys Glu His Val
1 5 10 15
Ala Asp Ser Thr Met Ser Ala Ala Ala Ile Asp Gly Val Ala Ala Leu
20 25 30
Arg Ser Val Phe Gln Arg Val Asn Gln Ala Ala Glu Lys Ala Gly Arg
35 40 45
Gly Ser Asp Gln Ile Arg Val Val Ala Val Ser Lys Thr Lys Pro Val
50 55 60
Ser Leu Ile Arg Gln Val Tyr Asp Ala Gly Gln Arg Ser Phe Gly Glu
65 70 75 80
Asn Tyr Val Gln Glu Ile Ile Glu Lys Ala Pro Gln Leu Pro Glu Asp
```



85 90 95  
Ile Glu Trp His Phe Ile Gly Asn Leu Gln Ser Asn Lys Val Lys Pro  
100 105 110  
Leu Leu Cys Lys Leu Thr Leu Leu Phe Gln Ser Pro His Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

Met Asn Glu Glu Glu Pro Asp Lys Glu His Val Ala Asp Ser Thr Met  
1 5 10 15  
Ser Ala Ala Ala Ile Asp Gly Val Ala Ala Leu Arg Ser Val Phe Gln  
20 25 30  
Arg Val Asn Gln Ala Ala Glu Lys Ala Gly Arg Gly Ser Asp Gln Ile  
35 40 45  
Arg Val Val Ala Val Ser Lys Thr Lys Pro Val Ser Leu Ile Arg Gln  
50 55 60  
Val Tyr Asp Ala Gly Gln Arg Ser Phe Gly Glu Asn Tyr Val Gln Glu  
65 70 75 80  
Ile Ile Glu Lys Ala Pro Gln Leu Pro Glu Asp Ile Glu Trp His Phe  
85 90 95  
Ile Gly Asn Leu Gln Ser Asn Lys Val Lys Pro Leu Leu Cys Lys Leu  
100 105 110  
Thr Leu Leu Phe Gln Ser Pro His Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

Met Ser Ala Ala Ala Ile Asp Gly Val Ala Ala Leu Arg Ser Val Phe  
1 5 10 15  
Gln Arg Val Asn Gln Ala Ala Glu Lys Ala Gly Arg Gly Ser Asp Gln  
20 25 30  
Ile Arg Val Val Ala Val Ser Lys Thr Lys Pro Val Ser Leu Ile Arg  
35 40 45  
Gln Val Tyr Asp Ala Gly Gln Arg Ser Phe Gly Glu Asn Tyr Val Gln  
50 55 60  
Glu Ile Ile Glu Lys Ala Pro Gln Leu Pro Glu Asp Ile Glu Trp His  
65 70 75 80  
Phe Ile Gly Asn Leu Gln Ser Asn Lys Val Lys Pro Leu Leu Cys Lys  
85 90 95  
Leu Thr Leu Leu Phe Gln Ser Pro His Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..676  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570852  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

aacaatccct acaacggcta catctacact tcttttcaag agagagcaac ttttatctcc 60  
cacgccaaca cggcgaaGct agccacgaca tacggcgaca caactctcgc caaaatctgt 120  
ggaacaatcg cggcggatga gaagcggcac gagatggcgt atacgcggat cgtcgagaag 180  
ctattcgaga ttgatccga tggtagccga caagctctag cgagtatgat gaggaagcga 240  
atcacgatgc cggctcagct gatgcacgac ggtcgcgatg acaatctgtt cgatcattac 300  
gctgctgtgg cgcagagaat cggagtgtat accgcgacgg attacgcagg gattttggag 360  
tttttgttgc ggcgggtgga ggtggagaag ttagggatgg gtttgtccgg tgaaggagg 420  
agagcacagg attatctgtg taccttgccg cagaggatca ggaggttaga ggaaagagct 480  
gacgatagag tcaaactgtc gtcaaagtct aaaccttctg tttcgttcag ctggatttac 540  
gggagagaag ttgaactata aacgacaatg gttgttgCgt ttcactgtat tagactctta 600  
aacgttatgg gccttactaa tgtaatatgg gaagtaaag taataaagaa acgctaaaag 660  
atcttgcgtt ttagtc

(2) INFORMATION FOR SEQ ID NO:1760:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 186 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..186  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570853  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

Asn Asn Pro Tyr Asn Gly Tyr Ile Tyr Thr Ser Phe Gln Glu Arg Ala  
1 5 10 15  
Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Thr Thr Tyr Gly  
20 25 30  
Asp Thr Thr Leu Ala Lys Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys  
35 40 45  
Arg His Glu Met Ala Tyr Thr Arg Ile Val Glu Lys Leu Phe Glu Ile  
50 55 60  
Asp Pro Asp Gly Thr Val Gln Ala Leu Ala Ser Met Met Arg Lys Arg  
65 70 75 80  
Ile Thr Met Pro Ala Gln Leu Met His Asp Gly Arg Asp Asp Asn Leu  
85 90 95  
Phe Asp His Tyr Ala Ala Val Ala Gln Arg Ile Gly Val Tyr Thr Ala  
100 105 110  
Thr Asp Tyr Ala Gly Ile Leu Glu Phe Leu Leu Arg Arg Trp Glu Val  
115 120 125  
Glu Lys Leu Gly Met Gly Leu Ser Gly Glu Gly Arg Arg Ala Gln Asp  
130 135 140  
Tyr Leu Cys Thr Leu Pro Gln Arg Ile Arg Arg Leu Glu Glu Arg Ala  
145 150 155 160  
Asp Asp Arg Val Lys Arg Ala Ser Lys Ser Lys Pro Ser Val Ser Phe  
165 170 175  
Ser Trp Ile Tyr Gly Arg Glu Val Glu Leu  
180 185

(2) INFORMATION FOR SEQ ID NO:1761:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1570854
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

Met Ala Tyr Thr Arg Ile Val Glu Lys Leu Phe Glu Ile Asp Pro Asp  
1 5 10 15  
Gly Thr Val Gln Ala Leu Ala Ser Met Met Arg Lys Arg Ile Thr Met  
20 25 30  
Pro Ala Gln Leu Met His Asp Gly Arg Asp Asp Asn Leu Phe Asp His  
35 40 45  
Tyr Ala Ala Val Ala Gln Arg Ile Gly Val Tyr Thr Ala Thr Asp Tyr  
50 55 60  
Ala Gly Ile Leu Glu Phe Leu Leu Arg Arg Trp Glu Val Glu Lys Leu  
65 70 75 80  
Gly Met Gly Leu Ser Gly Glu Gly Arg Arg Ala Gln Asp Tyr Leu Cys  
85 90 95  
Thr Leu Pro Gln Arg Ile Arg Arg Leu Glu Glu Arg Ala Asp Asp Arg  
100 105 110  
Val Lys Arg Ala Ser Lys Ser Lys Pro Ser Val Ser Phe Ser Trp Ile  
115 120 125  
Tyr Gly Arg Glu Val Glu Leu  
130 135

- (2) INFORMATION FOR SEQ ID NO:1762:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 111 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..111
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1570855
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

Met Met Arg Lys Arg Ile Thr Met Pro Ala Gln Leu Met His Asp Gly  
1 5 10 15  
Arg Asp Asp Asn Leu Phe Asp His Tyr Ala Ala Val Ala Gln Arg Ile  
20 25 30  
Gly Val Tyr Thr Ala Thr Asp Tyr Ala Gly Ile Leu Glu Phe Leu Leu  
35 40 45  
Arg Arg Trp Glu Val Glu Lys Leu Gly Met Gly Leu Ser Gly Glu Gly  
50 55 60  
Arg Arg Ala Gln Asp Tyr Leu Cys Thr Leu Pro Gln Arg Ile Arg Arg  
65 70 75 80  
Leu Glu Glu Arg Ala Asp Asp Arg Val Lys Arg Ala Ser Lys Ser Lys  
85 90 95  
Pro Ser Val Ser Phe Ser Trp Ile Tyr Gly Arg Glu Val Glu Leu  
100 105 110

- (2) INFORMATION FOR SEQ ID NO:1763:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 646 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:

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- (A) NAME/KEY: -  
(B) LOCATION: 1..646  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| tctcgagtac | acctcatcat | tcttcttcgt | gtgagagaga  | tcttttttga | aaacgaaagc | 60  |
| Gggatttagc | gtatagcagc | ttccaccggt | tgcgccgaatt | tcatcgagct | tcaagtgaac | 120 |
| atgagtaaac | caatggaaga | ggataccaac | cagggaaaga  | ctgaggagga | ggagttcaac | 180 |
| actggaccac | tctctgtttt | gatgatgagt | gttaagaata  | acactcaggt | gttgatcaat | 240 |
| tgccgtaaca | acaggaaact | ccttggccga | gttagggctt  | ttgacaggca | ctgcaacatg | 300 |
| gttcttgaaa | atgtcagaga | aatgtggact | gaggttccga  | aaaccggaaa | aggaaagaag | 360 |
| aaagctcttc | ctgttaacag | agatcgattc | atcagcaaga  | tgttcctgcg | tggagactca | 420 |
| gtcattatcg | tcctcaggaa | ccccaaagtg | gagaagctct  | tcttatgata | attctcgctt | 480 |
| cttcttggtc | aatcctaatt | gttgcacaa  | cagtgagaac  | atgttttgat | tatgagcttt | 540 |
| aaatctacta | gtgttgCctt | gtatttttca | cttgtcttct  | atctttgact | tgaaacgcag | 600 |
| ccagtgaact | ttgtaatatc | aaaagagaag | ttctttwwtt  | cttttt     |            |     |

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Pro | Met | Glu | Glu | Asp | Thr | Asn | Gln | Gly | Lys | Thr | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Glu | Phe | Asn | Thr | Gly | Pro | Leu | Ser | Val | Leu | Met | Met | Ser | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Asn | Thr | Gln | Val | Leu | Ile | Asn | Cys | Arg | Asn | Asn | Arg | Lys | Leu | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Arg | Val | Arg | Ala | Phe | Asp | Arg | His | Cys | Asn | Met | Val | Leu | Glu | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Arg | Glu | Met | Trp | Thr | Glu | Val | Pro | Lys | Thr | Gly | Lys | Gly | Lys | Lys |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Lys | Ala | Leu | Pro | Val | Asn | Arg | Asp | Arg | Phe | Ile | Ser | Lys | Met | Phe | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Gly | Asp | Ser | Val | Ile | Ile | Val | Leu | Arg | Asn | Pro | Lys |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..105  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Asp | Thr | Asn | Gln | Gly | Lys | Thr | Glu | Glu | Glu | Glu | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Gly | Pro | Leu | Ser | Val | Leu | Met | Met | Ser | Val | Lys | Asn | Asn | Thr | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Ile | Asn | Cys | Arg | Asn | Asn | Arg | Lys | Leu | Leu | Gly | Arg | Val | Arg |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Phe | Asp | Arg | His | Cys | Asn | Met | Val | Leu | Glu | Asn | Val | Arg | Glu | Met |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |

Trp Thr Glu Val Pro Lys Thr Gly Lys Gly Lys Lys Lys Ala Leu Pro  
65 70 75 80  
Val Asn Arg Asp Arg Phe Ile Ser Lys Met Phe Leu Arg Gly Asp Ser  
85 90 95  
Val Ile Ile Val Leu Arg Asn Pro Lys  
100 105

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1570865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

Met Met Ser Val Lys Asn Asn Thr Gln Val Leu Ile Asn Cys Arg Asn  
1 5 10 15  
Asn Arg Lys Leu Gly Arg Val Arg Ala Phe Asp Arg His Cys Asn  
20 25 30  
Met Val Leu Glu Asn Val Arg Glu Met Trp Thr Glu Val Pro Lys Thr  
35 40 45  
Gly Lys Gly Lys Lys Lys Ala Leu Pro Val Asn Arg Asp Arg Phe Ile  
50 55 60  
Ser Lys Met Phe Leu Arg Gly Asp Ser Val Ile Ile Val Leu Arg Asn  
65 70 75 80  
Pro Lys

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1570869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

atcagaaaac acaaattctta aaacttttctg gaaaaacaaa aatgtcagga agaggaaaag 60  
gaggaaaagg gttaggcaaa ggaggagcaa agagacacag aaaggttcta agagacaaca 120  
ttcaaggaat cacaaagcca gcgattcgct gtcttgctcg tagaggaggt gtgaagagaa 180  
tcagtggatt gatctatgaa gaaacgagag gtgtgttgaa gatttttctg gagaatgtga 240  
ttagagatgc tgttacttac actgagcatg cgaggaggaa gacggtgact gctatggatg 300  
ttgtttatgc cttgaagaga caaggaagaa ctctatatgg atttggtggt tgatcaattt 360  
gagatctggg ttttctggtg aatgatgata atttaagtct tgcgatcaag aaattccaga 420  
aattgggttg aattttaggg tttcgttttg tgttgtaatt agggcagcat tgtaatggat 480  
taatgataag tacCatttgc cc

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1570870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

Gln Lys Thr Gln Ile Leu Lys Leu Ser Gly Lys Thr Lys Met Ser Gly  
1 5 10 15  
Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala Lys Arg His  
20 25 30  
Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys Pro Ala Ile  
35 40 45  
Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser Gly Leu Ile  
50 55 60  
Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu Asn Val Ile  
65 70 75 80  
Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys Thr Val Thr  
85 90 95  
Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg Thr Leu Tyr  
100 105 110  
Gly Phe Gly Gly  
115

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1570871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala  
1 5 10 15  
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys  
20 25 30  
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser  
35 40 45  
Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu  
50 55 60  
Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys  
65 70 75 80  
Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg  
85 90 95  
Thr Leu Tyr Gly Phe Gly Gly  
100

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..634

(D) OTHER INFORMATION: / Ceres Seq. ID 1570895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atttgctcaga ttggtttgga tggctctcgt atgcttgatc caagtactag ccgaactttg | 60  |
| agaatatatc ctcttgagaa catcacaaaga tgcgaaaaac tagattcgtc tattctggct | 120 |
| ttctgggtcta agactccggt agacattgaa gctaaacgta tcagattgca atcaaatagt | 180 |
| tacaccacca acacccttct ggacactgtg acggctgcaa tgtttcaggc caaggagatc  | 240 |
| gggggaagta gcaggcctcc cacctctgga aaactggttg aacaaactgc tgagaagaaa  | 300 |

aaaggattgg gtgattggat gaacattata aagcctgtta atgaggagaa agatcattgg 360  
gtacctgatg aagctgtttc taagtgcaca tcatgtgggt cagatttcgg tgcatttata 420  
cgaaggcacc actgcaggaa ttgtggtgaa gtcttctgtg acaagtgtac tcaaggcagg 480  
attgctctca ctgctgagga taatgctcct caagtccgtg tttgtgaccg gtgcatggca 540  
gaagtgtcac aaaggttgag taatgCcaag gaaaccactg gcaggaatgt gagCctgcag 600  
agccatgaag accttgctag aaagttwcag gagg

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1570896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Ile Cys Gln Ile Gly Leu Asp Gly Leu Arg Met Leu Asp Pro Ser Thr  
1 5 10 15  
Ser Arg Thr Leu Arg Ile Tyr Pro Leu Glu Asn Ile Thr Arg Cys Glu  
20 25 30  
Lys Leu Asp Ser Ser Ile Leu Ala Phe Trp Ser Lys Thr Pro Val Asp  
35 40 45  
Ile Glu Ala Lys Arg Ile Arg Leu Gln Ser Asn Ser Tyr Thr Thr Asn  
50 55 60  
Thr Leu Leu Asp Thr Val Thr Ala Ala Met Phe Gln Ala Lys Glu Ile  
65 70 75 80  
Gly Gly Ser Ser Arg Pro Pro Thr Ser Gly Lys Leu Val Glu Gln Thr  
85 90 95  
Ala Glu Lys Lys Lys Gly Leu Gly Asp Trp Met Asn Ile Ile Lys Pro  
100 105 110  
Val Asn Glu Glu Lys Asp His Trp Val Pro Asp Glu Ala Val Ser Lys  
115 120 125  
Cys Thr Ser Cys Gly Ser Asp Phe Gly Ala Phe Ile Arg Arg His His  
130 135 140  
Cys Arg Asn Cys Gly Glu Val Phe Cys Asp Lys Cys Thr Gln Gly Arg  
145 150 155 160  
Ile Ala Leu Thr Ala Glu Asp Asn Ala Pro Gln Val Arg Val Cys Asp  
165 170 175  
Arg Cys Met Ala Glu Val Ser Gln Arg Leu Ser Asn Ala Lys Glu Thr  
180 185 190  
Thr Gly Arg Asn Val Ser Leu Gln Ser His Glu Asp Leu Ala Arg Lys  
195 200 205  
Xaa Gln Glu  
210

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1570897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

Met Leu Asp Pro Ser Thr Ser Arg Thr Leu Arg Ile Tyr Pro Leu Glu  
1 5 10 15  
Asn Ile Thr Arg Cys Glu Lys Leu Asp Ser Ser Ile Leu Ala Phe Trp

(ix) FEATURE:



- (A) NAME/KEY: -  
(B) LOCATION: 1..525  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aagatggcca | agtagaacga | gattgcgaag | aagaagagag  | aggctaaagc | cgatagaaaa | 60  |
| cgagccattc | acggcgatcc | tctcaccaat | aaattgaaga  | ccagaactcc | ggtcccctcc | 120 |
| gtctccggca | aacgtcagag | aaagctcctt | cgcaaagggc  | gcagagagca | gaaagatatg | 180 |
| gtggagaagg | gtcttggtac | tatggaagat | gtggagatgg  | cttctgctca | agctgcatca | 240 |
| gaagactcca | agaaatcccc | cagaaaattt | agcgttaaga  | agagcttgaa | gttgaacaaa | 300 |
| ctaaataata | aaggcaaaaa | gaagaaaaac | cagaaaagcca | gtggtgaaaa | atctgctgat | 360 |
| tgtatgctag | aatgagtgct | gtgtatacct | gtaaaccctat | ttcttctaac | ggatgataga | 420 |
| ggtttctcaa | tgtctgggta | gattctttca | aaaatgtgaa  | acgtgtgttt | ttgcatccgg | 480 |
| aggatGcgNa | aGcagaggaa | tggagggttt | gatatgattt  | tattt      |            |     |

(2) INFORMATION FOR SEQ ID NO:1775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Met | Ala | Lys | Tyr | Asn | Glu | Ile | Ala | Lys | Lys | Lys | Arg | Glu | Ala | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Asp | Arg | Lys | Arg | Ala | Ile | His | Gly | Asp | Pro | Leu | Thr | Asn | Lys | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Thr | Arg | Thr | Pro | Val | Pro | Ser | Val | Ser | Gly | Lys | Arg | Gln | Arg | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Leu | Arg | Lys | Trp | Arg | Arg | Glu | Gln | Lys | Asp | Met | Val | Glu | Lys | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Val | Thr | Met | Glu | Asp | Val | Glu | Met | Ala | Ser | Ala | Gln | Ala | Ala | Ser |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Glu | Asp | Ser | Lys | Lys | Ser | Pro | Arg | Lys | Phe | Ser | Val | Lys | Lys | Ser | Leu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Leu | Asn | Lys | Leu | Asn | Asn | Lys | Gly | Lys | Lys | Lys | Lys | Asn | Gln | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Ala | Ser | Gly | Glu | Lys | Ser | Ala | Asp | Cys | Met | Leu | Glu |     |     |     |     |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Tyr | Asn | Glu | Ile | Ala | Lys | Lys | Arg | Glu | Ala | Lys | Ala |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Arg | Lys | Arg | Ala | Ile | His | Gly | Asp | Pro | Leu | Thr | Asn | Lys | Leu | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Arg | Thr | Pro | Val | Pro | Ser | Val | Ser | Gly | Lys | Arg | Gln | Arg | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Arg | Lys | Trp | Arg | Arg | Glu | Gln | Lys | Asp | Met | Val | Glu | Lys | Gly | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Val Thr Met Glu Asp Val Glu Met Ala Ser Ala Gln Ala Ala Ser Glu  
65 70 75 80  
Asp Ser Lys Lys Ser Pro Arg Lys Phe Ser Val Lys Lys Ser Leu Lys  
85 90 95  
Leu Asn Lys Leu Asn Asn Lys Gly Lys Lys Lys Lys Asn Gln Lys Ala  
100 105 110  
Ser Gly Glu Lys Ser Ala Asp Cys Met Leu Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

Met Val Glu Lys Gly Leu Val Thr Met Glu Asp Val Glu Met Ala Ser  
1 5 10 15  
Ala Gln Ala Ala Ser Glu Asp Ser Lys Lys Ser Pro Arg Lys Phe Ser  
20 25 30  
Val Lys Lys Ser Leu Lys Leu Asn Lys Leu Asn Asn Lys Gly Lys Lys  
35 40 45  
Lys Lys Asn Gln Lys Ala Ser Gly Glu Lys Ser Ala Asp Cys Met Leu  
50 55 60  
Glu  
65

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aattttcaaa aaaagcagat taaaacagag attagcgagt gagagagaga gacaaagata  | 60  |
| tagagcttct cgtgaagcaa cagtgaagaa aaggaaagtg aatcgccatg gatgatcgcc  | 120 |
| ttcgcttaag ccgcagaatc cgctttcttc ttcttgcttg gctccgtcgt tctcgctccg  | 180 |
| gaagaataga gtttatcaga cgatttggat acaaggaaat aatcaaagca acagaaggtt  | 240 |
| tccgtaaggt tatttacacc aactatcacg ggtctgcata cagagctaaa ttcaaaggtg  | 300 |
| gtgaggttgc tttgggtcaaa gaactcactg ctcttgatct tggacgagaa aggtttgatg | 360 |
| aggaagttca gcttttgggt cgcttacgtc accgtcatct ccttacActt cgtgggtttt  | 420 |
| gcattttagt cttgaacaat catctcagtc tgtattttga atttggttca ctct        |     |

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570932

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

Met Asp Asp Arg Leu Arg Leu Ser Arg Arg Ile Arg Phe Leu Leu Leu  
1 5 10 15  
Ala Trp Leu Arg Arg Ser Arg Ser Gly Arg Ile Glu Phe Ile Arg Arg  
20 25 30  
Phe Gly Tyr Lys Glu Ile Ile Lys Ala Thr Glu Gly Phe Arg Lys Val  
35 40 45  
Ile Tyr Thr Asn Tyr His Gly Ser Ala Tyr Arg Ala Lys Phe Lys Gly  
50 55 60  
Gly Glu Val Ala Leu Val Lys Glu Leu Thr Ala Leu Asp Leu Gly Arg  
65 70 75 80  
Glu Arg Phe Asp Glu Val Gln Leu Leu Gly Arg Leu Arg His Arg  
85 90 95  
His Leu Leu Thr Leu Arg Gly Phe Cys Ile Leu Val Leu Asn Asn His  
100 105 110  
Leu Ser Leu Tyr Phe Glu Phe Gly Ser Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..850
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

acacacacac acatgttctt cggtgctgct tcggtgggtt aaaaactttt ttAtttgttt 60  
cttgcttttt gtaaagtcaa agataacaaa taaataagaa aaatggagaa tctaccacct 120  
ggttatcgtc ccaatgttgg tgtttgtcta atcaactcgg ataatctggt atttgtagct 180  
tctagattga atgttccagg agcatggcag atgccacagg gaggcattga agatggggag 240  
gatccaaagt cagcagccat gagagagtta caagaagaaa ctggtgttgt ttcagctgaa 300  
atcgtctcag aggtcccaaa ttggttgaca tatgattttc caccagcagt aaaagcaaaa 360  
gttaaccgctc tttggggcgg tgaatggcat ggtcaagctc agaaatggta tttagtgaga 420  
ctgaggaacg atgaggacga gaaagagatc aatctagcga acaacgaagc ggattcagag 480  
tttgcgaggt ggaaatgggc gaagccagaa gaagtggtag agcaagcagt ggattacaaa 540  
aggccaacct atgaagaagt catcaagact tttggttcgt tcttaaacga cacaggaaga 600  
gctgctaaat gtaaatcagc caagtgggtga tataagatac caagaaccaa tgtttgtctt 660  
tttatttttt ttgttaactg ttgtttttct ttttttgggc ggttcttttt agtagaacc 720  
ttttggaatg caaaagcttt ctctaggggt tttttacttt catttttgta aattgggttat 780  
tggtacgtag aaagtttttt ggttttattt taacgtgggg gtcattgtaa taaagtcggt 840  
gtctggattc

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

Met Glu Asn Leu Pro Pro Gly Tyr Arg Pro Asn Val Gly Val Cys Leu  
1 5 10 15  
Ile Asn Ser Asp Asn Leu Val Phe Val Ala Ser Arg Leu Asn Val Pro  
20 25 30  
Gly Ala Trp Gln Met Pro Gln Gly Gly Ile Glu Asp Gly Glu Asp Pro

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(2) INFORMATION FOR SEQ ID NO:1782:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1570938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1570939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

Met Arg Glu Leu Gln Glu Glu Thr Gly Val Val Ser Ala Glu Ile Val  
1 5 10 15

Ser Glu Val Pro Asn Trp Leu Thr Tyr Asp Phe Pro Pro Ala Val Lys  
20 25 30  
Ala Lys Val Asn Arg Leu Trp Gly Glu Trp His Gly Gln Ala Gln  
35 40 45  
Lys Trp Tyr Leu Val Arg Leu Arg Asn Asp Glu Asp Glu Lys Glu Ile  
50 55 60  
Asn Leu Ala Asn Asn Glu Ala Asp Ser Glu Phe Ala Glu Trp Lys Trp  
65 70 75 80  
Ala Lys Pro Glu Glu Val Val Glu Gln Ala Val Asp Tyr Lys Arg Pro  
85 90 95  
Thr Tyr Glu Glu Val Ile Lys Thr Phe Gly Ser Phe Leu Asn Asp Thr  
100 105 110  
Gly Arg Ala Ala Lys Cys Lys Ser Ala Lys Trp  
115 120

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..651
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cttttttgtc gaccattttt gtttctgagt tgttcttctt gattagcttt gtccgcttgg  | 60  |
| aaccaaacat ggcgagtctt ggccatatag ccagagaatc atcagacatc acacgcctcg  | 120 |
| cccagtttta caaagaggtg tttgggttcg aggagatcga aagtcctgat tttggagacc  | 180 |
| taaaggtggt gtggctaaac ttaccaggtg cttttgcaat gcacattatc cagagaaacc  | 240 |
| cttcaacaaa tcttcagaaa ggtccttaca gtgctacctc agcggttaag gatcctagcc  | 300 |
| atctcccaat gggcatcat atctgtttct ctgtcccaaa tttcgactct ttccttcatt   | 360 |
| ctctcaagga gaaagggata gaaacttttc agaagtctct gcctgatgga aaagtcaagc  | 420 |
| aagttttctt ctttgatcct gatggaaacg gattagaggt agcaagtcga tcatgagcct  | 480 |
| tgaacctgaa atatgtggta tctactacta tagaatgaaa taaaagtatt gtataaataa  | 540 |
| tcagtttggt gaaataaaaat ctatatgtat aggtttgatg ttaacttgtg acaGcttacg | 600 |
| cctcaaagtt cgtgtcatgt gctttgaatg ktggatgtaw cgratttatg c           |     |

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Phe Leu Ser Thr Ile Phe Val Ser Glu Leu Phe Phe Leu Ile Ser Phe  
1 5 10 15  
Val Arg Leu Glu Pro Asn Met Ala Ser Leu Gly His Ile Ala Arg Glu  
20 25 30  
Ser Ser Asp Ile Thr Arg Leu Ala Gln Phe Tyr Lys Glu Val Phe Gly  
35 40 45  
Phe Glu Glu Ile Glu Ser Pro Asp Phe Gly Asp Leu Lys Val Val Trp  
50 55 60  
Leu Asn Leu Pro Gly Ala Phe Ala Met His Ile Ile Gln Arg Asn Pro  
65 70 75 80  
Ser Thr Asn Leu Pro Glu Gly Pro Tyr Ser Ala Thr Ser Ala Val Lys  
85 90 95

Asp Pro Ser His Leu Pro Met Gly His His Ile Cys Phe Ser Val Pro  
100 105 110  
Asn Phe Asp Ser Phe Leu His Ser Leu Lys Glu Lys Gly Ile Glu Thr  
115 120 125  
Phe Gln Lys Ser Leu Pro Asp Gly Lys Val Lys Gln Val Phe Phe Phe  
130 135 140  
Asp Pro Asp Gly Asn Gly Leu Glu Val Ala Ser Arg Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1570953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

Met Ala Ser Leu Gly His Ile Ala Arg Glu Ser Ser Asp Ile Thr Arg  
1 5 10 15  
Leu Ala Gln Phe Tyr Lys Glu Val Phe Gly Phe Glu Glu Ile Glu Ser  
20 25 30  
Pro Asp Phe Gly Asp Leu Lys Val Val Trp Leu Asn Leu Pro Gly Ala  
35 40 45  
Phe Ala Met His Ile Ile Gln Arg Asn Pro Ser Thr Asn Leu Pro Glu  
50 55 60  
Gly Pro Tyr Ser Ala Thr Ser Ala Val Lys Asp Pro Ser His Leu Pro  
65 70 75 80  
Met Gly His His Ile Cys Phe Ser Val Pro Asn Phe Asp Ser Phe Leu  
85 90 95  
His Ser Leu Lys Glu Lys Gly Ile Glu Thr Phe Gln Lys Ser Leu Pro  
100 105 110  
Asp Gly Lys Val Lys Gln Val Phe Phe Phe Asp Pro Asp Gly Asn Gly  
115 120 125  
Leu Glu Val Ala Ser Arg Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1570954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met His Ile Ile Gln Arg Asn Pro Ser Thr Asn Leu Pro Glu Gly Pro  
1 5 10 15  
Tyr Ser Ala Thr Ser Ala Val Lys Asp Pro Ser His Leu Pro Met Gly  
20 25 30  
His His Ile Cys Phe Ser Val Pro Asn Phe Asp Ser Phe Leu His Ser  
35 40 45  
Leu Lys Glu Lys Gly Ile Glu Thr Phe Gln Lys Ser Leu Pro Asp Gly  
50 55 60  
Lys Val Lys Gln Val Phe Phe Phe Asp Pro Asp Gly Asn Gly Leu Glu  
65 70 75 80  
Val Ala Ser Arg Ser

85

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1092
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| aacttttggc  | gagaaaatca | gagacagaag  | aagaagaaaa  | gcgaaaaaaa  | gcaaaacatg  | 60   |
| aaggcgacga  | cgaagactcc | gatccacgtg  | gtgtggtcat  | gggttaggag  | acaacctccg  | 120  |
| aagggtgaagg | cttttctcgc | cgtgggtcact | ggcatggcgg  | ctttggttct  | tctcagattc  | 180  |
| attgttcacg  | atcacgacaa | tctcttcgtt  | gccgctgagg  | ctgttcattc  | catcgggatc  | 240  |
| tgtgtgctca  | tctacaaact | catgaaggag  | aagacctgtg  | cgggattgtc  | actgaaatct  | 300  |
| caggagctta  | cggcgatatt | tttagctgtt  | aggctgtatt  | gtagcattgt  | aatggaatat  | 360  |
| gatatacata  | ccattcttga | cttggctact  | ttgggaacaa  | ctctctgggt  | tatatattatg | 420  |
| attcgtttca  | agttaagagc | tagttacatg  | gaggacaaaag | acaactttcc  | tctctattat  | 480  |
| gtgcttgccg  | cctgtgttgc | attagctgtg  | ttcatccatc  | catcgacctc  | tcataacata  | 540  |
| ataaacagaa  | tttcatgggc | tttatgtgta  | taccttgaag  | ctgtttcagt  | actacctcag  | 600  |
| ctacgagtga  | tgcagaacac | aaagattgtt  | gaaccgttca  | cggctcatta  | tgtttttgca  | 660  |
| cttggagtag  | caaggttcct | cagctgtgcc  | cactgggttt  | tacaggttgt  | ggacacgcgg  | 720  |
| ggacggttgc  | ttgtagcatt | gggttatgga  | ttgtggccat  | caatggttct  | gatctcagaa  | 780  |
| attgttcaaa  | ctttcatctt | ggcagatttc  | tgttactact  | acgtcaaaaag | cgttttcgga  | 840  |
| ggccagcttg  | ttctccggct | accgtctgga  | gtagNtataa  | gttcaaaaaga | tagaaatact  | 900  |
| ccaacgatgt  | cctgcgatga | gcttgacgga  | aattctaatt  | gggaaagata  | gctcaatttt  | 960  |
| tctttacctc  | tgatttcatc | gtttatgtgt  | cttgaggttt  | caccaagtgt  | ctcgggttacg | 1020 |
| aattaatttt  | acagtgttgt | atattttgcc  | tatcaaggga  | tttaacgtct  | ttcagggtcga | 1080 |
| taagttatct  | tt         |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Cys | Arg | Glu | Asn | Gln | Arg | Gln | Lys | Lys | Lys | Lys | Ser | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Gln | Asn | Met | Lys | Ala | Thr | Thr | Lys | Thr | Pro | Ile | His | Val | Val | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Trp | Val | Arg | Arg | Gln | Pro | Pro | Lys | Val | Lys | Ala | Phe | Leu | Ala | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Thr | Gly | Met | Ala | Ala | Leu | Val | Leu | Leu | Arg | Phe | Ile | Val | His | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Asp | Asn | Leu | Phe | Val | Ala | Ala | Glu | Ala | Val | His | Ser | Ile | Gly | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Cys | Val | Leu | Ile | Tyr | Lys | Leu | Met | Lys | Glu | Lys | Thr | Cys | Ala | Gly | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Leu | Lys | Ser | Gln | Glu | Leu | Thr | Ala | Ile | Phe | Leu | Ala | Val | Arg | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Cys | Ser | Ile | Val | Met | Glu | Tyr | Asp | Ile | His | Thr | Ile | Leu | Asp | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Thr | Leu | Gly | Thr | Thr | Leu | Trp | Val | Ile | Phe | Met | Ile | Arg | Phe | Lys |

|                             |                                         |     |     |     |
|-----------------------------|-----------------------------------------|-----|-----|-----|
| 130                         |                                         | 135 |     | 140 |
| Leu Arg Ala Ser Tyr Met     | Glu Asp Lys Asp Asn Phe Pro Leu Tyr Tyr |     |     |     |
| 145                         | 150                                     | 155 | 160 |     |
| Val Leu Ala Pro Cys Val     | Ala Leu Ala Val Phe Ile His Pro Ser Thr |     |     |     |
|                             | 165                                     | 170 | 175 |     |
| Ser His Asn Ile Ile Asn Arg | Ile Ser Trp Ala Leu Cys Val Tyr Leu     |     |     |     |
|                             | 180                                     | 185 | 190 |     |
| Glu Ala Val Ser Val Leu Pro | Gln Leu Arg Val Met Gln Asn Thr Lys     |     |     |     |
|                             | 195                                     | 200 | 205 |     |
| Ile Val Glu Pro Phe Thr Ala | His Tyr Val Phe Ala Leu Gly Val Ala     |     |     |     |
|                             | 210                                     | 215 | 220 |     |
| Arg Phe Leu Ser Cys Ala His | Trp Val Leu Gln Val Val Asp Thr Arg     |     |     |     |
| 225                         | 230                                     | 235 | 240 |     |
| Gly Arg Leu Leu Val Ala Leu | Gly Tyr Gly Leu Trp Pro Ser Met Val     |     |     |     |
|                             | 245                                     | 250 | 255 |     |
| Leu Ile Ser Glu Ile Val Gln | Thr Phe Ile Leu Ala Asp Phe Cys Tyr     |     |     |     |
|                             | 260                                     | 265 | 270 |     |
| Tyr Tyr Val Lys Ser Val Phe | Gly Gly Gln Leu Val Leu Arg Leu Pro     |     |     |     |
|                             | 275                                     | 280 | 285 |     |
| Ser Gly Val Xaa Ile Ser Ser | Lys Asp Arg Asn Thr Pro Thr Met Ser     |     |     |     |
| 290                         | 295                                     | 300 |     |     |
| Cys Asp Glu Leu Asp Gly Asn | Ser Asn Trp Glu Arg                     |     |     |     |
| 305                         | 310                                     | 315 |     |     |

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1570976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

|                                 |                                 |
|---------------------------------|---------------------------------|
| Met Lys Ala Thr Thr Lys Thr Pro | Ile His Val Val Trp Ser Trp Val |
| 1                               | 5 10 15                         |
| Arg Arg Gln Pro Lys Val Lys Ala | Phe Leu Ala Val Val Thr Gly     |
|                                 | 20 25 30                        |
| Met Ala Ala Leu Val Leu Leu Arg | Phe Ile Val His Asp His Asp Asn |
|                                 | 35 40 45                        |
| Leu Phe Val Ala Ala Glu Ala Val | His Ser Ile Gly Ile Cys Val Leu |
|                                 | 50 55 60                        |
| Ile Tyr Lys Leu Met Lys Glu Lys | Thr Cys Ala Gly Leu Ser Leu Lys |
| 65                              | 70 75 80                        |
| Ser Gln Glu Leu Thr Ala Ile Phe | Leu Ala Val Arg Leu Tyr Cys Ser |
|                                 | 85 90 95                        |
| Ile Val Met Glu Tyr Asp Ile His | Thr Ile Leu Asp Leu Ala Thr Leu |
|                                 | 100 105 110                     |
| Gly Thr Thr Leu Trp Val Ile Phe | Met Ile Arg Phe Lys Leu Arg Ala |
|                                 | 115 120 125                     |
| Ser Tyr Met Glu Asp Lys Asp Asn | Phe Pro Leu Tyr Tyr Val Leu Ala |
|                                 | 130 135 140                     |
| Pro Cys Val Ala Leu Ala Val Phe | Ile His Pro Ser Thr Ser His Asn |
| 145                             | 150 155 160                     |
| Ile Ile Asn Arg Ile Ser Trp Ala | Leu Cys Val Tyr Leu Glu Ala Val |
|                                 | 165 170 175                     |
| Ser Val Leu Pro Gln Leu Arg Val | Met Gln Asn Thr Lys Ile Val Glu |
|                                 | 180 185 190                     |
| Pro Phe Thr Ala His Tyr Val Phe | Ala Leu Gly Val Ala Arg Phe Leu |
|                                 | 195 200 205                     |



Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg Gly Arg Leu  
210 215 220  
Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Leu Ile Ser  
225 230 235 240  
Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val  
245 250 255  
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val  
260 265 270  
Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser Cys Asp Glu  
275 280 285  
Leu Asp Gly Asn Ser Asn Trp Glu Arg  
290 295

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp His Asp Asn  
1 5 10 15  
Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile Cys Val Leu  
20 25 30  
Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys  
35 40 45  
Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser  
50 55 60  
Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu  
65 70 75 80  
Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys Leu Arg Ala  
85 90 95  
Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Tyr Val Leu Ala  
100 105 110  
Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr Ser His Asn  
115 120 125  
Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu Glu Ala Val  
130 135 140  
Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu  
145 150 155 160  
Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Leu  
165 170 175  
Ser Cys Ala His Trp Val Leu Gln Val Asp Thr Arg Gly Arg Leu  
180 185 190  
Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Leu Ile Ser  
195 200 205  
Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val  
210 215 220  
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val  
225 230 235 240  
Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser Cys Asp Glu  
245 250 255  
Leu Asp Gly Asn Ser Asn Trp Glu Arg  
260 265

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1710  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

```
tatcaagaat ttggacgagt ccatcgacca caaagcactg catgatactt tttcatcggt 60
tggaacatt gtgtcgtgca aggtagctgt cgattcttca ggccagtcaa aaggctatgg 120
gtttgtgcaa tacgccaatg aagaatctgc ccagaaagct atagagaaac tgaacggcat 180
gttgctcaat gacaagcaag tgtatgtggg tcctttcctg aggagacaag aaagagactc 240
cactgctaac aaaacgaaat tcaccaatgt gtatgtgaag aatctcgcgg aaagtactac 300
cgatgatgac ttgaagaatg cttttggcga gtatggaaag ataacaagtg ctgtcgtgat 360
gaaagatgga gaagggaagt ccaagggctt tgggtttgtc aactttgaaa atgctgatga 420
tgctgctagg gctgtggagt ctctcaatgg gcacaaattt gatgataagg agtggtatgt 480
tggtagagcc cagaagaagt cagagaggga aacakaacta agggtcctgt atgaacagaa 540
tttgaaggaa gctgcagaca agtttaaaag ttcaaacttg tatgttaaga atttggatcc 600
tagcatttca gatgagaaac ttaaagagat cttttctcct tttggtaccg ttacatctag 660
caagtgatg cggtatccta atggaacaag caaaggctca ggttttgttg ctttcgcaac 720
tcccgaagaa gcaactgaag ctatgtcaca gttgagcggg aaaatgatcg aaagcaagcc 780
actctatgtg gctattgcac agcgggaagg agacagaagg gtcagactac aggtcagtt 840
ttcccaagtg aggccagttg caatgcagcc gtctgttggg cccgcgatgc cagtttatcc 900
cccgggtggg cctgggtattg gacaacaaat gttctatggg caggcccctc ctgccatgat 960
tcctcccag cctgggtatg gataccaaca gcagcttggg cctggaatga gacctggtgg 1020
gggtcctgta ccagtttct tcatgcctat ggttcagcca cagcagcagc gtcctggagg 1080
aggaagacgt cctgggggaa tccaacactc ccagcagcaa aatcccatga tgcagcaaca 1140
gatgcatcca aggggtcgga tgttcogga tccccaaggg cgtggtggta gtggtgatgt 1200
gctcccatat gatatgggca acaacatgcc attgactatt ggagctttgg cttcaaactc 1260
gtctaattgt actccagagc aacagaggac gatgctgggt gaggtgctgt acccgttggg 1320
ggagcaggtt gaggcagagt ctgcagccaa agtgactggg atgcttttgg agatggacca 1380
gactgaagtg ctccatctgt tggagtcacc agaagctctc aaggccaaag ttgcagaggc 1440
tatggatgtt ctgaggagtg tcgctgctgg tgcgtgaacc gagcagctcg cttccttgaa 1500
cctctcttaa attgctttt atcatttgat ctttggtttt tgtctctccc atacaattgg 1560
agttgtttct ttgctattcg ttttctccct gggaatttgg attcctccac ataaCtgcgt 1620
ttgtgttatt ttaaaccctc gtttttaaac cacaaggaa aaacctatct gctttgttct 1680
tttgatttag ttgctgttgc tagcttgttc
```

(2) INFORMATION FOR SEQ ID NO:1793:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 502 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..502  
(D) OTHER INFORMATION: / Ceres Seq. ID 1570999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

```
Ile Lys Asn Leu Asp Glu Ser Ile Asp His Lys Ala Leu His Asp Thr
1 5 10 15
Phe Ser Ser Phe Gly Asn Ile Val Ser Cys Lys Val Ala Val Asp Ser
20 25 30
Ser Gly Gln Ser Lys Gly Tyr Gly Phe Val Gln Tyr Ala Asn Glu Glu
35 40 45
Ser Ala Gln Lys Ala Ile Glu Lys Leu Asn Gly Met Leu Leu Asn Asp
50 55 60
Lys Gln Val Tyr Val Gly Pro Phe Leu Arg Arg Gln Glu Arg Asp Ser
65 70 75 80
Thr Ala Asn Lys Thr Lys Phe Thr Asn Val Tyr Val Lys Asn Leu Ala
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Glu | Ser | Thr | Thr | Asp | Asp | Asp | Leu | Lys | Asn | Ala | Phe | Gly | Glu | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Lys | Ile | Thr | Ser | Ala | Val | Val | Met | Lys | Asp | Gly | Glu | Gly | Lys | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Phe | Gly | Phe | Val | Asn | Phe | Glu | Asn | Ala | Asp | Asp | Ala | Ala | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Glu | Ser | Leu | Asn | Gly | His | Lys | Phe | Asp | Asp | Lys | Glu | Trp | Tyr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Arg | Ala | Gln | Lys | Lys | Ser | Glu | Arg | Glu | Thr | Xaa | Leu | Arg | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Tyr | Glu | Gln | Asn | Leu | Lys | Glu | Ala | Ala | Asp | Lys | Phe | Lys | Ser | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Asn |
| Leu | Tyr | Val | Lys | Asn | Leu | Asp | Pro | Ser | Ile | Ser | Asp | Glu | Lys | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     | Lys |
| Glu | Ile | Phe | Ser | Pro | Phe | Gly | Thr | Val | Thr | Ser | Ser | Lys | Val | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     | Arg |
| Asp | Pro | Asn | Gly | Thr | Ser | Lys | Gly | Ser | Gly | Phe | Val | Ala | Phe | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | Thr |
| Pro | Glu | Glu | Ala | Thr | Glu | Ala | Met | Ser | Gln | Leu | Ser | Gly | Lys | Met |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | Ile |
| Glu | Ser | Lys | Pro | Leu | Tyr | Val | Ala | Ile | Ala | Gln | Arg | Lys | Glu | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 | Arg |
| Arg | Val | Arg | Leu | Gln | Ala | Gln | Phe | Ser | Gln | Val | Arg | Pro | Val | Ala |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     | Met |
| Gln | Pro | Ser | Val | Gly | Pro | Arg | Met | Pro | Val | Tyr | Pro | Pro | Gly | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     | Pro |
| Gly | Ile | Gly | Gln | Gln | Met | Phe | Tyr | Gly | Gln | Ala | Pro | Pro | Ala | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | Ile |
| Pro | Pro | Gln | Pro | Gly | Tyr | Gly | Tyr | Gln | Gln | Leu | Val | Pro | Gly | Met |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |
| Arg | Pro | Gly | Gly | Gly | Pro | Val | Pro | Ser | Phe | Phe | Met | Pro | Met | Val |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 | Gln |
| Pro | Gln | Gln | Gln | Arg | Pro | Gly | Gly | Gly | Arg | Arg | Pro | Gly | Gly | Ile |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     | Gln |
| His | Ser | Gln | Gln | Gln | Asn | Pro | Met | Met | Gln | Gln | Gln | Met | His | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     | Arg |
| Gly | Arg | Met | Phe | Arg | Tyr | Pro | Gln | Gly | Arg | Gly | Gly | Ser | Gly | Asp |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     | Val |
| Pro | Pro | Tyr | Asp | Met | Gly | Asn | Asn | Met | Pro | Leu | Thr | Ile | Gly | Ala |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 | Leu |
| Ala | Ser | Asn | Leu | Ser | Asn | Ala | Thr | Pro | Glu | Gln | Gln | Arg | Thr | Met |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 | Leu |
| Gly | Glu | Val | Leu | Tyr | Pro | Leu | Val | Glu | Gln | Val | Glu | Ala | Glu | Ser |
|     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     | Ala |
| Ala | Lys | Val | Thr | Gly | Met | Leu | Leu | Glu | Met | Asp | Gln | Thr | Glu | Val |
|     | 450 |     |     |     |     | 455 |     |     |     | 460 |     |     |     | Leu |
| His | Leu | Leu | Glu | Ser | Pro | Glu | Ala | Leu | Lys | Ala | Lys | Val | Ala | Glu |
| 465 |     |     |     |     | 470 |     |     |     | 475 |     |     |     |     | Ala |
| Met | Asp | Val | Leu | Arg | Ser | Val | Ala | Ala | Gly | Ala | Ala | Thr | Glu | Gln |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 | Leu |
| Ala | Ser | Leu | Asn | Leu | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     | 500 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1571000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Asn | Asp | Lys | Gln | Val | Tyr | Val | Gly | Pro | Phe | Leu | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Glu | Arg | Asp | Ser | Thr | Ala | Asn | Lys | Thr | Lys | Phe | Thr | Asn | Val | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Asn | Leu | Ala | Glu | Ser | Thr | Thr | Asp | Asp | Asp | Leu | Lys | Asn | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Gly | Glu | Tyr | Gly | Lys | Ile | Thr | Ser | Ala | Val | Val | Met | Lys | Asp | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Lys | Ser | Lys | Gly | Phe | Gly | Phe | Val | Asn | Phe | Glu | Asn | Ala | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Ala | Ala | Arg | Ala | Val | Glu | Ser | Leu | Asn | Gly | His | Lys | Phe | Asp | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Glu | Trp | Tyr | Val | Gly | Arg | Ala | Gln | Lys | Lys | Ser | Glu | Arg | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Xaa | Leu | Arg | Val | Arg | Tyr | Glu | Gln | Asn | Leu | Lys | Glu | Ala | Ala | Asp | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Lys | Ser | Ser | Asn | Leu | Tyr | Val | Lys | Asn | Leu | Asp | Pro | Ser | Ile | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Glu | Lys | Leu | Lys | Glu | Ile | Phe | Ser | Pro | Phe | Gly | Thr | Val | Thr | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Lys | Val | Met | Arg | Asp | Pro | Asn | Gly | Thr | Ser | Lys | Gly | Ser | Gly | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ala | Phe | Ala | Thr | Pro | Glu | Glu | Ala | Thr | Glu | Ala | Met | Ser | Gln | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Gly | Lys | Met | Ile | Glu | Ser | Lys | Pro | Leu | Tyr | Val | Ala | Ile | Ala | Gln |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Lys | Glu | Asp | Arg | Arg | Val | Arg | Leu | Gln | Ala | Gln | Phe | Ser | Gln | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Pro | Val | Ala | Met | Gln | Pro | Ser | Val | Gly | Pro | Arg | Met | Pro | Val | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Pro | Gly | Gly | Pro | Gly | Ile | Gly | Gln | Gln | Met | Phe | Tyr | Gly | Gln | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Pro | Ala | Met | Ile | Pro | Pro | Gln | Pro | Gly | Tyr | Gly | Tyr | Gln | Gln | Gln |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Val | Pro | Gly | Met | Arg | Pro | Gly | Gly | Gly | Pro | Val | Pro | Ser | Phe | Phe |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Met | Pro | Met | Val | Gln | Pro | Gln | Gln | Gln | Arg | Pro | Gly | Gly | Gly | Arg | Arg |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Gly | Gly | Ile | Gln | His | Ser | Gln | Gln | Gln | Asn | Pro | Met | Met | Gln | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Met | His | Pro | Arg | Gly | Arg | Met | Phe | Arg | Tyr | Pro | Gln | Gly | Arg | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Ser | Gly | Asp | Val | Pro | Pro | Tyr | Asp | Met | Gly | Asn | Asn | Met | Pro | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Ile | Gly | Ala | Leu | Ala | Ser | Asn | Leu | Ser | Asn | Ala | Thr | Pro | Glu | Gln |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Gln | Arg | Thr | Met | Leu | Gly | Glu | Val | Leu | Tyr | Pro | Leu | Val | Glu | Gln | Val |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Ala | Glu | Ser | Ala | Ala | Lys | Val | Thr | Gly | Met | Leu | Leu | Glu | Met | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gln | Thr | Glu | Val | Leu | His | Leu | Leu | Glu | Ser | Pro | Glu | Ala | Leu | Lys | Ala |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Lys | Val | Ala | Glu | Ala | Met | Asp | Val | Leu | Arg | Ser | Val | Ala | Ala | Gly | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Thr | Glu | Gln | Leu | Ala | Ser | Leu | Asn | Leu | Ser |     |     |     |     |     |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1795:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 383 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..383  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571001  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Met Lys Asp Gly Glu Gly Lys Ser Lys Gly Phe Gly Phe Val Asn Phe  
1                   5                   10                   15  
Glu Asn Ala Asp Asp Ala Ala Arg Ala Val Glu Ser Leu Asn Gly His  
                  20                   25                   30  
Lys Phe Asp Asp Lys Glu Trp Tyr Val Gly Arg Ala Gln Lys Lys Ser  
                  35                   40                   45  
Glu Arg Glu Thr Xaa Leu Arg Val Arg Tyr Glu Gln Asn Leu Lys Glu  
                  50                   55                   60  
Ala Ala Asp Lys Phe Lys Ser Ser Asn Leu Tyr Val Lys Asn Leu Asp  
65                   70                   75                   80  
Pro Ser Ile Ser Asp Glu Lys Leu Lys Glu Ile Phe Ser Pro Phe Gly  
                  85                   90                   95  
Thr Val Thr Ser Ser Lys Val Met Arg Asp Pro Asn Gly Thr Ser Lys  
                  100                   105                   110  
Gly Ser Gly Phe Val Ala Phe Ala Thr Pro Glu Glu Ala Thr Glu Ala  
                  115                   120                   125  
Met Ser Gln Leu Ser Gly Lys Met Ile Glu Ser Lys Pro Leu Tyr Val  
130                   135                   140  
Ala Ile Ala Gln Arg Lys Glu Asp Arg Arg Val Arg Leu Gln Ala Gln  
145                   150                   155                   160  
Phe Ser Gln Val Arg Pro Val Ala Met Gln Pro Ser Val Gly Pro Arg  
                  165                   170                   175  
Met Pro Val Tyr Pro Pro Gly Gly Pro Gly Ile Gly Gln Gln Met Phe  
                  180                   185                   190  
Tyr Gly Gln Ala Pro Pro Ala Met Ile Pro Pro Gln Pro Gly Tyr Gly  
195                   200                   205  
Tyr Gln Gln Gln Leu Val Pro Gly Met Arg Pro Gly Gly Gly Pro Val  
210                   215                   220  
Pro Ser Phe Phe Met Pro Met Val Gln Pro Gln Gln Gln Arg Pro Gly  
225                   230                   235                   240  
Gly Gly Arg Arg Pro Gly Gly Ile Gln His Ser Gln Gln Gln Asn Pro  
                  245                   250                   255  
Met Met Gln Gln Gln Met His Pro Arg Gly Arg Met Phe Arg Tyr Pro  
                  260                   265                   270  
Gln Gly Arg Gly Gly Ser Gly Asp Val Pro Pro Tyr Asp Met Gly Asn  
275                   280                   285  
Asn Met Pro Leu Thr Ile Gly Ala Leu Ala Ser Asn Leu Ser Asn Ala  
290                   295                   300  
Thr Pro Glu Gln Gln Arg Thr Met Leu Gly Glu Val Leu Tyr Pro Leu  
305                   310                   315                   320  
Val Glu Gln Val Glu Ala Glu Ser Ala Ala Lys Val Thr Gly Met Leu  
                  325                   330                   335  
Leu Glu Met Asp Gln Thr Glu Val Leu His Leu Leu Glu Ser Pro Glu  
340                   345                   350  
Ala Leu Lys Ala Lys Val Ala Glu Ala Met Asp Val Leu Arg Ser Val  
355                   360                   365  
Ala Ala Gly Ala Ala Thr Glu Gln Leu Ala Ser Leu Asn Leu Ser  
370                   375                   380

- (2) INFORMATION FOR SEQ ID NO:1796:  
    (i) SEQUENCE CHARACTERISTICS:

2025 RELEASE UNDER E.O. 14176

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..862

(D) OTHER INFORMATION: / Ceres Seq. ID 1571014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| agtttctctt | tacttccctc | tttctctgag | ctatggagat | tactgtaatc  | gcttcttctt  | 60  |
| caatcgatga | aggaattgga | agttgggac  | tcaaaaccgg | gacagagcag  | cttcaattca  | 120 |
| agccgtgtgc | ttctccggcg | catggtctca | ccgccgtcgg | caaaaatttc  | tcgcctcttc  | 180 |
| tcagctctcg | gcgagaaata | cttctggctc | gattttttac | tggctcttga  | ctaagcctca  | 240 |
| agctgaagtg | aagagctacc | cagtgggaac | aataaaggct | cttgacagca  | acaatgaagg  | 300 |
| aaottattta | gttgggtgtg | gaatctctgg | agatatttac | ctttgggagg  | ttgcgactgg  | 360 |
| gaagttgctt | aagaagtggc | atggttcaag | gccggttcac | agatcttcag  | cgacggagga  | 420 |
| ttggactact | tgggcaaccc | gagcttggtc | cacgctcaga | gcattcttagc | catttggggt  | 480 |
| actcaagtta | tcctcatggg | agctgttgaa | ggctacagag | tcgccggaga  | tggctccattg | 540 |
| ggagaagcag | aggacttgct | ttaccacagg | ggcagcttcg | acccattggg  | cctcgctact  | 600 |
| gaccccgagg | ctttcgcaga | gttgaagggt | aaggagctca | agaacggaag  | gttggctatg  | 660 |
| ttctctatgt | ttggattctt | cgttcaagcc | atcgtcaccg | gaaagggaac  | tttggagaac  | 720 |
| ctgcgcgacc | atttgccga  | cccagtcac  | aacaacgctt | gggccttcgc  | caccaaCttc  | 780 |
| gtccccggaa | agtgaagcgg | tgcttattat | gtgaatgaga | gcagagaaaag | agagtttgtt  | 840 |
| tgtggtctat | tctatgtaaa | ac         |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1571015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Thr | Val | Ile | Ala | Ser | Ser | Ser | Ile | Asp | Glu | Gly | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ser | Trp | Asp | Leu | Lys | Thr | Gly | Thr | Glu | Gln | Leu | Gln | Phe | Lys | Pro | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Pro | Ala | His | Gly | Leu | Thr | Ala | Val | Gly | Lys | Asn | Phe | Ser | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Leu | Ser | Ser | Arg | Arg | Glu | Ile | Leu | Leu | Ala | Arg | Phe | Phe | Thr | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Leu | Ser | Leu | Lys |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1571016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Glu | Leu | Glu | Val | Gly | Ile | Ser | Lys | Pro | Gly | Gln | Ser | Ser | Phe |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

Asn Ser Ser Arg Val Leu Leu Arg Arg Met Val Ser Pro Pro Ser Ala  
20 25 30  
Lys Ile Ser Arg Leu Leu Ser Ala Leu Gly Glu Lys Tyr Phe Trp Leu  
35 40 45  
Asp Phe Leu Leu Val Leu Asp  
50 55

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1571017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

Met Gly Ala Val Glu Gly Tyr Arg Val Ala Gly Asp Gly Pro Leu Gly  
1 5 10 15  
Glu Ala Glu Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly  
20 25 30  
Leu Ala Thr Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu  
35 40 45  
Lys Asn Gly Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln  
50 55 60  
Ala Ile Val Thr Gly Lys Gly Pro Leu Glu Asn Leu Ala Asp His Leu  
65 70 75 80  
Ala Asp Pro Val Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val  
85 90 95  
Pro Gly Lys

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1244

(D) OTHER INFORMATION: / Ceres Seq. ID 1571021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acaSRcatat acattcacat tactaatctc tcaagatttc acaattttct tgtgattttc  | 60   |
| tctcagtttc ttatttcggt tcataacatg gatgccatga gtagcgtaga cgagagctct  | 120  |
| acaactacag attccattcc ggcgagaaag tcatcgcttc cggcgagttt actatataga  | 180  |
| atgggaagcg gaacaagcgt ggtacttgat tcagagaacg gtgtcgaagt cgaagtcgaa  | 240  |
| gccgaatcaa gaaagcttcc ttcttcaaga ttcaaagggtg ttgttcctca accaaatgga | 300  |
| agatggggag ctcagattta cgagaaacat caacgcgtgt ggcttggtac tttcaacgag  | 360  |
| gaagacgaag cagctcgtgc ttacgacgtc gcggctcacc gtttcggtg ccgcgatgcc   | 420  |
| gttactaatt tcaaagacac gacgttcgaa gaagagggtg agttcttaaa cgcgcatcgc  | 480  |
| aaatcagaga tcgtagatat gttgagaaaa cacacttaca aagaagagtt agaccaaagg  | 540  |
| aaacgtaacc gtgacggtaa cggaaaagag acgacggcgt ttgctttggc ttcgatgggtg | 600  |
| gttatgacgg ggtttaaaac ggcggagtta ctgtttgaga aaacggtaac gccaaagtac  | 660  |
| tgcgggaac taaaccgttt agttatacca aaacaccaag cggagaaaca ttttcggtta   | 720  |
| ccgttaggta ataataacgt ctccgttaaa ggtatgctgt tgaatttcga agacgttaac  | 780  |
| gggaaagtgt ggaggttccg ttactcttat tggaatagta gtcaaagtta tgtgttgacc  | 840  |
| aaaggttgga gtagattcgt taaagagaag agactttgtg ctggtgattt gatcagtttt  | 900  |
| aaaagatcca acgatcaaga tcaaaaattc tttatcgggt ggaaatcgaa atccgggttg  | 960  |
| gatctagaga cgggtcgggt tatgagattg tttgggggtg atattttttt aaacgccgtc  | 1020 |

```
gttgtagtga aggaacaac ggaggtgtta atgtcgtcgt taagggtgtaa gaatcaacga 1080
gttttgtaat aacaatttaa caacttgga aagaaaaaaa aagctttttg attttaattt 1140
ctcttcaacg ttaattctgc tgagattatt tatgttgtaa gttgtaacaa gtggaaaaaa 1200
ttaattaggt gtcaaacaaa tcttggttta atattcttg tatg
```

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..362

(D) OTHER INFORMATION: / Ceres Seq. ID 1571022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

```
Thr Xaa Ile Tyr Ile His Ile Thr Asn Leu Ser Arg Phe His Asn Phe
1 5 10 15
Leu Val Ile Phe Ser Gln Phe Leu Ile Ser Phe His Asn Met Asp Ala
20 25 30
Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser Ile Pro Ala
35 40 45
Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met Gly Ser Gly
50 55 60
Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val Glu Val Glu
65 70 75 80
Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly Val Val Pro
85 90 95
Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg
100 105 110
Val Trp Leu Gly Thr Phe Asn Glu Asp Glu Ala Ala Arg Ala Tyr
115 120 125
Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe
130 135 140
Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn Ala His Ser
145 150 155 160
Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Lys Glu Glu
165 170 175
Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys Glu Thr Thr
180 185 190
Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe Lys Thr Ala
195 200 205
Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
210 215 220
Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His Phe Pro Leu
225 230 235
Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu Leu Asn Phe
245 250 255
Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
260 265 270
Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
275 280 285
Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys Arg Ser Asn
290 295 300
Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys Ser Gly Leu
305 310 315 320
Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val Asp Ile Ser
325 330 335
Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val Leu Met Ser
340 345 350
Ser Leu Arg Cys Lys Asn Gln Arg Val Leu
```



355 360  
(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1571023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser  
1 5 10 15  
Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met  
20 25 30  
Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val  
35 40 45  
Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly  
50 55 60  
Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys  
65 70 75 80  
His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala  
85 90 95  
Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val  
100 105 110  
Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn  
115 120 125  
Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr  
130 135 140  
Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys  
145 150 155 160  
Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe  
165 170 175  
Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val  
180 185 190  
Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His  
195 200 205  
Phe Pro Leu Pro Leu Gly Asn Asn Val Ser Val Lys Gly Met Leu  
210 215 220  
Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser  
225 230 235 240  
Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg  
245 250 255  
Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys  
260 265 270  
Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys  
275 280 285  
Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val  
290 295 300  
Asp Ile Ser Leu Asn Ala Val Val Val Val Lys Glu Thr Thr Glu Val  
305 310 315 320  
Leu Met Ser Ser Leu Arg Cys Lys Asn Gln Arg Val Leu  
325 330

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..330
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571024
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

```

Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser Ile Pro Ala
1 5 10 15
Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met Gly Ser Gly
 20 25 30
Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val Glu Val Glu
 35 40 45
Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly Val Val Pro
 50 55 60
Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg
 65 70 75 80
Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala Tyr
 85 90 95
Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe
 100 105 110
Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn Ala His Ser
 115 120 125
Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Lys Glu Glu
 130 135 140
Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys Glu Thr Thr
 145 150 155 160
Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe Lys Thr Ala
 165 170 175
Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
 180 185 190
Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His Phe Pro Leu
 195 200 205
Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu Leu Asn Phe
 210 215 220
Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
 225 230 235 240
Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
 245 250 255
Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys Arg Ser Asn
 260 265 270
Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys Ser Gly Leu
 275 280 285
Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val Asp Ile Ser
 290 295 300
Leu Asn Ala Val Val Val Lys Glu Thr Thr Glu Val Leu Met Ser
 305 310 315 320
Ser Leu Arg Cys Lys Asn Gln Arg Val Leu
 325 330

```

(2) INFORMATION FOR SEQ ID NO:1804:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1140 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

ctttctcaga ttctgctcttt cccgagaaaa ttggaagaaa cagagattca tcattttctc

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| ttcctctcaa  | aaatcagatc  | tgcaaaactc  | tcagatcact | catggggttg  | atttcaaacc  | 120  |
| ctacccggtt  | gattctcgtc  | gccaccatct  | tcttctcgt  | ttcttcaatc  | tccggtcagg  | 180  |
| attctgtcgt  | tgagaacaat  | gagagacaag  | aatctgaagg | atctggtaaa  | gagcttggtc  | 240  |
| gtcgtggaat  | ggttgggtact | gaacgaattg  | gagttgatac | tgttgtagac  | aatattgggtg | 300  |
| ctcttggttt  | gaatctagac  | cttgatgcta  | ctgctcctag | tgtatttgat  | gctttgtttt  | 360  |
| cgagtttctc  | gatgatactt  | gtcaccgaga  | ttggggatga | aacttttata  | atagcggcat  | 420  |
| tgatggctat  | gcgacatcct  | aaagctactg  | ttttatctgg | tgactctca   | gctttgtttg  | 480  |
| tkakgactat  | actGttctac  | tggtcttggt  | aggatagtgc | caaacttgat  | atcgaggaag  | 540  |
| cacaccaata  | gtgctgtctac | agtgtcttat  | gcattttttg | gtttgcgact  | actctacatt  | 600  |
| gcttgagggt  | ctactgattc  | aaagtcaaat  | cagaagaaag | aaatggagga  | agttgaagag  | 660  |
| aagctcgagt  | cagggtcaagg | gaagacaccc  | ttccgtcgtt | tattctcaag  | attttgtacc  | 720  |
| ccaatatttc  | tgagatcctt  | catcttaacc  | tttctagctg | aatgggggtga | ccgtagccag  | 780  |
| atcgctacaa  | tagctttggc  | gactcacaag  | aacgccatag | gagtggccat  | tggggcaagt  | 840  |
| attggacaca  | ctgtgtgtac  | ttcactagca  | gttgttgagg | gaagcatgct  | ggcttcaagg  | 900  |
| atctcgcaac  | gtacgggtgc  | aactgttgga  | ggcttactct | tcctcggctt  | ttcagtctcc  | 960  |
| tcctattttct | atcctccatt  | gtagtaaagt  | tgcttctttc | gaaaatgggt  | gttagagaca  | 1020 |
| atttctaagt  | aaagtttcaa  | tttttttttt  | gattttaatt | taagtttgat  | ttttgtttaa  | 1080 |
| tatcaatggc  | caaatggcc   | aaaccaaaaga | atccaacgcc | tatgctttta  | caatttactt  | 1140 |

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1571032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Ile | Ser | Asn | Pro | Thr | Arg | Leu | Ile | Leu | Val | Ala | Thr | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Phe | Leu | Val | Ser | Ser | Ile | Ser | Gly | Gln | Asp | Ser | Val | Val | Glu | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asn | Glu | Arg | Gln | Glu | Ser | Glu | Gly | Ser | Gly | Lys | Glu | Leu | Gly | Arg | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Met | Val | Gly | Thr | Glu | Arg | Ile | Gly | Val | Asp | Thr | Val | Val | Asp | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ile | Gly | Ala | Leu | Gly | Leu | Asn | Leu | Asp | Leu | Asp | Ala | Thr | Ala | Pro | Ser |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Val | Phe | Asp | Ala | Leu | Phe | Ser | Ser | Phe | Ser | Met | Ile | Leu | Val | Thr | Glu |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Gly | Asp | Glu | Thr | Phe | Ile | Ile | Ala | Ala | Leu | Met | Ala | Met | Arg | His |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Lys | Ala | Thr | Val | Leu | Ser | Gly | Ala | Leu | Ser | Ala | Leu | Phe | Xaa | Xaa |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ile | Leu | Phe | Tyr | Trp | Thr | Trp |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1571033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

00000000-00000000

Met Val Gly Thr Glu Arg Ile Gly Val Asp Thr Val Val Asp Asn Ile  
1 5 10 15  
Gly Ala Leu Gly Leu Asn Leu Asp Leu Asp Ala Thr Ala Pro Ser Val  
20 25 30  
Phe Asp Ala Leu Phe Ser Ser Phe Ser Met Ile Leu Val Thr Glu Ile  
35 40 45  
Gly Asp Glu Thr Phe Ile Ile Ala Ala Leu Met Ala Met Arg His Pro  
50 55 60  
Lys Ala Thr Val Leu Ser Gly Ala Leu Ser Ala Leu Phe Xaa Xaa Thr  
65 70 75 80  
Ile Leu Phe Tyr Trp Thr Trp  
85

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Met Glu Glu Val Glu Glu Lys Leu Glu Ser Gly Gln Gly Lys Thr Pro  
1 5 10 15  
Phe Arg Arg Leu Phe Ser Arg Phe Cys Thr Pro Ile Phe Leu Glu Ser  
20 25 30  
Phe Ile Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Ile Ala  
35 40 45  
Thr Ile Ala Leu Ala Thr His Lys Asn Ala Ile Gly Val Ala Ile Gly  
50 55 60  
Ala Ser Ile Gly His Thr Val Cys Thr Ser Leu Ala Val Val Gly Gly  
65 70 75 80  
Ser Met Leu Ala Ser Arg Ile Ser Gln Arg Thr Val Ala Thr Val Gly  
85 90 95  
Gly Leu Leu Phe Leu Gly Phe Ser Val Ser Ser Tyr Phe Tyr Pro Pro  
100 105 110  
Leu

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| atcaacaaa  | acaaaacata  | aaaaacaagt | ggaagcttta | aaacgagagg | gagagagcaa | 60  |
| aaatggcgac | gtcgggaacg  | tacgtgacgg | aagttccgct | aaaaggatcg | gccgagaaat | 120 |
| actacaagag | gtggaagaac  | gagaaccatg | tcttccctga | tgctatcggc | caccacatcc | 180 |
| aaaatgttac | cgttcacgaa  | ggcgaacatg | actctcacgg | Gtctatcagg | agttggaact | 240 |
| acacatggga | tggaaaaggag | gaggtgttca | aggagagaag | agagatagac | gatgagacca | 300 |
| aaacgttgac | gttaagagga  | cttgagggtc | acgtgatgga | gcagctcaaa | gtgtacgacg | 360 |
| tcgtctacca | attcattccc  | aaatctgagg | atacctgcat | cggcaaaatc | actttaatat | 420 |
| gggagaagcg | caacgatgat  | tccccagaac | caagcggcta | catgaaattc | gtcaagagct | 480 |
| tggttgctga | catgggaaac  | cacgttagca | aaacttaatc | atcattccca | cagtcgctcg | 540 |

catcatcatc atcatcatca tcatcatcat catcatcatc atcatcatca tcatcatcat 600  
catcatcatc atcatcacta tctcgattta taagttaaga tgttttcagt ataataaatg 660  
gggtcttggt gatcggttcat ttctatgtgt aaaccgtttg gttctgtatg atgcttcgat 720  
atattggtat gttcatgatc atatgtcggg ttcgatataa tgattcttaa gattaattta 780  
ct

(2) INFORMATION FOR SEQ ID NO:1809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser  
1 5 10 15  
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro  
20 25 30  
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu  
35 40 45  
His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly  
50 55 60  
Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys  
65 70 75 80  
Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys  
85 90 95  
Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys  
100 105 110  
Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro  
115 120 125  
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met  
130 135 140  
Gly Asn His Val Ser Lys Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:1810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..682
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

agtgagtgag agaagaatca gagaaaaatgc cgccgaaatt ggatccatct caaatcgctcg 60  
acgtctacgt ccgagtcacc ggaggKgagN gtcggagcag cgtcttcact cgctccaaag 120  
atcggtccac tcggtctggc accaaagaag atcggagaag acatcgccaa agagacagcg 180  
aaagaatgga aaggctcttcg agtcaccgtg aagcttacgg tacagaatcg tcaagctaag 240  
gtcacagtgg ttccatccgc agcggctcta gtcacaaaag ccctcaagga gccagagaga 300  
gataggaaga aagtgaagaa catcaaacat aatggcaaca ttctgtttga tgatgtgatt 360  
gagattgcta agataatgcg tcctagatct atcgctaagg aattgagtgg aacagtgaag 420  
gagatttttag gaacttggtg ctctgttggt tgcactgttg atggtaaaga ccctaaggat 480  
cttcaggaag aaattaacag tgggtgacatt gatattccta acgagtgata aaggttttta 540  
cttttgagtt ctctatcggt ttattttttg tatttgattt tgaggatttg gtattagtaa 600  
tactatatatt cggaagtga gaattgttg cttttgccca tttgaatcct ttcttgggat 660  
taatcaaaat gttcaatttt ct

(2) INFORMATION FOR SEQ ID NO:1811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

Val Ser Glu Arg Ile Arg Glu Asn Ala Ala Glu Ile Gly Ser Ile  
1 5 10 15  
Ser Asn Arg Arg Arg Leu Arg Pro Ser His Arg Arg Xaa Xaa Ser Glu  
20 25 30  
Gln Arg Leu His Ser Leu Gln Arg Ser Val His Ser Val Trp His Gln  
35 40 45  
Arg Arg Ser Glu Lys Thr Ser Pro Lys Arg Gln Arg Lys Asn Gly Lys  
50 55 60  
Val Phe Glu Ser Pro  
65

(2) INFORMATION FOR SEQ ID NO:1812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

Met Pro Pro Lys Leu Asp Pro Ser Gln Ile Val Asp Val Tyr Val Arg  
1 5 10 15  
Val Thr Gly Xaa Glu Xaa Arg Ser Ser Val Phe Thr Arg Ser Lys Asp  
20 25 30  
Arg Ser Thr Arg Ser Gly Thr Lys Glu Asp Arg Arg Arg His Arg Gln  
35 40 45  
Arg Asp Ser Glu Arg Met Glu Arg Ser Ser Ser His Arg Glu Ala Tyr  
50 55 60  
Gly Thr Glu Ser Ser Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

Met Arg Pro Arg Ser Ile Ala Lys Glu Leu Ser Gly Thr Val Lys Glu  
1 5 10 15  
Ile Leu Gly Thr Cys Val Ser Val Gly Cys Thr Val Asp Gly Lys Asp  
20 25 30  
Pro Lys Asp Leu Gln Glu Glu Ile Asn Ser Gly Asp Ile Asp Ile Pro

35 40 45  
Asn Glu  
50

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..585
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| ataaacaaaa  | agaatttgaa | ccaacaaagc | aaaacatgaa  | aggcacattc | actaacttgc | 60  |
| ttgtgctcct  | cctcattgca | cttgtttgtg | ccaatgtcgg  | tgctaggaaa | gttatctccg | 120 |
| aagataccca  | attcaaggat | gaaaaatctt | tcctcggagg  | cagtggcagc | ggtgatggct | 180 |
| tagggccttg  | ccttggtgga | ggagctggtc | ttggtgggct  | tgggattggg | gctgggatcg | 240 |
| gcgcgggagc  | cggactaggg | ttaggtggag | gcggccttgg  | gggaggagcc | ggtggcggac | 300 |
| tcgggtggcct | tccttgaacg | tattgacaag | tgtgcgtgtg  | agagctgatt | ctcagcttat | 360 |
| tactaattaa  | ttaagttact | ttcattctct | taataaaaatc | tagagggttt | gaatttcgga | 420 |
| tttcttcagc  | tttaatttaa | acttcaatat | ttgaacccaa  | aaaggtctta | gctactagag | 480 |
| gtaatgctcg  | taatcgattt | atgtgtAacg | ccggttctga  | tattcttatg | tgcaagtgtg | 540 |
| gaacgtttct  | cttttattca | ctatatagca | ttactttctt  | ttttt      |            |     |

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Lys | Glu | Glu | Pro | Thr | Lys | Gln | Asn | Met | Lys | Gly | Thr | Phe |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Asn | Leu | Leu | Val | Leu | Leu | Ile | Ala | Leu | Val | Cys | Ala | Asn | Val |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Ala | Arg | Lys | Val | Ile | Ser | Glu | Asp | Thr | Gln | Phe | Lys | Asp | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ser | Phe | Leu | Gly | Gly | Ser | Gly | Ser | Gly | Asp | Gly | Leu | Gly | Leu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Gly | Ala | Gly | Leu | Gly | Gly | Leu | Gly | Ile | Gly | Ala | Gly | Ile |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Gly | Ala | Gly | Leu | Gly | Leu | Gly | Gly | Gly | Phe | Gly | Gly | Gly | Ala |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Gly | Gly | Leu | Gly | Gly | Leu | Pro |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1571064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

Met Lys Gly Thr Phe Thr Asn Leu Leu Val Leu Leu Leu Ile Ala Leu  
1 5 10 15  
Val Cys Ala Asn Val Gly Ala Arg Lys Val Ile Ser Glu Asp Thr Gln  
20 25 30  
Phe Lys Asp Glu Lys Ser Phe Leu Gly Gly Ser Gly Ser Gly Asp Gly  
35 40 45  
Leu Gly Leu Gly Leu Gly Gly Gly Ala Gly Leu Gly Gly Leu Gly Ile  
50 55 60  
Gly Ala Gly Ile Gly Ala Gly Ala Gly Leu Gly Leu Gly Gly Gly Gly  
65 70 75 80  
Phe Gly Gly Gly Ala Gly Gly Gly Leu Gly Gly Leu Pro  
85 90

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..718

(D) OTHER INFORMATION: / Ceres Seq. ID 1571079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

attcaaagac atacaaaata attgagtttt ttttttttaa ttagaaaacaa atgggggttga 60  
gtggtgttct tcatgtggag gttgaggtta agtctccggc tgaaaagttc tgggtagccc 120  
tcggcgacgg catcaatctc ttcccaaag ctttccctaa cgactacaaa accatccaag 180  
ttctagccgg cgacggcaac gctcctggct ccattcgctt cattacttat ggagaaggat 240  
ctccactggt gaagatatcg gcggagagga tcgaagcagt ggatttggag aacaaaagca 300  
tgtcatacag catcattggc ggcgaaatgt tggagtacta caaacggtc aaaggaacca 360  
tcaccgttat tectaagaac ggtggcagcc ttctgaaatg gtctgtgag tttgagaaga 420  
ccgcccata gaattgatgac ccacacgtca tcaaggactt tgctgtcaag aacttcaaag 480  
agatagatga gtatctcctt aagcaaaacta gtgcctaaca ctagaacctt taaattatat 540  
Maagagggtt cgatcgcttc tataagattt ttctaattaa gaagttgaat aaagtgaac 600  
ctctttatga atatccaagt ttgtgatttc ggagtttatg cagcctagta ggccataagc 660  
tttttataaa agccaattta gtcgaacatt ttgaaaaaat cgaacctttt ggtaaaagc

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1571080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Gly Leu Ser Gly Val Leu His Val Glu Val Glu Val Lys Ser Pro  
1 5 10 15  
Ala Glu Lys Phe Trp Val Ala Leu Gly Asp Gly Ile Asn Leu Phe Pro  
20 25 30  
Lys Ala Phe Pro Asn Asp Tyr Lys Thr Ile Gln Val Leu Ala Gly Asp  
35 40 45  
Gly Asn Ala Pro Gly Ser Ile Arg Leu Ile Thr Tyr Gly Glu Gly Ser  
50 55 60  
Pro Leu Val Lys Ile Ser Ala Glu Arg Ile Glu Ala Val Asp Leu Glu  
65 70 75 80  
Asn Lys Ser Met Ser Tyr Ser Ile Ile Gly Gly Glu Met Leu Glu Tyr



85 90 95  
Tyr Lys Thr Phe Lys Gly Thr Ile Thr Val Ile Pro Lys Asn Gly Gly  
100 105 110  
Ser Leu Leu Lys Trp Ser Gly Glu Phe Glu Lys Thr Ala His Glu Ile  
115 120 125  
Asp Asp Pro His Val Ile Lys Asp Phe Ala Val Lys Asn Phe Lys Glu  
130 135 140  
Ile Asp Glu Tyr Leu Leu Lys Gln Thr Ser Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..499
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atcagttctg | cttctgcttt | agaaattagg | Gttccctttt  | tgaagaagac | gagtattcac | 60  |
| ttcttctcac | cgtgaagcga | tggcttcttt | gttcaaggag  | caagcaaagc | tatcagctta | 120 |
| tcgagataga | agattttcag | gaacacaaga | ggagtttgat  | gaagcgctaa | gagcatctac | 180 |
| aacggtttac | attggcaatg | tgtcttttta | cactactgaa  | gaacagcttt | acgagctttt | 240 |
| ctctagagct | ggagaaatca | aaaagatcat | catgggtttg  | gataagaaca | ctaaaacacc | 300 |
| ttgtggcttt | tgtttcgctc | tgttctactc | tagagaggat  | actgaagatg | cagtcaagta | 360 |
| tataagtggg | actattctcg | atgaccggcc | tattcgtgtg  | gattttgatt | ggggattcca | 420 |
| agaaggaaga | caatggggcc | gtggtagaag | cggtgggccag | gttcgtgatg | aataccgtac | 480 |
| agattacgat | cctggccac  |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Leu | Phe | Lys | Glu | Gln | Ala | Lys | Leu | Ser | Ala | Tyr | Arg | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Phe | Ser | Gly | Thr | Gln | Glu | Glu | Phe | Asp | Glu | Ala | Leu | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Thr | Val | Tyr | Ile | Gly | Asn | Val | Ser | Phe | Tyr | Thr | Thr | Glu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Leu | Tyr | Glu | Leu | Phe | Ser | Arg | Ala | Gly | Glu | Ile | Lys | Lys | Ile | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Met | Gly | Leu | Asp | Lys | Asn | Thr | Lys | Thr | Pro | Cys | Gly | Phe | Cys | Phe | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Phe | Tyr | Ser | Arg | Glu | Asp | Thr | Glu | Asp | Ala | Val | Lys | Tyr | Ile | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Thr | Ile | Leu | Asp | Asp | Arg | Pro | Ile | Arg | Val | Asp | Phe | Asp | Trp | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gln | Glu | Gly | Arg | Gln | Trp | Gly | Arg | Gly | Arg | Ser | Gly | Gly | Gln | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Arg | Asp | Glu | Tyr | Arg | Thr | Asp | Tyr | Asp | Pro | Gly | His |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571087  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:  
Met Gly Leu Asp Lys Asn Thr Lys Thr Pro Cys Gly Phe Cys Phe Val  
1                  5                  10                  15  
Leu Phe Tyr Ser Arg Glu Asp Thr Glu Asp Ala Val Lys Tyr Ile Ser  
                  20                  25                  30  
Gly Thr Ile Leu Asp Asp Arg Pro Ile Arg Val Asp Phe Asp Trp Gly  
                  35                  40                  45  
Phe Gln Glu Gly Arg Gln Trp Gly Arg Gly Arg Ser Gly Gly Gln Val  
50                  55                  60  
Arg Asp Glu Tyr Arg Thr Asp Tyr Asp Pro Gly His  
65                  70                  75

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 756 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..756  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

aaacaactac aaacaacatt tctgagattg cgccggagtc aaggagaggg agagagcgat 60  
ccaacggttg agatgtttct acgggcaatc ggacggccat tattggctaa agtgaagcag 120  
acgacgggga tcgtcgggct tgacgttggt cccaacgcga gacgggtgct gatcgatctc 180  
tacagcaaaa ccctaaagga gatccaagct gtgccggagg atgaagggtta ccgtNaaagc 240  
ggtggaatca ttcacgcgcc aacgtotcaa tgtgtgcaag gaagaagaag attgggagat 300  
gattgagaag cggcttggtt gtggtcaagt cgaagagctt atcgaagagg ctgcgcatga 360  
gctcacactc attgggaaaa tgatcgagtg ggatccttgg ggtgtaccag atgattacga 420  
gtgtgaagtg attgagaatg atgcgcgat tccaaagcat gttcctcagc accgacctgg 480  
tcctcttctc gagcagttct ataaaacgct tgaaggtcta attgcagagt ctaaaacaga 540  
gatcccagct gctacaccca gcgatccgca gttgaaggag taacttccag tttttacAYa 600  
tatbCgtRvt GcTTgttgct tttttggcta gagttgtttc cgaatcagtg gtcaagcctc 660  
tgaataaatt gcttaataat tttcataacg ataacaatgt ctgttcacaa atgttttata 720  
actcttatta aacaaatgat gtttcttccc ttttgc

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 101 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Lys Gln Leu Gln Thr Thr Phe Leu Arg Leu Arg Arg Ser Gln Gly Glu  
1                  5                  10                  15  
Gly Glu Ser Asp Pro Thr Val Glu Met Phe Leu Arg Ala Ile Gly Arg

20 25 30  
Pro Leu Leu Ala Lys Val Lys Gln Thr Thr Gly Ile Val Gly Leu Asp  
35 40 45  
Val Val Pro Asn Ala Arg Ala Val Leu Ile Asp Leu Tyr Ser Lys Thr  
50 55 60  
Leu Lys Glu Ile Gln Ala Val Pro Glu Asp Glu Gly Tyr Arg Xaa Ser  
65 70 75 80  
Gly Gly Ile Ile His Ala Pro Thr Ser Gln Cys Val Gln Gly Arg Arg  
85 90 95  
Arg Leu Gly Asp Asp  
100

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

Met Lys Gly Thr Xaa Lys Ala Val Glu Ser Phe Thr Arg Gln Arg Leu  
1 5 10 15  
Asn Val Cys Lys Glu Glu Glu Asp Trp Glu Met Ile Glu Lys Arg Leu  
20 25 30  
Gly Cys Gly Gln Val Glu Glu Leu Ile Glu Glu Ala Arg Asp Glu Leu  
35 40 45  
Thr Leu Ile Gly Lys Met Ile Glu Trp Asp Pro Trp Gly Val Pro Asp  
50 55 60  
Asp Tyr Glu Cys Glu Val Ile Glu Asn Asp Ala Pro Ile Pro Lys His  
65 70 75 80  
Val Pro Gln His Arg Pro Gly Pro Leu Pro Glu Gln Phe Tyr Lys Thr  
85 90 95  
Leu Glu Gly Leu Ile Ala Glu Ser Lys Thr Glu Ile Pro Ala Ala Thr  
100 105 110  
Pro Ser Asp Pro Gln Leu Lys Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

Met Ile Glu Lys Arg Leu Gly Cys Gly Gln Val Glu Glu Leu Ile Glu  
1 5 10 15  
Glu Ala Arg Asp Glu Leu Thr Leu Ile Gly Lys Met Ile Glu Trp Asp  
20 25 30  
Pro Trp Gly Val Pro Asp Asp Tyr Glu Cys Glu Val Ile Glu Asn Asp  
35 40 45  
Ala Pro Ile Pro Lys His Val Pro Gln His Arg Pro Gly Pro Leu Pro  
50 55 60  
Glu Gln Phe Tyr Lys Thr Leu Glu Gly Leu Ile Ala Glu Ser Lys Thr  
65 70 75 80

Glu Ile Pro Ala Ala Thr Pro Ser Asp Pro Gln Leu Lys Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aaaaaaactt gcaaaactct cgtccgagat atatcgactc cgcgaccctc cactactctt  | 60   |
| ctgctgatct acacacacac acacaaaaaa aaaaaaactc aatcgccagc aacaatggcg  | 120  |
| aagctcacac ttctcttctt cttttcttt ctcactttct cctcatccat cgctttccaa   | 180  |
| tcagacgagc tcctcggtga cgacgacgaa tttggtctag aaggagcaaa gccccgctcc  | 240  |
| accgatcttt acacatcttc ttcttcttcg ccacagcagc agcaacagac tccaactatc  | 300  |
| cggagaagat actcagatcc taccgatttg gattcaaaag tccaatttac tctcgaacat  | 360  |
| gccttcgggtg actctgattt ctccccgcc ggtactttct ccgctcgtct caaaacctgg  | 420  |
| agtcattggcg gaaagacatt aacgaagctg cgattctcta ggaatgattt ttctgctaaa | 480  |
| gagaaagatg cattcaagaa tctgctgaaa ggagatgact tttatcggat tcggcttcca  | 540  |
| tctaattgtg ttagtccacc agggagagag ttTgtgattg catcagttag agctagatgt  | 600  |
| ctaccacggg atggcttgga tgagcatttc attatacaca tggaagggtgc taacatcttg | 660  |
| gcagttagtt atggttctcc tggggcggtg caatatcctc gccaatgaa acttcagca    | 720  |
| aaatggctgt ttaactctca cacaattctg aaaagcagtg agcaggcgcc aagaactcca  | 780  |
| atattcactg aggagattct aggcagttag aatgtagagg gagaagtga accaccacca   | 840  |
| gagagatcat tttgggcgaa atattggatg tatttgatac cgctgggact cgtagtgtg   | 900  |
| aatgccgtta cacaagcatc aaacatggct gaagaaccgc cgggtggaca ggcaggaggg  | 960  |
| gcacaagtgc aaccagctgc caggagaaga tgattccact tttacttctc ccaaagcaat  | 1020 |
| gaaagctgca gctgggttaga gatgatgatt caacagatct tcatgtaaac catcttgcca | 1080 |
| tcatttggtt ttatgtaacc tttaatttta atcctcgatc ggtgtgtttt tgtactcacc  | 1140 |
| aatcgggaaa tcaaaaatct tgtcttcatt acatatcaag aacaaagaca tttagcagct  | 1200 |
| tccatatctt gttttgata                                               |      |

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Thr | Cys | Lys | Thr | Leu | Val | Arg | Asp | Ile | Ser | Thr | Pro | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Thr | Leu | Leu | Leu | Ile | Tyr | Thr | His | Thr | His | Lys | Lys | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Gln | Ser | Pro | Ala | Thr | Met | Ala | Lys | Leu | Thr | Leu | Leu | Phe | Phe | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Phe | Leu | Ile | Phe | Ser | Ser | Ser | Ile | Ala | Phe | Gln | Ser | Asp | Glu | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Val | Asp | Asp | Asp | Glu | Phe | Gly | Leu | Glu | Gly | Ala | Lys | Pro | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Asp | Leu | Tyr | Thr | Ser | Ser | Ser | Ser | Ser | Pro | Gln | Gln | Gln | Gln | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Pro | Thr | Ile | Arg | Arg | Arg | Tyr | Ser | Asp | Pro | Thr | Asp | Leu | Asp | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Gln | Phe | Thr | Leu | Glu | His | Ala | Phe | Gly | Asp | Ser | Asp | Phe | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Ala | Gly | Thr | Phe | Ser | Ala | Arg | Leu | Lys | Thr | Trp | Ser | His | Gly | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Thr | Leu | Thr | Lys | Leu | Arg | Phe | Ser | Arg | Asn | Asp | Phe | Ser | Ala | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Lys | Asp | Ala | Phe | Lys | Asn | Leu | Leu | Lys | Gly | Asp | Asp | Phe | Tyr | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Arg | Leu | Pro | Ser | Asn | Val | Val | Ser | Pro | Pro | Gly | Arg | Glu | Phe | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ala | Ser | Val | Arg | Ala | Arg | Cys | Leu | Pro | Arg | Asp | Gly | Leu | Asp | Glu |
|     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| His | Phe | Ile | Ile | His | Met | Glu | Gly | Ala | Asn | Ile | Leu | Ala | Val | Ser | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ser | Pro | Gly | Ala | Cys | Gln | Tyr | Pro | Arg | Gln | Leu | Lys | Leu | Pro | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Trp | Ser | Phe | Asn | Ser | His | Thr | Ile | Leu | Lys | Ser | Ser | Glu | Gln | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Arg | Thr | Pro | Ile | Phe | Thr | Glu | Glu | Ile | Leu | Gly | Ser | Glu | Asn | Val |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Glu | Gly | Glu | Val | Glu | Pro | Pro | Pro | Glu | Arg | Ser | Phe | Trp | Ala | Lys | Tyr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Met | Tyr | Leu | Ile | Pro | Leu | Gly | Leu | Val | Val | Met | Asn | Ala | Val | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Ala | Ser | Asn | Met | Ala | Glu | Glu | Pro | Ala | Gly | Gly | Gln | Ala | Gly | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Gln | Val | Gln | Pro | Ala | Ala | Arg | Arg | Arg |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Leu | Thr | Leu | Leu | Phe | Phe | Leu | Ser | Phe | Leu | Ile | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Ile | Ala | Phe | Gln | Ser | Asp | Glu | Leu | Leu | Val | Asp | Asp | Asp | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Leu | Glu | Gly | Ala | Lys | Pro | Arg | Ser | Thr | Asp | Leu | Tyr | Thr | Ser |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Ser | Ser | Pro | Gln | Gln | Gln | Gln | Gln | Thr | Pro | Thr | Ile | Arg | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Tyr | Ser | Asp | Pro | Thr | Asp | Leu | Asp | Ser | Lys | Val | Gln | Phe | Thr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | His | Ala | Phe | Gly | Asp | Ser | Asp | Phe | Ser | Pro | Ala | Gly | Thr | Phe | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Arg | Leu | Lys | Thr | Trp | Ser | His | Gly | Lys | Thr | Leu | Thr | Lys | Leu |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Arg | Phe | Ser | Arg | Asn | Asp | Phe | Ser | Ala | Lys | Glu | Lys | Asp | Ala | Phe | Lys |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Leu | Lys | Gly | Asp | Asp | Phe | Tyr | Arg | Ile | Arg | Leu | Pro | Ser | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Val | Ser | Pro | Pro | Gly | Arg | Glu | Phe | Val | Ile | Ala | Ser | Val | Arg | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Cys | Leu | Pro | Arg | Asp | Gly | Leu | Asp | Glu | His | Phe | Ile | Ile | His | Met |

165 170 175  
Glu Gly Ala Asn Ile Leu Ala Val Ser Tyr Gly Ser Pro Gly Ala Cys  
180 185 190  
Gln Tyr Pro Arg Gln Leu Lys Leu Pro Ala Lys Trp Ser Phe Asn Ser  
195 200 205  
His Thr Ile Leu Lys Ser Ser Glu Gln Ala Pro Arg Thr Pro Ile Phe  
210 215 220  
Thr Glu Glu Ile Leu Gly Ser Glu Asn Val Glu Gly Glu Val Glu Pro  
225 230 235 240  
Pro Pro Glu Arg Ser Phe Trp Ala Lys Tyr Trp Met Tyr Leu Ile Pro  
245 250 255  
Leu Gly Leu Val Val Met Asn Ala Val Thr Gln Ala Ser Asn Met Ala  
260 265 270  
Glu Glu Pro Ala Gly Gly Gln Ala Gly Gly Ala Gln Val Gln Pro Ala  
275 280 285  
Ala Arg Arg Arg  
290

(2) INFORMATION FOR SEQ ID NO:1829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaagtacaaa aaccaacatg gctttgcaaa agtttctct cttggggctg tttctggtcc   | 60  |
| taaccatcct cgtctcttca gcgacagcGg atggacatgt ttgcccgccg tcaacaaaac  | 120 |
| taagccggag atgcaataac gataaagaaa atgtggttgt cagtttcttc catcgttata  | 180 |
| aggttataag tgagtatcct gttccataa aatatttggt gatgtttttc gtttttgttt   | 240 |
| tttattttct atttgtggat aaccaagaac ctatggacta ttggtcgata attccattgg  | 300 |
| gccggggacc gaagaatttg ttggtgttta gtattttatt ttattttaat ttttatatac  | 360 |
| tatgatatgg gacatttatc tataatctttt ggtatcatat atgtaaatat gtgatttgca | 420 |
| aatgtttaaa agataattca ttaccggaaa tggtgaaatc aatagttttt             |     |

(2) INFORMATION FOR SEQ ID NO:1830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

Ser Thr Lys Thr Asn Met Ala Leu Gln Lys Phe Pro Leu Leu Gly Leu  
1 5 10 15  
Phe Leu Val Leu Thr Ile Leu Val Ser Ser Ala Thr Ala Asp Gly His  
20 25 30  
Val Cys Pro Pro Ser Thr Lys Leu Ser Arg Arg Cys Asn Asn Asp Lys  
35 40 45  
Glu Asn Val Val Val Ser Phe Phe His Arg Tyr Lys Val Ile Ser Glu  
50 55 60  
Tyr Pro Val Ser Ile Lys Tyr Leu Leu Met Phe Phe Val Phe Val Phe  
65 70 75 80  
Tyr Phe Leu Phe Val Asp Asn Gln Glu Pro Met Asp Tyr Trp Ser Ile  
85 90 95

Ile Pro Leu Gly Arg Gly Pro Lys Asn Leu Leu Val Phe Ser Ile Leu  
100 105 110  
Phe Tyr Phe Asn Phe Tyr Ile Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:1831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

Met Ala Leu Gln Lys Phe Pro Leu Leu Gly Leu Phe Leu Val Leu Thr  
1 5 10 15  
Ile Leu Val Ser Ser Ala Thr Ala Asp Gly His Val Cys Pro Pro Ser  
20 25 30  
Thr Lys Leu Ser Arg Arg Cys Asn Asn Asp Lys Glu Asn Val Val Val  
35 40 45  
Ser Phe Phe His Arg Tyr Lys Val Ile Ser Glu Tyr Pro Val Ser Ile  
50 55 60  
Lys Tyr Leu Leu Met Phe Phe Val Phe Val Phe Tyr Phe Leu Phe Val  
65 70 75 80  
Asp Asn Gln Glu Pro Met Asp Tyr Trp Ser Ile Ile Pro Leu Gly Arg  
85 90 95  
Gly Pro Lys Asn Leu Leu Val Phe Ser Ile Leu Phe Tyr Phe Asn Phe  
100 105 110  
Tyr Ile Leu  
115

(2) INFORMATION FOR SEQ ID NO:1832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aatattcttc gttccaaacg aaaaccctaa aagagaaaag gaggcgaaaa tgggtgcagcg | 60  |
| tcttgtttac cggtcgcgac acagCtacgc caccaaatacg aaccagcacc gtatcgtaa  | 120 |
| gactccagga ggtaaattgg tgtatcaaac cacaagaag aaagctagtg gccccaaatg   | 180 |
| tcctgttact ggcaagcgta ttcaaggaat ccctcacttg aggcctctg agtacaagag   | 240 |
| gtcaagatta tcaagaaaca ggaggactgt aaaccgagca tacgggtggag tcttgtctgg | 300 |
| ttctgcagtc agggaaagga tcattcgggc attccttgtc gaagagcaaa agattgtgaa  | 360 |
| gaaagtgttg aaactccaaa aggctaagga gaaagttagc cccaaggctt aagcttttat  | 420 |
| gttttattct tctctgtttt ggaattatgg ctatgttcaa gtgataggac ttggtgcagt  | 480 |
| catgtgagga catctatggt actcgaccaa ttttt                             |     |

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

Ile Phe Phe Val Pro Asn Glu Asn Pro Lys Arg Glu Lys Glu Ala Lys  
1 5 10 15  
Met Val Gln Arg Leu Val Tyr Arg Ser Arg His Ser Tyr Ala Thr Lys  
20 25 30  
Ser Asn Gln His Arg Ile Val Lys Thr Pro Gly Gly Lys Leu Val Tyr  
35 40 45  
Gln Thr Thr Lys Lys Lys Ala Ser Gly Pro Lys Cys Pro Val Thr Gly  
50 55 60  
Lys Arg Ile Gln Gly Ile Pro His Leu Arg Pro Ser Glu Tyr Lys Arg  
65 70 75 80  
Ser Arg Leu Ser Arg Asn Arg Arg Thr Val Asn Arg Ala Tyr Gly Gly  
85 90 95  
Val Leu Ser Gly Ser Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu  
100 105 110  
Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Leu Gln Lys Ala  
115 120 125  
Lys Glu Lys Val Ala Pro Lys Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

Tyr Ser Ser Phe Gln Thr Lys Thr Leu Lys Glu Lys Arg Arg Arg Lys  
1 5 10 15  
Trp Cys Ser Val Leu Phe Thr Gly Arg Asp Thr Ala Thr Pro Pro Asn  
20 25 30  
Arg Thr Ser Thr Val Ser Ser Arg Leu Gln Glu Val Asn Trp Cys Ile  
35 40 45  
Lys Pro Gln Arg Arg Lys Leu Val Ala Pro Asn Val Leu Leu Leu Ala  
50 55 60  
Ser Val Phe Lys Glu Ser Leu Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

Met Val Gln Arg Leu Val Tyr Arg Ser Arg His Ser Tyr Ala Thr Lys  
1 5 10 15  
Ser Asn Gln His Arg Ile Val Lys Thr Pro Gly Gly Lys Leu Val Tyr  
20 25 30  
Gln Thr Thr Lys Lys Lys Ala Ser Gly Pro Lys Cys Pro Val Thr Gly



35 40 45  
Lys Arg Ile Gln Gly Ile Pro His Leu Arg Pro Ser Glu Tyr Lys Arg  
50 55 60  
Ser Arg Leu Ser Arg Asn Arg Arg Thr Val Asn Arg Ala Tyr Gly Gly  
65 70 75 80  
Val Leu Ser Gly Ser Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu  
85 90 95  
Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Leu Gln Lys Ala  
100 105 110  
Lys Glu Lys Val Ala Pro Lys Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..705
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| acatctcaact | gctcactact | ctcactgtaa  | tcccttagat  | cttcttttca | aatttcaatg  | 60  |
| gcgtccggtg  | atgttgagta | tcggtgcttc  | gttgagggtc  | tagcatgggc | caactgatgac | 120 |
| agagctcttg  | agactgcctt | cgctcaatac  | ggcgacgtta  | ttgattccaa | gatcattaac  | 180 |
| gatcgtgaga  | ctggaagatc | aaggggattc  | ggattcgtca  | ccttcaagga | tgagaaagcc  | 240 |
| atgaaggatg  | cgattgaggg | aatgaacgga  | caagatctcg  | atggccgtag | catcaactgtt | 300 |
| aacgaggctc  | agtcacgagg | aagcgggtggc | ggcggaggcc  | accgtggagg | tggtggcggt  | 360 |
| ggataCgcga  | gcggcgggtg | tggaggttac  | tccggtggag  | gtggtagcta | cggagggtggc | 420 |
| ggcggttagac | Gcgagggtg  | aggaggatac  | agcggcggcg  | gcggttactc | ctcaagaggt  | 480 |
| ggtggtggcg  | gaagctacgg | tgggtggaaga | cgtgaggggag | gaggaggata | cgggtggtggt | 540 |
| gaaggaggag  | gttacggagg | aagcgggtggt | ggtggaggat  | ggtaattcct | ttaattaggt  | 600 |
| ttgggattac  | caatgaatgt | tctctctctc  | gcttggttatg | cttctacttg | gttttgtgtg  | 660 |
| ttctctattt  | tgttattctt | ccgttaatgt  | aatgaaagag  | ttggt      |             |     |

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Gly | Asp | Val | Glu | Tyr | Arg | Cys | Phe | Val | Gly | Gly | Leu | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Ala | Thr | Asp | Asp | Arg | Ala | Leu | Glu | Thr | Ala | Phe | Ala | Gln | Tyr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Ile | Asp | Ser | Lys | Ile | Ile | Asn | Asp | Arg | Glu | Thr | Gly | Arg | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Gly | Phe | Gly | Phe | Val | Thr | Phe | Lys | Asp | Glu | Lys | Ala | Met | Lys | Asp |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Ala | Ile | Glu | Gly | Met | Asn | Gly | Gln | Asp | Leu | Asp | Gly | Arg | Ser | Ile | Thr |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Val | Asn | Glu | Ala | Gln | Ser | Arg | Gly | Ser | Gly | Gly | Gly | Gly | Gly | His | Arg |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Gly | Gly | Gly | Gly | Gly | Gly | Tyr | Arg | Ser | Gly | Gly | Gly | Gly | Gly | Tyr | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     | 110 |     |

Gly Gly Gly Gly Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly  
115 120 125  
Gly Gly Tyr Ser Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly  
130 135 140  
Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly  
145 150 155 160  
Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly Gly Trp  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1571136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg  
1 5 10 15  
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly  
20 25 30  
Gly His Arg Gly Gly Gly Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly  
35 40 45  
Gly Tyr Ser Gly Gly Gly Gly Ser Tyr Gly Gly Gly Gly Gly Arg Arg  
50 55 60  
Glu Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Tyr Ser Ser Arg Gly  
65 70 75 80  
Gly Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly  
85 90 95  
Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly  
100 105 110  
Gly Trp

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1571137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr Val Asn Glu Ala  
1 5 10 15  
Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly His Arg Gly Gly Gly Gly  
20 25 30  
Gly Gly Tyr Arg Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly  
35 40 45  
Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Ser  
50 55 60  
Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Gly Ser Tyr Gly  
65 70 75 80  
Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly Gly Glu Gly Gly  
85 90 95  
Gly Tyr Gly Gly Ser Gly Gly Gly Gly Gly Trp

100 105  
(2) INFORMATION FOR SEQ ID NO:1840:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 873 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..873  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571138  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:  
gaaaccacaa caaacacaaa aatcaaaagg ggtcatttac tatcttttaa gagacgacat 60  
atatagttct cgaccaagaa aagaaaaggg ggtgacctga gttcttcaac acataacata 120  
atggccggag ttttcaaaac gggtacgttt cttgttttgg ttttcgctgc cgttggtgtc 180  
ttcgcgaggg actacgatgt tggatgatgat acggaatgga cgagacctat ggaccccgag 240  
ttctatacta cttggggtac cggtaaaact ttccgtgtag gcgacgagct cgaatttgat 300  
ttcgctgctg ggaggcatga tgtggcagtt gtatcagaag ctgcatttga aaactgtgag 360  
aaagagaaac ccattagcca catgaccggt cCtccggtca aaattatgct aaacaccact 420  
ggaccacaat actttatctg caccgtcggg gaccattgtc gttttgggtca aaaactttcc 480  
atcactgtag ttgctgctgg tgcaactgga ggtgctactc ctggtgccgg tgctacccca 540  
gcacctggat caaccccaag tactggagga accactcctc ccactgcggg tgggaccaca 600  
acaccttcag gctctagcgg aaccactact ccagctggaa atgccgcttc ctcatagggt 660  
ggtgctactt ttctggtcgc ttttgtttct gctgtgtgtg ctctcttttg agtcacactc 720  
gaaacctagt tatgtgtttg ttttacctta ctctccttat ttaaatagtc atgtatttga 780  
ttatttgtga gaataaggac ttgttttcaa gtcattataa acgtcttata cttgtgatta 840  
gtattgagtt tcaatatatg attattcggg tgc

(2) INFORMATION FOR SEQ ID NO:1841:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..196  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571139  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:  
Met Ala Gly Val Phe Lys Thr Val Thr Phe Leu Val Leu Val Phe Ala  
1 5 10 15  
Ala Val Val Val Phe Ala Glu Asp Tyr Asp Val Gly Asp Asp Thr Glu  
20 25 30  
Trp Thr Arg Pro Met Asp Pro Glu Phe Tyr Thr Thr Trp Ala Thr Gly  
35 40 45  
Lys Thr Phe Arg Val Gly Asp Glu Leu Glu Phe Asp Phe Ala Ala Gly  
50 55 60  
Arg His Asp Val Ala Val Val Ser Glu Ala Ala Phe Glu Asn Cys Glu  
65 70 75 80  
Lys Glu Lys Pro Ile Ser His Met Thr Val Pro Pro Val Lys Ile Met  
85 90 95  
Leu Asn Thr Thr Gly Pro Gln Tyr Phe Ile Cys Thr Val Gly Asp His  
100 105 110  
Cys Arg Phe Gly Gln Lys Leu Ser Ile Thr Val Val Ala Ala Gly Ala  
115 120 125  
Thr Gly Gly Ala Thr Pro Gly Ala Gly Ala Thr Pro Ala Pro Gly Ser  
130 135 140  
Thr Pro Ser Thr Gly Gly Thr Thr Pro Pro Thr Ala Gly Gly Thr Thr  
145 150 155 160  
Thr Pro Ser Gly Ser Ser Gly Thr Thr Thr Pro Ala Gly Asn Ala Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Ser | Leu | Gly | Gly | Ala | Thr | Phe | Leu | Val | Ala | Phe | Val | Ser | Ala | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ala | Leu | Phe |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Glu | Phe | Tyr | Thr | Thr | Trp | Ala | Thr | Gly | Lys | Thr | Phe | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gly | Asp | Glu | Leu | Glu | Phe | Asp | Phe | Ala | Ala | Gly | Arg | His | Asp | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Val | Ser | Glu | Ala | Ala | Phe | Glu | Asn | Cys | Glu | Lys | Glu | Lys | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | His | Met | Thr | Val | Pro | Pro | Val | Lys | Ile | Met | Leu | Asn | Thr | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Pro | Gln | Tyr | Phe | Ile | Cys | Thr | Val | Gly | Asp | His | Cys | Arg | Phe | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Lys | Leu | Ser | Ile | Thr | Val | Val | Ala | Ala | Gly | Ala | Thr | Gly | Gly | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Pro | Gly | Ala | Gly | Ala | Thr | Pro | Ala | Pro | Gly | Ser | Thr | Pro | Ser | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Thr | Thr | Pro | Pro | Thr | Ala | Gly | Gly | Thr | Thr | Thr | Pro | Ser | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Gly | Thr | Thr | Thr | Pro | Ala | Gly | Asn | Ala | Ala | Ser | Ser | Leu | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Gly | Ala | Thr | Phe | Leu | Val | Ala | Phe | Val | Ser | Ala | Val | Val | Ala | Leu | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Pro | Pro | Val | Lys | Ile | Met | Leu | Asn | Thr | Thr | Gly | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Phe | Ile | Cys | Thr | Val | Gly | Asp | His | Cys | Arg | Phe | Gly | Gln | Lys | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Ile | Thr | Val | Val | Ala | Ala | Gly | Ala | Thr | Gly | Gly | Ala | Thr | Pro | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Ala | Thr | Pro | Ala | Pro | Gly | Ser | Thr | Pro | Ser | Thr | Gly | Gly | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Pro | Pro | Thr | Ala | Gly | Gly | Thr | Thr | Thr | Pro | Ser | Gly | Ser | Ser | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |

Thr Thr Thr Pro Ala Gly Asn Ala Ala Ser Ser Leu Gly Gly Ala Thr  
85 90 95  
Phe Leu Val Ala Phe Val Ser Ala Val Val Ala Leu Phe  
100 105

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ctcgtcagca atctgGatct aatccaccac tctctccaat tgtcattcac tccggttttg   | 60  |
| ctattttccaa ggagagaaaag atgatagctg tgatcggatt gcttctgggt tttctagtat | 120 |
| cagcattggt cttaatccaa ggaaagcgaa gaagaacaaa cgacaatcaa gagaagaaga   | 180 |
| gatctagcag tgagcctgta gaagatgtgg taagaccaa aagttacagc aagagtgaag    | 240 |
| tcgcagtaca taacaaaagg aacgattggt ggatcataat caaagataaa gtctatgata   | 300 |
| ttacttctta tgttgaagaa catcctgggt gtgacgctat tcttgatcat gctgggtgatg  | 360 |
| attctactga tggcttcttc ggacctcaac acgccactcg tgttttcgac atgattgaag   | 420 |
| atttctacat cggggaactt cattagtaaa agcttaaaga tttgagattt gattgaagat   | 480 |
| ttgagatttc ttcttaagta agcttaaaga tggctttttt aattctcttc tcattgaaga   | 540 |
| tttgagattg cattaccttt ttgtcttgct agtgtaAcac ttcttcttcc attgtattgc   | 600 |
| caaagtttcc tcatttctcc                                               |     |

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Gln Gln Ser Gly Ser Asn Pro Pro Leu Ser Pro Ile Val Ile His |  |
| 1 5 10 15                                                       |  |
| Ser Gly Phe Ala Ile Ser Lys Glu Arg Lys Met Ile Ala Val Ile Gly |  |
| 20 25 30                                                        |  |
| Leu Leu Leu Gly Phe Leu Val Ser Ala Leu Phe Leu Ile Gln Gly Lys |  |
| 35 40 45                                                        |  |
| Arg Arg Arg Thr Asn Asp Asn Gln Glu Lys Lys Arg Ser Ser Ser Glu |  |
| 50 55 60                                                        |  |
| Pro Val Glu Asp Val Val Arg Pro Lys Ser Tyr Ser Lys Ser Glu Val |  |
| 65 70 75 80                                                     |  |
| Ala Val His Asn Lys Arg Asn Asp Cys Trp Ile Ile Ile Lys Asp Lys |  |
| 85 90 95                                                        |  |
| Val Tyr Asp Ile Thr Ser Tyr Val Glu Glu His Pro Gly Gly Asp Ala |  |
| 100 105 110                                                     |  |
| Ile Leu Asp His Ala Gly Asp Asp Ser Thr Asp Gly Phe Phe Gly Pro |  |
| 115 120 125                                                     |  |
| Gln His Ala Thr Arg Val Phe Asp Met Ile Glu Asp Phe Tyr Ile Gly |  |
| 130 135 140                                                     |  |
| Glu Leu His                                                     |  |
| 145                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..121
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

Met Ile Ala Val Ile Gly Leu Leu Leu Gly Phe Leu Val Ser Ala Leu  
1 5 10 15  
Phe Leu Ile Gln Gly Lys Arg Arg Arg Thr Asn Asp Asn Gln Glu Lys  
20 25 30  
Lys Arg Ser Ser Ser Glu Pro Val Glu Asp Val Val Arg Pro Lys Ser  
35 40 45  
Tyr Ser Lys Ser Glu Val Ala Val His Asn Lys Arg Asn Asp Cys Trp  
50 55 60  
Ile Ile Ile Lys Asp Lys Val Tyr Asp Ile Thr Ser Tyr Val Glu Glu  
65 70 75 80  
His Pro Gly Gly Asp Ala Ile Leu Asp His Ala Gly Asp Asp Ser Thr  
85 90 95  
Asp Gly Phe Phe Gly Pro Gln His Ala Thr Arg Val Phe Asp Met Ile  
100 105 110  
Glu Asp Phe Tyr Ile Gly Glu Leu His  
115 120

(2) INFORMATION FOR SEQ ID NO:1847:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 290 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..290
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

aaaaWaWaga aatgatgact tcgcataacc ggaagtttagc tcaacccccg gaaggtaacg 60  
aggaagctag ggcagatcca aaaggaccag ctaaattgttg tgtgatgtga agagaggttg 120  
gtgggaatca gctatttgtg ttaatagaag gaacagtgtg tataaaacat catttgaagc 180  
tttgaaattc cctacaactt cctaattgtg tagtcttggt tgagaatata tatatgtccg 240  
ccaaaaacag ttgatgatta ttttaataaaa cctcatctct actttctctt

(2) INFORMATION FOR SEQ ID NO:1848:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..35
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

Xaa Xaa Glu Met Thr Ser His Asn Arg Lys Leu Ala Gln Pro Pro  
1 5 10 15  
Glu Gly Asn Glu Glu Ala Arg Ala Asp Pro Lys Gly Pro Ala Lys Cys  
20 25 30  
Cys Val Met  
35

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Thr | Ser | His | Asn | Arg | Lys | Leu | Ala | Gln | Pro | Pro | Glu | Gly | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Glu | Ala | Arg | Ala | Asp | Pro | Lys | Gly | Pro | Ala | Lys | Cys | Cys | Val | Met |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |     |

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Cys | Asp | Val | Lys | Arg | Gly | Trp | Trp | Glu | Ser | Ala | Ile | Cys | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Arg | Arg | Asn | Ser | Val | Tyr | Lys | Thr | Ser | Phe | Glu | Ala | Leu | Lys | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Pro | Thr | Thr | Ser |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..560
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

|              |            |            |            |            |            |     |
|--------------|------------|------------|------------|------------|------------|-----|
| atcaaaaaaaaa | gtaataaagt | aaagtatttc | gccgtgagag | aaagaacaat | caccatcgtc | 60  |
| tagggtttca   | attcattgtt | ccagtacttc | atcgtagcgc | cgctcctctc | ttgtccagac | 120 |
| tccagaagat   | tcaatggcac | ccaagaaaga | caaagttcct | cctccgtcct | ctaaacccgc | 180 |
| caaatccggt   | ggcggcaagc | aaaagaaaaa | gaagtggagc | aaaggaaagc | aaaaggagaa | 240 |
| agtgaacaac   | atggttttgt | ttgaccaagc | aacttacgac | aagcttctct | ctgaggctcc | 300 |
| caagttcaaa   | cttatcactc | cttctatcct | ctctgaccgt | ttgaggatca | atggatcgct | 360 |
| tgctagaagg   | gcatcgagag | aattgatggc | taagggaaca | atcaggatgg | tctctgtca  | 420 |
| ctcaagccag   | cagatctaca | ctagggcaac | ccacggctaa | cttccttcga | atgttttagt | 480 |
| tgtttccttg   | tattttactc | aatgtcttta | tgaaccatta | tctttctaga | atgcaccttt | 540 |
| acttgcaaAc   | attggtctac |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..108
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571164
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

Met Ala Pro Lys Lys Asp Lys Val Pro Pro Pro Ser Ser Lys Pro Ala  
1 5 10 15  
Lys Ser Gly Gly Gly Lys Gln Lys Lys Lys Lys Trp Ser Lys Gly Lys  
20 25 30  
Gln Lys Glu Lys Val Asn Asn Met Val Leu Phe Asp Gln Ala Thr Tyr  
35 40 45  
Asp Lys Leu Leu Ser Glu Ala Pro Lys Phe Lys Leu Ile Thr Pro Ser  
50 55 60  
Ile Leu Ser Asp Arg Leu Arg Ile Asn Gly Ser Leu Ala Arg Arg Ala  
65 70 75 80  
Ile Arg Glu Leu Met Ala Lys Gly Thr Ile Arg Met Val Ser Ala His  
85 90 95  
Ser Ser Gln Gln Ile Tyr Thr Arg Ala Thr His Gly  
100 105

(2) INFORMATION FOR SEQ ID NO:1853:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..69
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571165
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

Met Val Leu Phe Asp Gln Ala Thr Tyr Asp Lys Leu Leu Ser Glu Ala  
1 5 10 15  
Pro Lys Phe Lys Leu Ile Thr Pro Ser Ile Leu Ser Asp Arg Leu Arg  
20 25 30  
Ile Asn Gly Ser Leu Ala Arg Arg Ala Ile Arg Glu Leu Met Ala Lys  
35 40 45  
Gly Thr Ile Arg Met Val Ser Ala His Ser Ser Gln Gln Ile Tyr Thr  
50 55 60  
Arg Ala Thr His Gly  
65

(2) INFORMATION FOR SEQ ID NO:1854:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 748 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..748
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571166
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aacacaaaaca aaacaaaaca aaaaaaacac gagtggaagc ttttaaaca aattagaaaa  | 60  |
| agagagagag aaatggcgac gtccggaaca tacgtgacgg aggtgccgct aaaaggaacg  | 120 |
| gtggagaaac acttcaagag gtacaggaac gagaactatc tcttcocctga cactatcggc | 180 |
| caccacatcc aaagtgttac tggtcacgat ggcgaatggg acactcaagg aggcacaaag  | 240 |



atttggaact acacactcgg agatggaaag gaggaggtat tcaaggagag gagagagata 300  
gacgatgaca ataagatagt aaagggttgta ggattggaag gtcacgtgat ggagcagttc 360  
aaggtgtatg agattgactt ccaatttatt cccaagtctg aagaagattg cgtctgcaaa 420  
atcactatga tatgggagaa gcgcaacgat gatttccccg aaccaagcag ctacatgcaa 480  
ctcctcaaga gtatggttat tgatatggag gaccacgtcc ttaaagctta atcaatatca 540  
caaccaccac catcatcaca accaccatca tcatcatcct atatgtttat taaattgttt 600  
tcattttat ataatagact agataagaac ctgtataatg tgcgggataa aatgattgaa 660  
ataaattatt atgcgtaaac ttattgtatg agatatcata tatgtttgta tacaagaaaa 720  
tatgtaatta aagtBttttg ttttattt

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1571167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

Asn Gln Asn Lys Thr Lys Gln Lys Lys His Glu Trp Lys Leu Leu Asn  
1 5 10 15  
Lys Ile Arg Lys Arg Glu Arg Glu Met Ala Thr Ser Gly Thr Tyr Val  
20 25 30  
Thr Glu Val Pro Leu Lys Gly Thr Val Glu Lys His Phe Lys Arg Tyr  
35 40 45  
Arg Asn Glu Asn Tyr Leu Phe Pro Asp Thr Ile Gly His His Ile Gln  
50 55 60  
Ser Val Thr Val His Asp Gly Glu Trp Asp Thr Gln Gly Gly Ile Lys  
65 70 75 80  
Ile Trp Asn Tyr Thr Leu Gly Asp Gly Lys Glu Glu Val Phe Lys Glu  
85 90 95  
Arg Arg Glu Ile Asp Asp Asp Asn Lys Ile Val Lys Val Val Gly Leu  
100 105 110  
Glu Gly His Val Met Glu Gln Phe Lys Val Tyr Glu Ile Asp Phe Gln  
115 120 125  
Phe Ile Pro Lys Ser Glu Glu Asp Cys Val Cys Lys Ile Thr Met Ile  
130 135 140  
Trp Glu Lys Arg Asn Asp Phe Pro Glu Pro Ser Ser Tyr Met Gln  
145 150 155 160  
Leu Leu Lys Ser Met Val Ile Asp Met Glu Asp His Val Leu Lys Ala  
165 170 175

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1571168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Thr  
1 5 10 15  
Val Glu Lys His Phe Lys Arg Tyr Arg Asn Glu Asn Tyr Leu Phe Pro  
20 25 30

Asp Thr Ile Gly His His Ile Gln Ser Val Thr Val His Asp Gly Glu  
35 40 45  
Trp Asp Thr Gln Gly Gly Ile Lys Ile Trp Asn Tyr Thr Leu Gly Asp  
50 55 60  
Gly Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Asp Asn  
65 70 75 80  
Lys Ile Val Lys Val Val Gly Leu Glu Gly His Val Met Glu Gln Phe  
85 90 95  
Lys Val Tyr Glu Ile Asp Phe Gln Phe Ile Pro Lys Ser Glu Glu Asp  
100 105 110  
Cys Val Cys Lys Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe  
115 120 125  
Pro Glu Pro Ser Ser Tyr Met Gln Leu Leu Lys Ser Met Val Ile Asp  
130 135 140  
Met Glu Asp His Val Leu Lys Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1066
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| aagactctgt tttttcccaa gatgtctggt ttcctctttt gtttcgtcca aatctctact | 60   |
| ttttagggat cttgtccttc tcttttctgc tgattaaaac cctcgaattt gctccaattc | 120  |
| gacgcgaaaa agggcattga gatggtgaat ggagaatcat caactagtac gtcttactct | 180  |
| gataataaca atgacacaaa tgatcaagga ggagactttg aatgtaacat ttgtttcgaa | 240  |
| ctagctcaag atccgattgt cactctctgt ggccatctct tttgctggcc ttgcttatac | 300  |
| cgtttggttc accaccattc acattctcaa gaatgtccgg tttgtaaagc cgtggttcaa | 360  |
| gacgataagc ttgttctctt ttacggtaga ggcaagaacc agactgacc gagatcaaaa  | 420  |
| cgttatccgg gtttacggat tcctaaccga ccaacaggtc aaagacctga gactgctgct | 480  |
| cctcctcctc agcctgaagc tgcgagtaat tttttcaact acggtattgg tttgatgggt | 540  |
| ggaattatgc cgatgatggc gactacgagg tttgggaatt tcagtatggg gtttggtggt | 600  |
| ttgttacctt ctttgtttaa ctttcagttt catggatttc atgatgCtac gctttatggt | 660  |
| tcaacaccgg gttatcctta cggtggttat cataacggtt tccgtggagt tcctcctcgt | 720  |
| ggacaagagc gtccatggc tgcgtgagga aaccaaagtg atgcatttct gaagaatatc  | 780  |
| ctcttttttg ttggaatctg tgtggtgata tttctcatct ggtgaaaacg aatcacattt | 840  |
| ggtgtatttc caggtatgat caaacttact tacttggtgc aagttgtgta tgtaaatatg | 900  |
| gtaatagctg agtgtacttg tctgctattt cgacgttggt attgtatttt tgttttgaag | 960  |
| atgaaccatg agtctacaag cttttttaca caactctttt gttgcttttg tgttttgtct | 1020 |
| aagcatctta tgaaaactag ttgtgaaata aatgggtcgt gttatg                |      |

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

Met Val Asn Gly Glu Ser Ser Thr Ser Thr Ser Tyr Ser Asp Asn Asn  
1 5 10 15  
Asn Asp Thr Asn Asp Gln Gly Gly Asp Phe Glu Cys Asn Ile Cys Phe

20 25 30  
Glu Leu Ala Gln Asp Pro Ile Val Thr Leu Cys Gly His Leu Phe Cys  
35 40 45  
Trp Pro Cys Leu Tyr Arg Trp Leu His His His Ser His Ser Gln Glu  
50 55 60  
Cys Pro Val Cys Lys Ala Val Val Gln Asp Asp Lys Leu Val Pro Leu  
65 70 75 80  
Tyr Gly Arg Gly Lys Asn Gln Thr Asp Pro Arg Ser Lys Arg Tyr Pro  
85 90 95  
Gly Leu Arg Ile Pro Asn Arg Pro Thr Gly Gln Arg Pro Glu Thr Ala  
100 105 110  
Ala Pro Pro Pro Gln Pro Glu Ala Ser Asn Phe Phe Asn Tyr Gly  
115 120 125  
Ile Gly Leu Met Gly Gly Ile Met Pro Met Met Ala Thr Thr Arg Phe  
130 135 140  
Gly Asn Phe Ser Met Gly Phe Gly Gly Leu Leu Pro Ser Leu Phe Asn  
145 150 155 160  
Phe Gln Phe His Gly Phe His Asp Ala Thr Leu Tyr Gly Ser Thr Pro  
165 170 175  
Gly Tyr Pro Tyr Gly Gly Tyr His Asn Gly Phe Arg Gly Val Pro Pro  
180 185 190  
Arg Gly Gln Glu Arg Pro Met Ala Arg Gly Gly Asn Gln Ser Asp Ala  
195 200 205  
Phe Leu Lys Asn Ile Leu Phe Phe Val Gly Ile Cys Val Val Ile Phe  
210 215 220  
Leu Ile Trp  
225

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..520
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

|            |            |            |            |            |              |            |            |     |
|------------|------------|------------|------------|------------|--------------|------------|------------|-----|
| aagttctaaa | gtcctcaa   | at         | ccgc       | aaagc      | tttttcagct   | tctttgttga | attgcgagca | 60  |
| gaggtagaaa | tcagcaggaa | acaaaaatgt | tggtcttttc | ttacttcaag | gatttgggtg   |            |            | 120 |
| gacaagaagt | gacggttgag | ctgaagaatg | atttagccat | aagaggaa   | actctcactcag |            |            | 180 |
| ttgatcagta | tctgaatatc | aagctcgaga | acactagggt | tggtgaccag | gaagtaccct   |            |            | 240 |
| cacatgcttt | cagtga     | gaaa       | ctgtttcatc | agaggatctg | tggttaaggta  | cgtgcagtta |            | 300 |
| cctaaagatg | gagtcgatgt | tgatttgctt | cacggcgcag | Ctagaagaga | agctaggggt   |            |            | 360 |
| ggctgattct | gaaatatctt | tgtatctcca | aaacttgaat | acttttcatt | cggcgtaatg   |            |            | 420 |
| gctttataat | gaatatttcc | ctgatgtaga | gccaatggta | tggccatgaa | tcttgttcca   |            |            | 480 |
| ttttattaac | aatggataat | ttaatttctt | ttcctcgtcc |            |              |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

Met Leu Phe Phe Ser Tyr Phe Lys Asp Leu Val Gly Gln Glu Val Thr

1 5 10 15  
Val Glu Leu Lys Asn Asp Leu Ala Ile Arg Gly Thr Leu His Ser Val  
20 25 30  
Asp Gln Tyr Leu Asn Ile Lys Leu Glu Asn Thr Arg Val Val Asp Gln  
35 40 45  
Glu Val Pro Ser His Ala Phe Ser Glu Lys Leu Phe His Gln Arg Ile  
50 55 60  
Cys Gly Lys Val Arg Ala Val Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1571222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

Met Leu Ser Val Arg Asn Cys Phe Ile Arg Gly Ser Val Val Arg Tyr  
1 5 10 15  
Val Gln Leu Pro Lys Asp Gly Val Asp Val Asp Leu Leu His Gly Ala  
20 25 30  
Ala Arg Arg Glu Ala Arg Gly Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1571223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

Met Glu Ser Met Leu Ile Cys Phe Thr Ala Gln Leu Glu Glu Lys Leu  
1 5 10 15  
Gly Val Ala Asp Ser Glu Ile Ser Leu Tyr Leu Gln Asn Leu Asn Thr  
20 25 30  
Phe His Ser Ala  
35

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2401

(D) OTHER INFORMATION: / Ceres Seq. ID 1571228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

acaaatcttt ctctttctct ttctctctct aacacaattt agaacaaaag tttcttcttt 60  
cttctctccc gagaggcctc tcgctgttca ttgaagtctt cttagaattt tctatcacct 120  
tggttctgta atttgcaaaa cagacaacaa tggttgagcg tgggaagagg actcacaatc 180  
gtttcagaga caacaacaat gacaacaacc ggaatcaaag gagaagactt tcttacgaat 240

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ccgaagaaaa  | aaagatcgat  | aacaaagacg  | atctcgttgt  | tgtttacaga  | atcttatgcc  | 300  |
| caagtgggtg  | catgggaagt  | gttataggca  | aaagtggcaa  | agttattaac  | ttgattaggg  | 360  |
| aagaaactag  | agctaggatc  | aaagttgttg  | atccttttcc  | aggttgtagc  | gaaagagtca  | 420  |
| taacgatctt  | ttgctcgggt  | tcggagaaga  | aagacattgt  | tgacattgag  | tatagtgaat  | 480  |
| tggtactctc  | tgttcctttg  | tgttctgctc  | aagctgctct  | tcttaaagtc  | catgatgcta  | 540  |
| ttgtggcttc  | tttagctact  | gctgctgaga  | acactaagat  | tgatagagat  | gacttttagag | 600  |
| aatgtcgtct  | tttagttccg  | tctagtcagt  | gttctattgt  | cattggtaaa  | tctgggtcga  | 660  |
| ttattaagaa  | cattagaggt  | agaactagag  | ctaactgtta  | ggttgtctct  | aaagatgctt  | 720  |
| ctgacccctc  | tcacacttgt  | gccatggatt  | ttgacaacat  | tgttatgata  | tctgggtgaga | 780  |
| McTtgaatcc  | gtgaagaagg  | cacttttccg  | tgtttctgca  | atcatgtaca  | aagtcagtc   | 840  |
| tcgagaacag  | attcctctgg  | atacaactgt  | ccaagaagtt  | cccgcctagta | ttataattcc  | 900  |
| gtctgatctg  | tctatctatc  | cacaagccgg  | tttataccca  | agtcaggatt  | ctattttcca  | 960  |
| acatggggcc  | aatgtttcat  | cgtttatcgg  | tacactacct  | cagggctatg  | gagaaaaatgc | 1020 |
| tgcaaatcca  | ctgccgggtt  | tttctgcttc  | tgctcttctc  | gtgggttcctg | gttttggtgg  | 1080 |
| gtcttccaga  | tcagaaaagt  | tggtataaaa  | agttatttgc  | gcttcttcca  | aaattggtcg  | 1140 |
| tgttatcggg  | aaaggaggat  | taaccattaa  | gggaataaga  | caagcaagcg  | ggtctcatat  | 1200 |
| cgaagttaat  | gactcgagga  | caaactcatga | tgatgactgt  | gttatcactg  | tcactgctac  | 1260 |
| agagtctcct  | gatgatttga  | agtctatggc  | ggttgaagct  | gttcttctac  | ttcaagagaa  | 1320 |
| aattaatgat  | gaagacgagg  | acaaagttaa  | aatgcaactc  | cttgtatctt  | ctaaggtaat  | 1380 |
| aggatgcatt  | atagggaaaa  | gtggctcaat  | cataagtga   | atcaggaaaa  | ggacaaaggc  | 1440 |
| tgatattcat  | atctcgaaaag | gaaataatac  | gcctaagagc  | tgatcccaat  | gatgagctcg  | 1500 |
| ttgagatata  | tggtgaagta  | agcaatgtga  | gagatgctct  | tattcagata  | gttctgaggc  | 1560 |
| ttcgagatga  | tgttttaagg  | gatagagaga  | ctggttccag  | gaatcaacct  | cctgcaagat  | 1620 |
| ctgagaataa  | caatttcttc  | tcttcaagta  | gtagtaatac  | tggtcttgca  | cttccctcaat | 1680 |
| ctttcatgtc  | ttctgttccg  | caagttgctt  | ctgtagattt  | cgataggaga  | ccagaaaccg  | 1740 |
| ggagcagcat  | gagcatgctt  | ccttcgagtg  | gtggaatcta  | tggttatgga  | agttttcccg  | 1800 |
| tgggcaatac  | aagttatgga  | tccaactcct  | cttactcatc  | caatctatat  | ggaggattgc  | 1860 |
| ctcagctctac | tactatggag  | gttcgaatcc  | cagcaaatgc  | agtgggtaaa  | gttatgggca  | 1920 |
| gaggaggagg  | caacttggac  | aacataagaa  | ggatatcagg  | agccatgata  | gaaatttctg  | 1980 |
| attccaaaaa  | ttcccatggc  | ggtcgcgttg  | ctctcatttc  | cgggacatct  | gaacagaaGc  | 2040 |
| gtaccgcaga  | gaacttggtc  | caagctttta  | tcattgtccac | ttgaataatt  | tgctctgccc  | 2100 |
| cctaactcct  | ttccatggaa  | gtgtgttcca  | tcaatctacc  | tctcagtggg  | tttctttgat  | 2160 |
| cggtttctc   | aggttttctc  | ccttccatca  | agctcatggt  | tagatatggg  | tgcactctctc | 2220 |
| atcaaacatt  | tcggtatctc  | atctcgactc  | agttactttt  | ggtttctcgt  | gctagacatt  | 2280 |
| ttatagtctt  | tcaggaccat  | tcttttcccc  | tttctgtg    | agctgttcgt  | actataacta  | 2340 |
| cttatctccg  | tcgagtaaaa  | caaaatcggt  | cttatatcaa  | tcaaactttg  | cttattctSc  | 2400 |

c

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Arg | Gly | Lys | Arg | Thr | His | Asn | Arg | Phe | Arg | Asp | Asn | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asp | Asn | Asn | Arg | Asn | Gln | Arg | Arg | Arg | Leu | Ser | Tyr | Glu | Ser | Glu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Glu | Lys | Lys | Ile | Asp | Asn | Lys | Asp | Asp | Leu | Val | Val | Val | Tyr | Arg | Ile |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |
| Leu | Cys | Pro | Ser | Gly | Val | Met | Gly | Ser | Val | Ile | Gly | Lys | Ser | Gly | Lys |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |
| Val | Ile | Asn | Leu | Ile | Arg | Gln | Glu | Thr | Arg | Ala | Arg | Ile | Lys | Val | Val |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     | 80  |
| Asp | Pro | Phe | Pro | Gly | Cys | Ser | Glu | Arg | Val | Ile | Thr | Ile | Phe | Cys | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Val Ser Glu Lys Lys Asp Ile Val Asp Ile Glu Tyr Ser Glu Leu Asp  
100 105 110  
Tyr Ser Val Pro Leu Cys Ser Ala Gln Ala Ala Leu Leu Lys Val His  
115 120 125  
Asp Ala Ile Val Ala Ser Leu Ala Thr Ala Ala Glu Asn Thr Lys Ile  
130 135 140  
Asp Arg Asp Asp Phe Arg Glu Cys Arg Leu Leu Val Pro Ser Ser Gln  
145 150 155 160  
Cys Ser Ile Val Ile Gly Lys Ser Gly Ser Ile Ile Lys Asn Ile Arg  
165 170 175  
Gly Arg Thr Arg Ala Asn Val Lys Val Val Ser Lys Asp Ala Ser Asp  
180 185 190  
Pro Ser His Thr Cys Ala Met Asp Phe Asp Asn Ile Val Met Ile Ser  
195 200 205  
Gly Glu Xaa Leu Asn Pro  
210

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

Met Gly Ser Val Ile Gly Lys Ser Gly Lys Val Ile Asn Leu Ile Arg  
1 5 10 15  
Gln Glu Thr Arg Ala Arg Ile Lys Val Val Asp Pro Phe Pro Gly Cys  
20 25 30  
Ser Glu Arg Val Ile Thr Ile Phe Cys Ser Val Ser Glu Lys Lys Asp  
35 40 45  
Ile Val Asp Ile Glu Tyr Ser Glu Leu Asp Tyr Ser Val Pro Leu Cys  
50 55 60  
Ser Ala Gln Ala Ala Leu Leu Lys Val His Asp Ala Ile Val Ala Ser  
65 70 75 80  
Leu Ala Thr Ala Ala Glu Asn Thr Lys Ile Asp Arg Asp Asp Phe Arg  
85 90 95  
Glu Cys Arg Leu Leu Val Pro Ser Ser Gln Cys Ser Ile Val Ile Gly  
100 105 110  
Lys Ser Gly Ser Ile Ile Lys Asn Ile Arg Gly Arg Thr Arg Ala Asn  
115 120 125  
Val Lys Val Val Ser Lys Asp Ala Ser Asp Pro Ser His Thr Cys Ala  
130 135 140  
Met Asp Phe Asp Asn Ile Val Met Ile Ser Gly Glu Xaa Leu Asn Pro  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

Met Tyr Lys Val Ser Pro Arg Glu Gln Ile Pro Leu Asp Thr Thr Val  
1 5 10 15  
Gln Glu Val Pro Ala Ser Ile Ile Ile Pro Ser Asp Leu Ser Ile Tyr  
20 25 30  
Pro Gln Ala Gly Leu Tyr Pro Ser Gln Asp Ser Ile Phe Gln His Gly  
35 40 45  
Ala Asn Val Ser Ser Phe Ile Gly Thr Leu Pro Gln Gly Tyr Gly Glu  
50 55 60  
Asn Ala Ala Asn Pro Leu Pro Val Phe Ser Ala Ser Ala Leu Pro Val  
65 70 75 80  
Val His Gly Phe Gly Gly Ser Ser Arg Ser Glu Lys Leu Ala Ile Lys  
85 90 95  
Val Ile Cys Ala Ser Ser Lys Ile Gly Arg Val Ile Gly Lys Gly Gly  
100 105 110  
Leu Thr Ile Lys Gly Ile Arg Gln Ala Ser Gly Ser His Ile Glu Val  
115 120 125  
Asn Asp Ser Arg Thr Asn His Asp Asp Asp Cys Val Ile Thr Val Thr  
130 135 140  
Ala Thr Glu Ser Pro Asp Asp Leu Lys Ser Met Ala Val Glu Ala Val  
145 150 155 160  
Leu Leu Leu Gln Glu Lys Ile Asn Asp Glu Asp Glu Asp Lys Val Lys  
165 170 175  
Met Gln Leu Leu Val Ser Ser Lys Val Ile Gly Cys Ile Ile Gly Lys  
180 185 190  
Ser Gly Ser Ile Ile Ser Glu Ile Arg Lys Arg Thr Lys Ala Asp Ile  
195 200 205  
His Ile Ser Lys Gly Asn Asn Thr Pro Lys Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..731
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

aaaaacacaa actctctata ctacacaacat tgtttaactc atcttttctaa gttggtttcg 60  
attcaagaat atcacaaatga ctaatgttcg ccttcctatt ctcgctctcct cggtcttgtt 120  
ccttgtcttt atttcatcgt cctcttgggt ccctacacct agttttgctg ctgagagtaag 180  
tcattctctg gtgcaagaag aggtcaaaaa gggtccagaa tacacagaac ctgaggagcc 240  
ggaagttcca gaagagcccg agctgccctc accggaggag cctgagattc cagaagagcc 300  
tgagattcca gaagagcctg aggttccttg agaacccgaa gttcctgaag agcccgaaga 360  
accagaagag ccagcagggt caacatttga atttccatca tggtttccga gctttcctat 420  
tcccgggtgtt aatggcgggt tgccaaagac tgaaaagaca aaacctacat caacagttga 480  
agaggttaac gtttctaaca agaagccata gatcaatggg taaagaacgt caaatgatta 540  
tataaactat atatgcaHtt atagtttttg tttgtttttg gttaaagatg agagattaca 600  
tatgtattac agtattagag tcctcaccat gtcattgatt agtctctaaa cgctcctgat 660  
ataatctcgt actaattctc tcttgtaaca tgtatatctc ttgtggtaca aaaaatatat 720  
atataactct t

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Asn | Val | Arg | Leu | Pro | Ile | Leu | Val | Ser | Ser | Val | Leu | Phe | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Phe | Ile | Ser | Ser | Ser | Leu | Leu | Phe | Pro | Thr | Pro | Ser | Phe | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Ser | His | Ser | Leu | Val | Gln | Glu | Glu | Val | Lys | Lys | Val | Pro | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Thr | Glu | Pro | Glu | Glu | Pro | Glu | Val | Pro | Glu | Glu | Pro | Glu | Leu | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Glu | Glu | Pro | Glu | Ile | Pro | Glu | Glu | Pro | Glu | Ile | Pro | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Glu | Val | Pro | Gly | Glu | Pro | Glu | Val | Pro | Glu | Glu | Pro | Glu | Glu | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Pro | Ala | Gly | Ser | Thr | Phe | Glu | Phe | Pro | Ser | Trp | Phe | Pro | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Pro | Ile | Pro | Gly | Val | Asn | Gly | Gly | Leu | Pro | Lys | Thr | Glu | Lys | Thr |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Lys | Pro | Thr | Ser | Thr | Val | Glu | Glu | Val | Asn | Val | Ser | Asn | Lys | Lys | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..941
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| atagaatata | aaagttgcta | aatttgatta  | aagatatgga  | caaagttcca  | agattttttg  | 60  |
| tttggttaac | ttaaaatggt | ttatggttatt | acttggtttt  | ggtttttggt  | ggagttctcg  | 120 |
| gtgatggatt | tatggctcgt | gatttacta   | tagagaacac  | ggcaggagca  | gatgcgcacc  | 180 |
| aagcggttgc | gtttagatca | gacagtgtt   | tttcggtact  | tgaaaactgc  | gagtttcttg  | 240 |
| ggaaccaaga | cactctttat | gctcactctc  | tccgtcagtt  | ctacaaacaa  | tgtcgaatcc  | 300 |
| aaggcaacgt | agacttcac  | tttggttaact | cagctgccgt  | attccaagat  | tgtgatatcc  | 360 |
| taatcgcttc | aaaacactcc | aaactcgagc  | aaggcgggtgc | aaacaacgcg  | atcacagcac  | 420 |
| acgggaggat | tgatgcgtcg | cagtcacagg  | gatttgtgtt  | tttgaactgt  | tcgattaacg  | 480 |
| gaacagagga | atacatgaag | gagtttcaag  | ctaaccctga  | aaggcataag  | aacttcttgg  | 540 |
| gaagaccgtg | gaaggagttt | tcgaggacgg  | tttttgtaaa  | ctgtaatctt  | gagtccttga  | 600 |
| ttagtcctga | tggatggatg | ccttggaacg  | gggatttcgc  | attgaagact  | ttgtattacg  | 660 |
| gtgagtataa | gaatacgggt | cggggatcgg  | ttagatcgag  | tagggttcca  | tggagtagtg  | 720 |
| agataccaga | gaagcatggt | gatgtttact  | ctgttgccaa  | ttttattcag  | gctgatgagt  | 780 |
| gggcttccac | gactgcttga | tttttgTtaa  | aggaaacatg  | aggttttagg  | attttgaaaa  | 840 |
| gaagagaaga | gaagtcgtca | ttgtaacttt  | attgtagtgt  | caaataattag | tgtgggtttct | 900 |
| ttatcgctca | ttggggattc | ataatagatt  | aataattgaa  | g           |             |     |

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: peptide  
(B) LOCATION: 1..222  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

Met Ala Arg Asp Leu Thr Ile Glu Asn Thr Ala Gly Ala Asp Ala His  
1 5 10 15  
Gln Ala Val Ala Phe Arg Ser Asp Ser Asp Phe Ser Val Leu Glu Asn  
20 25 30  
Cys Glu Phe Leu Gly Asn Gln Asp Thr Leu Tyr Ala His Ser Leu Arg  
35 40 45  
Gln Phe Tyr Lys Gln Cys Arg Ile Gln Gly Asn Val Asp Phe Ile Phe  
50 55 60  
Gly Asn Ser Ala Ala Val Phe Gln Asp Cys Asp Ile Leu Ile Ala Ser  
65 70 75 80  
Lys His Ser Lys Leu Glu Gln Gly Gly Ala Asn Asn Ala Ile Thr Ala  
85 90 95  
His Gly Arg Ile Asp Ala Ser Gln Ser Thr Gly Phe Val Phe Leu Asn  
100 105 110  
Cys Ser Ile Asn Gly Thr Glu Glu Tyr Met Lys Glu Phe Gln Ala Asn  
115 120 125  
Pro Glu Arg His Lys Asn Phe Leu Gly Arg Pro Trp Lys Glu Phe Ser  
130 135 140  
Arg Thr Val Phe Val Asn Cys Asn Leu Glu Ser Leu Ile Ser Pro Asp  
145 150 155 160  
Gly Trp Met Pro Trp Asn Gly Asp Phe Ala Leu Lys Thr Leu Tyr Tyr  
165 170 175  
Gly Glu Tyr Lys Asn Thr Gly Pro Gly Ser Val Arg Ser Ser Arg Val  
180 185 190  
Pro Trp Ser Ser Glu Ile Pro Glu Lys His Val Asp Val Tyr Ser Val  
195 200 205  
Ala Asn Phe Ile Gln Ala Asp Glu Trp Ala Ser Thr Thr Ala  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..543  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

ctcagaacat ctcaatctca attgaaatct taaaatccaa aattttcccg agaaaaatta 60  
aagtttctctg agaaaatgtc aggtcgtggg aaggaggagca aaggattggg caaaggagga 120  
gctaaacgtc acaggaaggt tctgagagac aacatccaag gaatcactaa gccggcgatt 180  
cggagattgg ctctagaggg tggagtcaag cgtattagtg gtttdRatct acgaggagac 240  
acgtggcggt ctcaagatct ttttgagaa tggtatccgt gacgcggtta cttacactga 300  
gcacgctcgg aggaagacgg tgactgctat ggatgttggt tatgctctta agagacaagg 360  
aagaactctc tacggattcg gcggtaggg tttttgattg ttgttttttg tgtttctacg 420  
tttattagga tgtaatttt cagaatttgg tgtaacttc gaaaaaatta aagaattgaa 480  
ggttgttggt gcaatttcgt gattgttgaa ggtgtgttg caaacttyya gtaatttcag 540  
ttt

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1571244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala  
1 5 10 15  
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys  
20 25 30  
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser  
35 40 45  
Gly Xaa Xaa Leu Arg Gly Asp Thr Trp Arg Ser Gln Asp Leu Phe Gly  
50 55 60  
Glu Cys Tyr Pro  
65

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2135

(D) OTHER INFORMATION: / Ceres Seq. ID 1571245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

atcacctctc tcttctcctg aaatcaccat gagtatggaa gcaacggagc tacaagatct 60  
ctctgacgac gccgattacg ccgcttctca acaacaagga tcggctagta tgatgcgtaS 120  
cgatagcgga aagagaagtt tacaaagtga acacgaagac gctgtattga tttatttgaa 180  
agataacggt gcaattcatc ctacacagtt cgcactctgag aggattagtg gtagattgaa 240  
gttgactaag caagattctg ttctctttct gtcgtggatt ccgtacaagg gacaaacatc 300  
aaatgcaaag ctatcagaga aagacaggag tctttatacc atcacgcggg ttccggtttac 360  
tgaagtggag tccattagga gacacactcc tgctctcgga tggcagtatg taattgttgt 420  
cctgtcttct ggacttgcac ttccacctct gtacttctac aatggaggag tcagggagtt 480  
tctggccatg gtgaagcagc atgtttttct tgcaagggtcg tcagaagatc aaaatgtgtt 540  
cattgtgaat gattttcaga gtcccttgca gagaactttg tcttcattgg agctgccaag 600  
ttcactgcct gtagcaagtg gacaatccgt ataccatta gacggagggt cttctagtga 660  
aaatcaaagg agaacaagtt cagatgttgg taatagagta tctagtgttt occagttctg 720  
cttcagaaag caaaagagtc atgatccaac tcgggatctt tcaatccatc tactagagaa 780  
gttttctctg gttaccaaatt ttgctcgaga tacaactact cagctgtttt cggaaaacaa 840  
tggtcttggg tccattgaca agagatggaa taaccaaccc gtacatagtt atcctgaaaa 900  
gttgctgaac attgctgagg aaaagcatca tgaaatccgt catagttatt ctgaaaatga 960  
ccttctcaag gatgacgaaa tttcttatat tgatgtccct gctgatccct tagagtttga 1020  
taaattaagt ttgatgtggg gaaaaccaag gcaaccacca atggggcata aagagttcac 1080  
agcattgttg gattctgaag ggcgagttgt ggaatcaaaa gctcttcggg agagagtttt 1140  
ctatggaggc attgagcacc agttgcgtag agaggtatgg ccctttctct tgggatatta 1200  
tgcatatgac tcgacatatg cagagagaga atatcttcga tctgtcaaac ggatggaata 1260  
tgcaacattg aaacagcaat ggcagagcat ttccctgaa caagcaaaaa gggtcacaaa 1320  
atatcgggag agaaaaggat tgatagataa agatgtggta agaactgata gggcatttga 1380  
atactatgaa ggggatgaca atctacatgt caatagcatg cgtgatattc tgttgacct 1440  
ctccttctac aattttgacc tgggttactg ccagggaatg agtgattatc tgtctcctat 1500  
cttggtcgtg atggaggatg aatcagaatc tttttggtgW ttcRtggcac tgatggaacg 1560  
acttggaacc aactttaacc gtgaccagaa tgggatgcac actcagctct ttgcactctc 1620  
aaagctggtg gagttgctcg atagcccgt acataattac ttaaggaga atgactgctt 1680  
gaattacttc ttctgtttcc gctggattct gattcagttt aaaagggaat ttgagtatga 1740  
gaagacaatg cagctgtggg aggtgatgtg gaccactac ctctcagaac attttcacct 1800  
atatgtttgt gtggcgtgt tgaagcgatg ccgcagcaag ataatgggag aacagatgga 1860  
ttttgatact ctcttaaagt tcatcaatga gctgtctggg catattgatc tcgattcaac 1920  
agtcagagat gccgaagcac tttgcataga agctgggtgaa aatgggtgctg ctagattcc 1980  
tccaggaacc cctccttctc tacccttga tgacggtacc ttatatcctc aggaagatga 2040

tggttttgtaa gtaatacgac ttttcttttt tcttctggac atgttaccaa aatttggatt 2100  
gcttttacta gaaatcccat acaatgatta aggcc

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 682 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..682

(D) OTHER INFORMATION: / Ceres Seq. ID 1571246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Leu | Ser | Ser | Pro | Glu | Ile | Thr | Met | Ser | Met | Glu | Ala | Thr | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gln | Asp | Leu | Ser | Asp | Asp | Ala | Asp | Tyr | Ala | Ala | Ser | Gln | Gln | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Ala | Ser | Met | Met | Arg | Xaa | Asp | Ser | Gly | Lys | Arg | Ser | Leu | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Glu | His | Glu | Asp | Ala | Val | Leu | Ile | Tyr | Leu | Lys | Asp | Asn | Val | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | His | Pro | Thr | Gln | Phe | Ala | Ser | Glu | Arg | Ile | Ser | Gly | Arg | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Thr | Lys | Gln | Asp | Ser | Val | Leu | Phe | Leu | Ser | Trp | Ile | Pro | Tyr | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gln | Thr | Ser | Asn | Ala | Lys | Leu | Ser | Glu | Lys | Asp | Arg | Ser | Leu | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Ile | Thr | Ala | Val | Pro | Phe | Thr | Glu | Val | Arg | Ser | Ile | Arg | Arg | His |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Pro | Ala | Leu | Gly | Trp | Gln | Tyr | Val | Ile | Val | Val | Leu | Ser | Ser | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ala | Phe | Pro | Pro | Leu | Tyr | Phe | Tyr | Asn | Gly | Gly | Val | Arg | Glu | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Ala | Met | Val | Lys | Gln | His | Val | Phe | Leu | Ala | Arg | Ser | Ser | Glu | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asn | Val | Phe | Ile | Val | Asn | Asp | Phe | Gln | Ser | Pro | Leu | Gln | Arg | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ser | Ser | Leu | Glu | Leu | Pro | Ser | Ser | Leu | Pro | Val | Ala | Ser | Gly | Gln |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Val | Tyr | Pro | Leu | Asp | Gly | Gly | Ser | Ser | Ser | Glu | Asn | Gln | Arg | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Ser | Ser | Asp | Val | Gly | Asn | Arg | Val | Ser | Ser | Val | Ser | Gln | Ser | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Phe | Arg | Lys | Gln | Lys | Ser | His | Asp | Pro | Thr | Arg | Asp | Leu | Ser | Ile | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Leu | Glu | Lys | Phe | Ser | Leu | Val | Thr | Lys | Phe | Ala | Arg | Asp | Thr | Thr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Gln | Leu | Phe | Ser | Glu | Asn | Asn | Gly | Phe | Gly | Ser | Ile | Asp | Lys | Arg |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Asn | Asn | Gln | Pro | Val | His | Ser | Tyr | Pro | Glu | Lys | Leu | Ser | Asn | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Glu | Glu | Lys | His | His | Glu | Ile | Arg | His | Ser | Tyr | Ser | Glu | Asn | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Leu | Lys | Asp | Asp | Glu | Ile | Ser | Tyr | Ile | Asp | Val | Pro | Ala | Asp | Pro |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Glu | Phe | Asp | Lys | Leu | Ser | Leu | Met | Trp | Gly | Lys | Pro | Arg | Gln | Pro |
|     | 340 |     |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Met | Gly | His | Lys | Glu | Phe | Thr | Ala | Leu | Leu | Asp | Ser | Glu | Gly | Arg |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |
| Val | Val | Glu | Ser | Lys | Ala | Leu | Arg | Glu | Arg | Val | Phe | Tyr | Gly | Gly | Ile |

|                         |                     |                     |
|-------------------------|---------------------|---------------------|
| 370                     | 375                 | 380                 |
| Glu His Gln Leu Arg Arg | Glu Val Trp Pro Phe | Leu Leu Gly Tyr Tyr |
| 385                     | 390                 | 395                 |
| Ala Tyr Asp Ser Thr     | Ala Glu Arg Glu Tyr | Leu Arg Ser Val Lys |
| 405                     | 410                 | 415                 |
| Arg Met Glu Tyr Ala Thr | Leu Lys Gln Gln Trp | Gln Ser Ile Ser Pro |
| 420                     | 425                 | 430                 |
| Glu Gln Ala Lys Arg Phe | Thr Lys Tyr Arg Glu | Arg Lys Gly Leu Ile |
| 435                     | 440                 | 445                 |
| Asp Lys Asp Val Val Arg | Thr Asp Arg Ala Phe | Glu Tyr Tyr Glu Gly |
| 450                     | 455                 | 460                 |
| Asp Asp Asn Leu His Val | Asn Ser Met Arg Asp | Ile Leu Leu Thr Tyr |
| 465                     | 470                 | 475                 |
| Ser Phe Tyr Asn Phe Asp | Leu Gly Tyr Cys Gln | Gly Met Ser Asp Tyr |
| 485                     | 490                 | 495                 |
| Leu Ser Pro Ile Leu Phe | Val Met Glu Asp Glu | Ser Glu Ser Phe Trp |
| 500                     | 505                 | 510                 |
| Xaa Phe Xaa Ala Leu Met | Glu Arg Leu Gly Pro | Asn Phe Asn Arg Asp |
| 515                     | 520                 | 525                 |
| Gln Asn Gly Met His Thr | Gln Leu Phe Ala Leu | Ser Lys Leu Val Glu |
| 530                     | 535                 | 540                 |
| Leu Leu Asp Ser Pro Leu | His Asn Tyr Phe Lys | Glu Asn Asp Cys Leu |
| 545                     | 550                 | 555                 |
| Asn Tyr Phe Phe Cys Phe | Arg Trp Ile Leu Ile | Gln Phe Lys Arg Glu |
| 565                     | 570                 | 575                 |
| Phe Glu Tyr Glu Lys Thr | Met Gln Leu Trp Glu | Val Met Trp Thr His |
| 580                     | 585                 | 590                 |
| Tyr Leu Ser Glu His Phe | His Leu Tyr Val Cys | Val Ala Val Leu Lys |
| 595                     | 600                 | 605                 |
| Arg Cys Arg Ser Lys Ile | Met Gly Glu Gln Met | Asp Phe Asp Thr Leu |
| 610                     | 615                 | 620                 |
| Leu Lys Phe Ile Asn Glu | Leu Ser Gly His Ile | Asp Leu Asp Ser Thr |
| 625                     | 630                 | 635                 |
| Val Arg Asp Ala Glu Ala | Leu Cys Ile Glu Ala | Gly Glu Asn Gly Ala |
| 645                     | 650                 | 655                 |
| Ala Ser Ile Pro Pro Gly | Thr Pro Pro Ser Leu | Pro Leu Asp Asp Gly |
| 660                     | 665                 | 670                 |
| Thr Leu Tyr Pro Gln Glu | Asp Asp Val Leu     |                     |
| 675                     | 680                 |                     |

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 673 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..673

(D) OTHER INFORMATION: / Ceres Seq. ID 1571247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Glu | Ala | Thr | Glu | Leu | Gln | Asp | Leu | Ser | Asp | Asp | Ala | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ala | Ala | Ser | Gln | Gln | Gln | Gly | Ser | Ala | Ser | Met | Met | Arg | Xaa | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Lys | Arg | Ser | Leu | Gln | Ser | Glu | His | Glu | Asp | Ala | Val | Leu | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Leu | Lys | Asp | Asn | Val | Ala | Ile | His | Pro | Thr | Gln | Phe | Ala | Ser | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ile | Ser | Gly | Arg | Leu | Lys | Leu | Thr | Lys | Gln | Asp | Ser | Val | Leu | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Leu | Ser | Trp | Ile | Pro | Tyr | Lys | Gly | Gln | Thr | Ser | Asn | Ala | Lys | Leu | Ser |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Glu | Lys | Asp | Arg | Ser | Leu | Tyr | Thr | Ile | Thr | Ala | Val | Pro | Phe | Thr | Glu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Val | Arg | Ser | Ile | Arg | Arg | His | Thr | Pro | Ala | Leu | Gly | Trp | Gln | Tyr | Val |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ile | Val | Val | Leu | Ser | Ser | Gly | Leu | Ala | Phe | Pro | Pro | Leu | Tyr | Phe | Tyr |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Asn | Gly | Gly | Val | Arg | Glu | Phe | Leu | Ala | Met | Val | Lys | Gln | His | Val | Phe |  |  |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Leu | Ala | Arg | Ser | Ser | Glu | Asp | Gln | Asn | Val | Phe | Ile | Val | Asn | Asp | Phe |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Gln | Ser | Pro | Leu | Gln | Arg | Thr | Leu | Ser | Ser | Leu | Glu | Leu | Pro | Ser | Ser |  |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Leu | Pro | Val | Ala | Ser | Gly | Gln | Ser | Val | Tyr | Pro | Leu | Asp | Gly | Gly | Ser |  |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |
| Ser | Ser | Glu | Asn | Gln | Arg | Arg | Thr | Ser | Ser | Asp | Val | Gly | Asn | Arg | Val |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Ser | Ser | Val | Ser | Gln | Ser | Gly | Phe | Arg | Lys | Gln | Lys | Ser | His | Asp | Pro |  |  |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Thr | Arg | Asp | Leu | Ser | Ile | His | Leu | Leu | Glu | Lys | Phe | Ser | Leu | Val | Thr |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Lys | Phe | Ala | Arg | Asp | Thr | Thr | Thr | Gln | Leu | Phe | Ser | Glu | Asn | Asn | Gly |  |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Phe | Gly | Ser | Ile | Asp | Lys | Arg | Trp | Asn | Asn | Gln | Pro | Val | His | Ser | Tyr |  |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Pro | Glu | Lys | Leu | Ser | Asn | Ile | Ala | Glu | Glu | Lys | His | His | Glu | Ile | Arg |  |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |  |
| His | Ser | Tyr | Ser | Glu | Asn | Asp | Leu | Leu | Lys | Asp | Asp | Glu | Ile | Ser | Tyr |  |  |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Ile | Asp | Val | Pro | Ala | Asp | Pro | Leu | Glu | Phe | Asp | Lys | Leu | Ser | Leu | Met |  |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Trp | Gly | Lys | Pro | Arg | Gln | Pro | Pro | Met | Gly | His | Lys | Glu | Phe | Thr | Ala |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Leu | Leu | Asp | Ser | Glu | Gly | Arg | Val | Val | Glu | Ser | Lys | Ala | Leu | Arg | Glu |  |  |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |  |  |
| Arg | Val | Phe | Tyr | Gly | Gly | Ile | Glu | His | Gln | Leu | Arg | Arg | Glu | Val | Trp |  |  |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |  |  |
| Pro | Phe | Leu | Leu | Gly | Tyr | Tyr | Ala | Tyr | Asp | Ser | Thr | Tyr | Ala | Glu | Arg |  |  |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Glu | Tyr | Leu | Arg | Ser | Val | Lys | Arg | Met | Glu | Tyr | Ala | Thr | Leu | Lys | Gln |  |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |
| Gln | Trp | Gln | Ser | Ile | Ser | Pro | Glu | Gln | Ala | Lys | Arg | Phe | Thr | Lys | Tyr |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Arg | Glu | Arg | Lys | Gly | Leu | Ile | Asp | Lys | Asp | Val | Val | Arg | Thr | Asp | Arg |  |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |
| Ala | Phe | Glu | Tyr | Tyr | Glu | Gly | Asp | Asp | Asn | Leu | His | Val | Asn | Ser | Met |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |
| Arg | Asp | Ile | Leu | Leu | Thr | Tyr | Ser | Phe | Tyr | Asn | Phe | Asp | Leu | Gly | Tyr |  |  |
|     | 465 |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |  |  |
| Cys | Gln | Gly | Met | Ser | Asp | Tyr | Leu | Ser | Pro | Ile | Leu | Phe | Val | Met | Glu |  |  |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |  |  |
| Asp | Glu | Ser | Glu | Ser | Phe | Trp | Xaa | Phe | Xaa | Ala | Leu | Met | Glu | Arg | Leu |  |  |
|     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |     |  |  |
| Gly | Pro | Asn | Phe | Asn | Arg | Asp | Gln | Asn | Gly | Met | His | Thr | Gln | Leu | Phe |  |  |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |
| Ala | Leu | Ser | Lys | Leu | Val | Glu | Leu | Leu | Asp | Ser | Pro | Leu | His | Asn | Tyr |  |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |
| Phe | Lys | Glu | Asn | Asp | Cys | Leu | Asn | Tyr | Phe | Phe | Cys | Phe | Arg | Trp | Ile |  |  |
|     | 545 |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |
| Leu | Ile | Gln | Phe | Lys | Arg | Glu | Phe | Glu | Tyr | Glu | Lys | Thr | Met | Gln | Leu |  |  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Thr | Glu | Leu | Gln | Asp | Leu | Ser | Asp | Asp | Ala | Asp | Tyr | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Ser | Gln | Gln | Gln | Gly | Ser | Ala | Ser | Met | Met | Arg | Xaa | Asp | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Arg | Ser | Leu | Gln | Ser | Glu | His | Glu | Asp | Ala | Val | Leu | Ile | Tyr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Asp | Asn | Val | Ala | Ile | His | Pro | Thr | Gln | Phe | Ala | Ser | Glu | Arg | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Arg | Leu | Lys | Leu | Thr | Lys | Gln | Asp | Ser | Val | Leu | Phe | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Trp | Ile | Pro | Tyr | Lys | Gly | Gln | Thr | Ser | Asn | Ala | Lys | Leu | Ser | Glu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Arg | Ser | Leu | Tyr | Thr | Ile | Thr | Ala | Val | Pro | Phe | Thr | Glu | Val | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ile | Arg | Arg | His | Thr | Pro | Ala | Leu | Gly | Trp | Gln | Tyr | Val | Ile | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Leu | Ser | Ser | Gly | Leu | Ala | Phe | Pro | Pro | Leu | Tyr | Phe | Tyr | Asn | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Val | Arg | Glu | Phe | Leu | Ala | Met | Val | Lys | Gln | His | Val | Phe | Leu | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Ser | Ser | Glu | Asp | Gln | Asn | Val | Phe | Ile | Val | Asn | Asp | Phe | Gln | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Leu | Gln | Arg | Thr | Leu | Ser | Ser | Leu | Glu | Leu | Pro | Ser | Ser | Leu | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Val | Ala | Ser | Gly | Gln | Ser | Val | Tyr | Pro | Leu | Asp | Gly | Gly | Ser | Ser | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Asn | Gln | Arg | Arg | Thr | Ser | Ser | Asp | Val | Gly | Asn | Arg | Val | Ser | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Ser | Gln | Ser | Gly | Phe | Arg | Lys | Gln | Lys | Ser | His | Asp | Pro | Thr | Arg |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Leu | Ser | Ile | His | Leu | Leu | Glu | Lys | Phe | Ser | Leu | Val | Thr | Lys | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Arg | Asp | Thr | Thr | Thr | Gln | Leu | Phe | Ser | Glu | Asn | Asn | Gly | Phe | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

Ser Ile Asp Lys Arg Trp Asn Asn Gln Pro Val His Ser Tyr Pro Glu  
275 280 285  
Lys Leu Ser Asn Ile Ala Glu Lys His His Glu Ile Arg His Ser  
290 295 300  
Tyr Ser Glu Asn Asp Leu Leu Lys Asp Asp Glu Ile Ser Tyr Ile Asp  
305 310 315 320  
Val Pro Ala Asp Pro Leu Glu Phe Asp Lys Leu Ser Leu Met Trp Gly  
325 330 335  
Lys Pro Arg Gln Pro Pro Met Gly His Lys Glu Phe Thr Ala Leu Leu  
340 345 350  
Asp Ser Glu Gly Arg Val Val Glu Ser Lys Ala Leu Arg Glu Arg Val  
355 360 365  
Phe Tyr Gly Gly Ile Glu His Gln Leu Arg Arg Glu Val Trp Pro Phe  
370 375 380  
Leu Leu Gly Tyr Tyr Ala Tyr Asp Ser Thr Tyr Ala Glu Arg Glu Tyr  
385 390 395 400  
Leu Arg Ser Val Lys Arg Met Glu Tyr Ala Thr Leu Lys Gln Gln Trp  
405 410 415  
Gln Ser Ile Ser Pro Glu Gln Ala Lys Arg Phe Thr Lys Tyr Arg Glu  
420 425 430  
Arg Lys Gly Leu Ile Asp Lys Asp Val Val Arg Thr Asp Arg Ala Phe  
435 440 445  
Glu Tyr Tyr Glu Gly Asp Asp Asn Leu His Val Asn Ser Met Arg Asp  
450 455 460  
Ile Leu Leu Thr Tyr Ser Phe Tyr Asn Phe Asp Leu Gly Tyr Cys Gln  
465 470 475 480  
Gly Met Ser Asp Tyr Leu Ser Pro Ile Leu Phe Val Met Glu Asp Glu  
485 490 495  
Ser Glu Ser Phe Trp Xaa Phe Xaa Ala Leu Met Glu Arg Leu Gly Pro  
500 505 510  
Asn Phe Asn Arg Asp Gln Asn Gly Met His Thr Gln Leu Phe Ala Leu  
515 520 525  
Ser Lys Leu Val Glu Leu Leu Asp Ser Pro Leu His Asn Tyr Phe Lys  
530 535 540  
Glu Asn Asp Cys Leu Asn Tyr Phe Phe Cys Phe Arg Trp Ile Leu Ile  
545 550 555 560  
Gln Phe Lys Arg Glu Phe Glu Tyr Glu Lys Thr Met Gln Leu Trp Glu  
565 570 575  
Val Met Trp Thr His Tyr Leu Ser Glu His Phe His Leu Tyr Val Cys  
580 585 590  
Val Ala Val Leu Lys Arg Cys Arg Ser Lys Ile Met Gly Glu Gln Met  
595 600 605  
Asp Phe Asp Thr Leu Leu Lys Phe Ile Asn Glu Leu Ser Gly His Ile  
610 615 620  
Asp Leu Asp Ser Thr Val Arg Asp Ala Glu Ala Leu Cys Ile Glu Ala  
625 630 635 640  
Gly Glu Asn Gly Ala Ala Ser Ile Pro Pro Gly Thr Pro Pro Ser Leu  
645 650 655  
Pro Leu Asp Asp Gly Thr Leu Tyr Pro Gln Glu Asp Asp Val Leu  
660 665 670

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..726
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571257

SEQUENCE 1877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| aagagatcac | ttctccgacg | cagaaatgac | gaagtTcagg | aagcttggtc  | ggccggcggg  | 60  |
| tcaccgtatg | tccatgctta | ggactatggt | ttctcagttg | gtgaagcacg  | agcgtattga  | 120 |
| gaccactgtc | actaaggcta | aagaggttcg | tcgtcttgct | gataaatatga | ttcaactcgg  | 180 |
| caaagagggg | tcactctctg | ctgcaaggcg | agcagctggt | tttgtgagag  | gagatgatgt  | 240 |
| ccttcacaag | attttcacag | aactggcaca | tagatacaaa | gatagagctg  | gtggatacac  | 300 |
| aagactgcta | cgtactcgca | tacgagttgg | tgatgctgct | cctatggcct  | atatacgagtt | 360 |
| tattgacaga | gagaacgagc | ttaggcaatc | aaaaccagca | acacctcaac  | caccgcaacg  | 420 |
| agtgccattg | gacccatggg | aaagatctcg | gctcaccagg | cagttcgCtc  | cgcctaagga  | 480 |
| ggagaaaatc | cctgattctg | agctgtaatg | tggcataaag | aatttcocctc | tgttcaccaa  | 540 |
| atatcttgct | tctgtctcaa | aaatgtatgt | tcgtgatcat | ttatcatatg  | ccacaatatg  | 600 |
| tttttacaga | aggcaaacaa | taagttagct | ttttcatttg | tttgaacatt  | gaaaatgtac  | 660 |
| tcttgaaaac | attaacaggc | ttagagagac | tctttctttg | cctatctacc  | tatgaactaa  | 720 |

actggtt

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1571258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | His | Phe | Ser | Asp | Ala | Glu | Met | Thr | Lys | Phe | Arg | Lys | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Ala | Gly | His | Arg | Met | Ser | Met | Leu | Arg | Thr | Met | Val | Ser | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Lys | His | Glu | Arg | Ile | Glu | Thr | Thr | Val | Thr | Lys | Ala | Lys | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Arg | Leu | Ala | Asp | Asn | Met | Ile | Gln | Leu | Gly | Lys | Glu | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Ala | Ala | Arg | Arg | Ala | Ala | Gly | Phe | Val | Arg | Gly | Asp | Asp | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | His | Lys | Ile | Phe | Thr | Glu | Leu | Ala | His | Arg | Tyr | Lys | Asp | Arg | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Gly | Tyr | Thr | Arg | Leu | Leu | Arg | Thr | Arg | Ile | Arg | Val | Gly | Asp | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Pro | Met | Ala | Tyr | Ile | Glu | Phe | Ile | Asp | Arg | Glu | Asn | Glu | Leu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ser | Lys | Pro | Ala | Thr | Pro | Gln | Pro | Pro | Gln | Arg | Val | Pro | Leu | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Trp | Glu | Arg | Ser | Arg | Leu | Thr | Arg | Gln | Phe | Ala | Pro | Pro | Lys | Glu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Glu | Lys | Ile | Pro | Asp | Ser | Glu | Leu |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     | 165 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1571259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Leu | Arg | Thr | Met | Val | Ser | Gln | Leu | Val | Lys | His | Glu | Arg | Ile | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Thr | Val | Thr | Lys | Ala | Lys | Glu | Val | Arg | Arg | Leu | Ala | Asp | Asn | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gln | Leu | Gly | Lys | Glu | Gly | Ser | Leu | Ser | Ala | Ala | Arg | Arg | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Phe | Val | Arg | Gly | Asp | Asp | Val | Leu | His | Lys | Ile | Phe | Thr | Glu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | His | Arg | Tyr | Lys | Asp | Arg | Ala | Gly | Gly | Tyr | Thr | Arg | Leu | Leu | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Arg | Ile | Arg | Val | Gly | Asp | Ala | Ala | Pro | Met | Ala | Tyr | Ile | Glu | Phe |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asp | Arg | Glu | Asn | Glu | Leu | Arg | Gln | Ser | Lys | Pro | Ala | Thr | Pro | Gln |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Pro | Gln | Arg | Val | Pro | Leu | Asp | Pro | Trp | Glu | Arg | Ser | Arg | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Gln | Phe | Ala | Pro | Pro | Lys | Glu | Glu | Lys | Ile | Pro | Asp | Ser | Glu | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

(2) INFORMATION FOR SEQ ID NO:1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1571260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Leu | Arg | Thr | Met | Val | Ser | Gln | Leu | Val | Lys | His | Glu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Glu | Thr | Thr | Val | Thr | Lys | Ala | Lys | Glu | Val | Arg | Arg | Leu | Ala | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Met | Ile | Gln | Leu | Gly | Lys | Glu | Gly | Ser | Leu | Ser | Ala | Ala | Arg | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Gly | Phe | Val | Arg | Gly | Asp | Asp | Val | Leu | His | Lys | Ile | Phe | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Leu | Ala | His | Arg | Tyr | Lys | Asp | Arg | Ala | Gly | Gly | Tyr | Thr | Arg | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Arg | Thr | Arg | Ile | Arg | Val | Gly | Asp | Ala | Ala | Pro | Met | Ala | Tyr | Ile |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Phe | Ile | Asp | Arg | Glu | Asn | Glu | Leu | Arg | Gln | Ser | Lys | Pro | Ala | Thr |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Gln | Pro | Pro | Gln | Arg | Val | Pro | Leu | Asp | Pro | Trp | Glu | Arg | Ser | Arg |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Arg | Gln | Phe | Ala | Pro | Pro | Lys | Glu | Glu | Lys | Ile | Pro | Asp | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..576  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| atgaatgtaa | tgccgtatag | tcagcctatg  | tccgctggtc  | aattggctac | ttcccttgct | 60  |
| aatgctacac | ctgctcaaca | gagaacactt  | cttgggtgaga | gtctatatcc | attagtggac | 120 |
| cagatagaga | gtgagcacgc | tgcgaaagtg  | actgggtatgc | ttctggaaat | ggatcagacc | 180 |
| gaggttttgc | atctgctcga | gtcaccagag  | gctctaaatg  | ccaaagtttc | agaggcatta | 240 |
| gatgtgttga | gaaacgtgaa | tcagccatct  | tcacagggaa  | gtgaaggcaa | caaaagtgga | 300 |
| agtccaagtg | atctcttggc | ttcactttcc  | atcaatgatc  | acttatgaga | agcttttgtt | 360 |
| cgagtttttt | ttttttactt | tgactctctt  | cctctctatc  | tctctctctg | attgacaaat | 420 |
| ttttgcggga | atctatttgc | tgtttttagac | tttttttgct  | cgatatgatt | gtttctgttt | 480 |
| tgGacttctt | acttttttgg | gttgacttaa  | aaaaggatgg  | ttttatttta | ttttgttggg | 540 |
| ttatatatta | ctgttgcaaa | attttgcgct  | cagttt      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..115  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Val | Met | Pro | Tyr | Ser | Gln | Pro | Met | Ser | Ala | Gly | Gln | Leu | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Thr | Ser | Leu | Ala | Asn | Ala | Thr | Pro | Ala | Gln | Gln | Arg | Thr | Leu | Leu | Gly |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Ser | Leu | Tyr | Pro | Leu | Val | Asp | Gln | Ile | Glu | Ser | Glu | His | Ala | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Val | Thr | Gly | Met | Leu | Leu | Glu | Met | Asp | Gln | Thr | Glu | Val | Leu | His |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Leu | Glu | Ser | Pro | Glu | Ala | Leu | Asn | Ala | Lys | Val | Ser | Glu | Ala | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Asp | Val | Leu | Arg | Asn | Val | Asn | Gln | Pro | Ser | Ser | Gln | Gly | Ser | Glu | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asn | Lys | Ser | Gly | Ser | Pro | Ser | Asp | Leu | Leu | Ala | Ser | Leu | Ser | Ile | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Asp | His | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..112  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Tyr | Ser | Gln | Pro | Met | Ser | Ala | Gly | Gln | Leu | Ala | Thr | Ser | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ala | Asn | Ala | Thr | Pro | Ala | Gln | Gln | Arg | Thr | Leu | Leu | Gly | Glu | Ser | Leu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Pro | Leu | Val | Asp | Gln | Ile | Glu | Ser | Glu | His | Ala | Ala | Lys | Val | Thr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Met | Leu | Leu | Glu | Met | Asp | Gln | Thr | Glu | Val | Leu | His | Leu | Leu | Glu |  |

(2) INFORMATION FOR SEQ ID NO:1884:

(A) LENGTH: 632 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..632

(D) OTHER INFORMATION: 11:35Z

(D) OTHER INFORMATION: / Ceres Seq. ID 1571265

| (XI) SEQUENCE ALIGNMENT: SEQ ID NO: 1 |            |             |             |            |            |     |
|---------------------------------------|------------|-------------|-------------|------------|------------|-----|
| attccccatc                            | gcacagacc  | gccctaagaat | ccgagagaga  | agaagagata | atgcagatct | 60  |
| tcgtcaaaac                            | cctcaccgcg | aaaactataa  | ccctagaggt  | tgagagcagc | gacaccatcg | 120 |
| acaatgttaa                            | agccaaaatc | caggacaaat  | agggcatacc  | acctgatcaa | cagaggctga | 180 |
| tttttgctgg                            | taagcaattg | gaagatggcc  | ggaccttagc  | tgactacaac | atccagaaag | 240 |
| agtctactct                            | tcattcttgc | ctcagggtca  | gaggtggaac  | catgatcaag | gtgaagacac | 300 |
| tactggaaa                             | agaaatcgag | attgatatcg  | aaccaaccga  | cactattgat | cggatcaaag | 360 |
| aacgtgttga                            | agagaaagaa | ggcatccctc  | ctgttcaaca  | aaggctcatc | tatgccggaa | 420 |
| aacagcttgc                            | tgatgcacaa | acggccaaag  | attatgcgat  | agagggaggc | tctgttcttc | 480 |
| attttggttct                           | tgctcttagg | ggtgggtctc  | tcctgatctga | ataataaagc | ttttcaacaa | 540 |
| acatctttcc                            | cctcactatt | gtcctccttt  | tgtggaAttc  | atgacacaca | aaaattgcta | 600 |
| tgggaaattg                            | gaatattatg | atgttttttc  | tc          |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1571266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Lys | Val | Lys | Thr | Leu | Thr | Gly | Lys | Glu | Ile | Glu | Ile | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Pro | Thr | Asp | Thr | Ile | Asp | Arg | Ile | Lys | Glu | Arg | Val | Glu | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Ile | Pro | Pro | Val | Gln | Gln | Arg | Leu | Ile | Tyr | Ala | Gly | Lys | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Ala | Asp | Asp | Lys | Thr | Ala | Lys | Asp | Tyr | Ala | Ile | Glu | Gly | Gly | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | His | Leu | Val | Leu | Ala | Leu | Arg | Gly | Gly | Leu | Leu |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1120

(D) OTHER INFORMATION: / Ceres Seq. ID 1571271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| aaaactcaag  | ggtttgattt | ttcttcttca | actacgttaa  | gattttctcct | acacttttct  | 60   |
| ttttcaccgt  | attctctttt | agtcctcgat | tctctacgcy  | tttcagcgtc  | aagtcttcta  | 120  |
| gatctctaaa  | gccttcgctg | tcgccaatat | aaatctctga  | gatcggtccc  | gtaaaaatcg  | 180  |
| attcgcgctg  | tttttgagta | aaaaaaatgg | cgcaacaatc  | gttgatctac  | agtttcgctg  | 240  |
| ctcggtgtac  | cgttatcctc | gttgagttca | cagattttcaa | aggcaatttc  | acatcaatcg  | 300  |
| ctgctcagtg  | ccttcagaag | cttccttctt | ctaacaacaa  | gtttacctac  | aactgcgatg  | 360  |
| gtcacacggt  | caattacctc | gtcgaaaatg | gattcaccta  | ttgtgttggt  | gcagttgatt  | 420  |
| ctgctgggag  | gcagattcct | atggctttct | tggaaacgag  | taaggaggat  | ttcaacaaga  | 480  |
| gatatggtgg  | tggaaaggct | gcaactgctc | aagcaaacag  | cttgaataaa  | gaatttgggt  | 540  |
| cgaaactgaa  | agagcatatg | cagtattgca | tggatcatcc  | tgatgagatt  | agcaagcttg  | 600  |
| ctaagggttaa | agctcaagtg | tctgaagtta | aaggtgttat  | gatggaaaac  | attgagaagg  | 660  |
| ttcttgaccg  | tggtgagaag | attgagcttt | tggttgacaa  | aacagaaaac  | cttcgctcac  | 720  |
| aggcgcaaga  | ttttagaaca | caaggaactc | aatgagaag   | aaagatgtgg  | tttcagaaca  | 780  |
| tgaagataaa  | gctcattgtc | cttgcaatta | tcattgcctt  | gattctcatc  | atcatcctct  | 840  |
| caatttgtgg  | gggattcaac | tgcggtaaat | aagtctggaa  | catttcttcc  | cggcggtatc  | 900  |
| gactgcgctc  | tgtgcttccc | aagatctctg | agaatatctt  | cattcagttc  | gttggtgctac | 960  |
| cttttttttg  | ttWttgtttt | tgwgatttct | atattctcat  | actatatgtt  | tcttcttaga  | 1020 |
| ttgtacttct  | tgaattttgt | tttgtatagg | ctatatatat  | tatacatata  | tgtatgcatg  | 1080 |
| ttcgacaatc  | tgcaatgttg | ctattgctgg | tactgacact  |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1571272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gln | Gln | Ser | Leu | Ile | Tyr | Ser | Phe | Val | Ala | Arg | Gly | Thr | Val |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ile | Leu | Val | Glu | Phe | Thr | Asp | Phe | Lys | Gly | Asn | Phe | Thr | Ser | Ile | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Gln | Cys | Leu | Gln | Lys | Leu | Pro | Ser | Ser | Asn | Asn | Lys | Phe | Thr | Tyr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Cys | Asp | Gly | His | Thr | Phe | Asn | Tyr | Leu | Val | Glu | Asn | Gly | Phe | Thr |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Tyr | Cys | Val | Val | Ala | Val | Asp | Ser | Ala | Gly | Arg | Gln | Ile | Pro | Met | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Phe | Leu | Glu | Arg | Val | Lys | Glu | Asp | Phe | Asn | Lys | Arg | Tyr | Gly | Gly | Gly |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Ala | Ala | Thr | Ala | Gln | Ala | Asn | Ser | Leu | Asn | Lys | Glu | Phe | Gly | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Leu | Lys | Glu | His | Met | Gln | Tyr | Cys | Met | Asp | His | Pro | Asp | Glu | Ile |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Lys | Leu | Ala | Lys | Val | Lys | Ala | Gln | Val | Ser | Glu | Val | Lys | Gly | Val |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Met | Met | Glu | Asn | Ile | Glu | Lys | Val | Leu | Asp | Arg | Gly | Glu | Lys | Ile | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Leu | Leu | Val | Asp | Lys | Thr | Glu | Asn | Leu | Arg | Ser | Gln | Ala | Gln | Asp | Phe |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Arg | Thr | Gln | Gly | Thr | Gln | Met | Arg | Arg | Lys | Met | Trp | Phe | Gln | Asn | Met |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |  |
| Lys | Ile | Lys | Leu | Ile | Val | Leu | Ala | Ile | Ile | Ile | Ala | Leu | Ile | Leu | Ile |  |

195 200 205  
Ile Ile Leu Ser Ile Cys Gly Gly Phe Asn Cys Gly Lys  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Met Ala Phe Leu Glu Arg Val Lys Glu Asp Phe Asn Lys Arg Tyr Gly  
1 5 10 15  
Gly Gly Lys Ala Ala Thr Ala Gln Ala Asn Ser Leu Asn Lys Glu Phe  
20 25 30  
Gly Ser Lys Leu Lys Glu His Met Gln Tyr Cys Met Asp His Pro Asp  
35 40 45  
Glu Ile Ser Lys Leu Ala Lys Val Lys Ala Gln Val Ser Glu Val Lys  
50 55 60  
Gly Val Met Met Glu Asn Ile Glu Lys Val Leu Asp Arg Gly Glu Lys  
65 70 75 80  
Ile Glu Leu Leu Val Asp Lys Thr Glu Asn Leu Arg Ser Gln Ala Gln  
85 90 95  
Asp Phe Arg Thr Gln Gly Thr Gln Met Arg Arg Lys Met Trp Phe Gln  
100 105 110  
Asn Met Lys Ile Lys Leu Ile Val Leu Ala Ile Ile Ala Leu Ile  
115 120 125  
Leu Ile Ile Ile Leu Ser Ile Cys Gly Gly Phe Asn Cys Gly Lys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

aaacarGcaa caacaacaat gtctttcttct ctccgatcta ccaccgccgc ttctcttthtc 60  
ctccgctcct cctcctcctc ctccagatcc actctcactc tctccgcttc ctctctcttc 120  
tccttcgtca gatctctcgt ctcttctcca cgtctctctt cttcttcacc cctctctcag 180  
aaatgtcgaa ttgcgctcgt gaatcggagt ttcaactcca ccaccgccgc tactaaatct 240  
tcctcttcag atcctgatca gttgaagaac gctagagaag atatcaaaga gcttctcagc 300  
accaaattct gccatccgat tttggttaga ttaggttggc atgatgctgg tacgtataac 360  
aagaacatta aggaatggcc acaaagaggt ggagctaata gaagtttgag attcgatatt 420  
gagcttaaac atactgctaa tgctggctct gtgaatgctt taaacttgat taaggatatc 480  
aaagagaaat actctgggat cagttatgct gatttgttcc agttagctag tgctactgct 540  
atagaggaag ctggaggacc gaaaataccg atgaaatatg gtagagttga tgccctctggt 600  
cctgaggatt gtccagaaga aggaaggctt ccagatgctg gtcctccttc gcctgctact 660  
catctcagag aagtttttta cagaatggga ttagatgaca aggacatagt tgcattatct 720  
ggtgctcaca cgttaggaag atctaggcca gaacgtagtg gttgggggaa gcctgagacg 780  
aagtacacga aagaaggacc tggagcacca ggaggacagt catggacacc agagtggctg 840  
aagtttgata attcgtactt caaggagatc aaggaaaaga gagatgaaga tctccttgtc 900  
ctaccactg atgctgccat cttcgaagat tcttctttca aggtctatgc tgaaaagtat 960

```
gctgcagatc aggatgcatt tttcaaggat tacgctgtag cgcattgcgaa actcagcaat 1020
cttggcgcag aattttaaccc tccggagggt atcattatct aatggggcac ctaatttact 1080
caaccagact tatgatttta gagaaacgta gttcaataat gaaagagaag aaaaagtga 1140
cggagaactt ttcattgcgag tacttttoga gatacctttt ggacaaatgt ttctggctgt 1200
tcaaaggatt ttgttttagcc gaaagtatit gatcgttttc atgggttttgt gctttcatgt 1260
ttttttcttg taataaattg cggaagtgat tatccaaaat ctatacaaat tttgtctgga 1320
attgaattat tttatcgatg ttataact
```

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1571292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

```
Lys Xaa Ala Thr Thr Thr Met Ser Ser Ser Leu Arg Ser Thr Thr Ala
1 5 10 15
Ala Ser Leu Xaa Leu Arg Ser Ser Ser Ser Ser Ser Arg Ser Thr Leu
20 25 30
Thr Leu Ser Ala Ser Ser Ser Leu Ser Phe Val Arg Ser Leu Val Ser
35 40 45
Ser Pro Arg Leu Ser Ser Ser Ser Pro Leu Ser Gln Lys Cys Arg Ile
50 55 60
Ala Ser Val Asn Arg Ser Phe Asn Ser Thr Thr Ala Ala Thr Lys Ser
65 70 75 80
Ser Ser Ser Asp Pro Asp Gln Leu Lys Asn Ala Arg Glu Asp Ile Lys
85 90 95
Glu Leu Leu Ser Thr Lys Phe Cys His Pro Ile Leu Val Arg Leu Gly
100 105 110
Trp His Asp Ala Gly Thr Tyr Asn Lys Asn Ile Lys Glu Trp Pro Gln
115 120 125
Arg Gly Gly Ala Asn Gly Ser Leu Arg Phe Asp Ile Glu Leu Lys His
130 135 140
Thr Ala Asn Ala Gly Leu Val Asn Ala Leu Asn Leu Ile Lys Asp Ile
145 150 155 160
Lys Glu Lys Tyr Ser Gly Ile Ser Tyr Ala Asp Leu Phe Gln Leu Ala
165 170 175
Ser Ala Thr Ala Ile Glu Glu Ala Gly Gly Pro Lys Ile Pro Met Lys
180 185 190
Tyr Gly Arg Val Asp Ala Ser Gly Pro Glu Asp Cys Pro Glu Glu Gly
195 200 205
Arg Leu Pro Asp Ala Gly Pro Pro Ser Pro Ala Thr His Leu Arg Glu
210 215 220
Val Phe Tyr Arg Met Gly Leu Asp Asp Lys Asp Ile Val Ala Leu Ser
225 230 235 240
Gly Ala His Thr Leu Gly Arg Ser Arg Pro Glu Arg Ser Gly Trp Gly
245 250 255
Lys Pro Glu Thr Lys Tyr Thr Lys Glu Gly Pro Gly Ala Pro Gly Gly
260 265 270
Gln Ser Trp Thr Pro Glu Trp Leu Lys Phe Asp Asn Ser Tyr Phe Lys
275 280 285
Glu Ile Lys Glu Lys Arg Asp Glu Asp Leu Leu Val Leu Pro Thr Asp
290 295 300
Ala Ala Ile Phe Glu Asp Ser Ser Phe Lys Val Tyr Ala Glu Lys Tyr
305 310 315 320
Ala Ala Asp Gln Asp Ala Phe Phe Lys Asp Tyr Ala Val Ala His Ala
325 330 335
```

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Lys Leu Ser Asn Leu Gly Ala Glu Phe Asn Pro Pro Glu Gly Ile Ile  
340 345 350  
Ile

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

Met Ser Ser Ser Leu Arg Ser Thr Thr Ala Ala Ser Leu Xaa Leu Arg  
1 5 10 15  
Ser Ser Ser Ser Ser Ser Arg Ser Thr Leu Thr Leu Ser Ala Ser Ser  
20 25 30  
Ser Leu Ser Phe Val Arg Ser Leu Val Ser Ser Pro Arg Leu Ser Ser  
35 40 45  
Ser Ser Pro Leu Ser Gln Lys Cys Arg Ile Ala Ser Val Asn Arg Ser  
50 55 60  
Phe Asn Ser Thr Thr Ala Ala Thr Lys Ser Ser Ser Ser Asp Pro Asp  
65 70 75 80  
Gln Leu Lys Asn Ala Arg Glu Asp Ile Lys Glu Leu Leu Ser Thr Lys  
85 90 95  
Phe Cys His Pro Ile Leu Val Arg Leu Gly Trp His Asp Ala Gly Thr  
100 105 110  
Tyr Asn Lys Asn Ile Lys Glu Trp Pro Gln Arg Gly Gly Ala Asn Gly  
115 120 125  
Ser Leu Arg Phe Asp Ile Glu Leu Lys His Thr Ala Asn Ala Gly Leu  
130 135 140  
Val Asn Ala Leu Asn Leu Ile Lys Asp Ile Lys Glu Lys Tyr Ser Gly  
145 150 155 160  
Ile Ser Tyr Ala Asp Leu Phe Gln Leu Ala Ser Ala Thr Ala Ile Glu  
165 170 175  
Glu Ala Gly Gly Pro Lys Ile Pro Met Lys Tyr Gly Arg Val Asp Ala  
180 185 190  
Ser Gly Pro Glu Asp Cys Pro Glu Glu Gly Arg Leu Pro Asp Ala Gly  
195 200 205  
Pro Pro Ser Pro Ala Thr His Leu Arg Glu Val Phe Tyr Arg Met Gly  
210 215 220  
Leu Asp Asp Lys Asp Ile Val Ala Leu Ser Gly Ala His Thr Leu Gly  
225 230 235 240  
Arg Ser Arg Pro Glu Arg Ser Gly Trp Gly Lys Pro Glu Thr Lys Tyr  
245 250 255  
Thr Lys Glu Gly Pro Gly Ala Pro Gly Gly Gln Ser Trp Thr Pro Glu  
260 265 270  
Trp Leu Lys Phe Asp Asn Ser Tyr Phe Lys Glu Ile Lys Glu Lys Arg  
275 280 285  
Asp Glu Asp Leu Leu Val Leu Pro Thr Asp Ala Ala Ile Phe Glu Asp  
290 295 300  
Ser Ser Phe Lys Val Tyr Ala Glu Lys Tyr Ala Ala Asp Gln Asp Ala  
305 310 315 320  
Phe Phe Lys Asp Tyr Ala Val Ala His Ala Lys Leu Ser Asn Leu Gly  
325 330 335  
Ala Glu Phe Asn Pro Pro Glu Gly Ile Ile Ile  
340 345

(2) INFORMATION FOR SEQ ID NO:1892:

SEQUENCE

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1532
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atatataagc  | tccaggtctt  | gtacatcttc  | atcatctgat  | ctcggggaag  | ctccgatctg  | 60   |
| agtttttttt  | agcaatggcg  | aaaatgattc  | ctagcctcgt  | ctctctaatt  | cttatcggtc  | 120  |
| ttgtttgcgat | cgcctccgcc  | gcagttattt  | tgcaggagcg  | ctttgatgat  | ggctgggaga  | 180  |
| acagatgggt  | taaatctgag  | tggaagaagg  | atgataacac  | tgctggggag  | tggaagcaca  | 240  |
| ctgcgggaaa  | ttggtctggt  | gacgctaacg  | ataaagggtat | ccagaccagt  | gaagactaca  | 300  |
| gattctacgc  | catttcagct  | gagttccctg  | aattcagtaa  | caaggacaag  | accttagtct  | 360  |
| tccaattctc  | agtcaagcac  | gagcaaaagc  | ttgactgcgg  | tgggtggctac | atgaagctac  | 420  |
| taagtgggtga | tgttgacca   | aagaaatttg  | gtggagacac  | accatacagt  | atcatgtttg  | 480  |
| gtcctgatata | ctgtggctac  | agcacaaa    | aagtgcattg  | tatccttacc  | tataatgaag  | 540  |
| ccaaccacct  | gatcaagaaa  | gatgttccat  | gtgAaactga  | ccagctcacc  | catgtgtaca  | 600  |
| catttatcct  | ccgcccagat  | gctaactaca  | gcattctcat  | cgacaatgtt  | gagaaacaaa  | 660  |
| ctggtagcct  | ttactctgac  | tgggatcttc  | tcccacccaa  | gaagatcaag  | gaccccagcg  | 720  |
| ccaagaagcc  | tgaggactgg  | gacgaacaag  | aatacatttc  | tgaccctgaa  | gacaagaaac  | 780  |
| ctgacgggta  | cgatgatata  | cctaaggaga  | tcccagacac  | cgactcaaag  | aagcctgagg  | 840  |
| actgggatga  | tgaagaagat  | ggtgagtggg  | ctgccccaac  | aatccccaac  | cctgagtaca  | 900  |
| tgggtgaatg  | gaagcctaag  | caaatacaaga | accccaacta  | caagggcaag  | tgggagggtc  | 960  |
| cattgattga  | caaccctgac  | ttcaaggatg  | acccagagct  | ctacgtcttc  | cccaagctga  | 1020 |
| aatatgttgg  | actcgaattg  | tggcagggtga | aatcaggatc  | attgttcgac  | aatgtcttga  | 1080 |
| tctgcgatga  | cccagactat  | gccaaagaag  | tggcagatga  | aacatgggga  | aagctcaagg  | 1140 |
| atgcggagaa  | agcagctttc  | gatgaggctg  | agaagaagaa  | tgaggaagag  | gaatccaagg  | 1200 |
| acgcacCctgc | ggaatctgat  | gctgaagacg  | aaccagagga  | tgatgaagga  | ggagatgatt  | 1260 |
| ccgattctga  | atctaaggcc  | gaggagacca  | aatcagaaga  | tagcgaggaa  | acctctgaga  | 1320 |
| aagacgccac  | cgctcatgat  | gagctatagg  | tgaagggttg  | aagatttgaa  | gaccaaagtt  | 1380 |
| ttcagtcctc  | ttattgtttt  | atcgttttct  | tttgaagtat  | tttagcatct  | agtttgctcg  | 1440 |
| agatagaaaac | aagtttttagc | aaaactaaaa  | gggggataca  | atgtctgtca  | gatgtctcatt | 1500 |
| ttagacttta  | aaaaaccatg  | aagaagtttt  | gc          |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..424
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Met | Ile | Pro | Ser | Leu | Val | Ser | Leu | Ile | Leu | Ile | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ala | Ile | Ala | Ser | Ala | Ala | Val | Ile | Phe | Glu | Glu | Arg | Phe | Asp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Gly | Trp | Glu | Asn | Arg | Trp | Val | Lys | Ser | Glu | Trp | Lys | Lys | Asp | Asp | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Gly | Glu | Trp | Lys | His | Thr | Ala | Gly | Asn | Trp | Ser | Gly | Asp | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | Asp | Lys | Gly | Ile | Gln | Thr | Ser | Glu | Asp | Tyr | Arg | Phe | Tyr | Ala | Ile |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ser | Ala | Glu | Phe | Pro | Glu | Phe | Ser | Asn | Lys | Asp | Lys | Thr | Leu | Val | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |



Gln Phe Ser Val Lys His Glu Gln Lys Leu Asp Cys Gly Gly Gly Tyr  
100 105 110  
Met Lys Leu Ser Gly Asp Val Asp Gln Lys Lys Phe Gly Gly Asp  
115 120 125  
Thr Pro Tyr Ser Ile Met Phe Gly Pro Asp Ile Cys Gly Tyr Ser Thr  
130 135 140  
Lys Lys Val His Ala Ile Leu Thr Tyr Asn Glu Ala Asn His Leu Ile  
145 150 155 160  
Lys Lys Asp Val Pro Cys Glu Thr Asp Gln Leu Thr His Val Tyr Thr  
165 170 175  
Phe Ile Leu Arg Pro Asp Ala Thr Tyr Ser Ile Leu Ile Asp Asn Val  
180 185 190  
Glu Lys Gln Thr Gly Ser Leu Tyr Ser Asp Trp Asp Leu Leu Pro Pro  
195 200 205  
Lys Lys Ile Lys Asp Pro Ser Ala Lys Lys Pro Glu Asp Trp Asp Glu  
210 215 220  
Gln Glu Tyr Ile Ser Asp Pro Glu Asp Lys Lys Pro Asp Gly Tyr Asp  
225 230 235 240  
Asp Ile Pro Lys Glu Ile Pro Asp Thr Asp Ser Lys Lys Pro Glu Asp  
245 250 255  
Trp Asp Asp Glu Glu Asp Gly Glu Trp Thr Ala Pro Thr Ile Pro Asn  
260 265 270  
Pro Glu Tyr Met Gly Glu Trp Lys Pro Lys Gln Ile Lys Asn Pro Asn  
275 280 285  
Tyr Lys Gly Lys Trp Glu Ala Pro Leu Ile Asp Asn Pro Asp Phe Lys  
290 295 300  
Asp Asp Pro Glu Leu Tyr Val Phe Pro Lys Leu Lys Tyr Val Gly Leu  
305 310 315 320  
Glu Leu Trp Gln Val Lys Ser Gly Ser Leu Phe Asp Asn Val Leu Ile  
325 330 335  
Cys Asp Asp Pro Asp Tyr Ala Lys Lys Leu Ala Asp Glu Thr Trp Gly  
340 345 350  
Lys Leu Lys Asp Ala Glu Lys Ala Ala Phe Asp Glu Ala Glu Lys Lys  
355 360 365  
Asn Glu Glu Glu Glu Ser Lys Asp Ala Pro Ala Glu Ser Asp Ala Glu  
370 375 380  
Asp Glu Pro Glu Asp Asp Glu Gly Gly Asp Asp Ser Asp Ser Glu Ser  
385 390 395 400  
Lys Ala Glu Glu Thr Lys Ser Glu Asp Ser Glu Glu Thr Ser Glu Lys  
405 410 415  
Asp Ala Thr Ala His Asp Glu Leu  
420

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1571306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

Met Ile Pro Ser Leu Val Ser Leu Ile Leu Ile Gly Leu Val Ala Ile  
1 5 10 15  
Ala Ser Ala Ala Val Ile Phe Glu Glu Arg Phe Asp Asp Gly Trp Glu  
20 25 30  
Asn Arg Trp Val Lys Ser Glu Trp Lys Lys Asp Asp Asn Thr Ala Gly  
35 40 45  
Glu Trp Lys His Thr Ala Gly Asn Trp Ser Gly Asp Ala Asn Asp Lys

|                                                                 |                                             |                     |
|-----------------------------------------------------------------|---------------------------------------------|---------------------|
| 50                                                              | 55                                          | 60                  |
| Gly Ile Gln Thr Ser                                             | Glu Asp Tyr Arg Phe Tyr                     | Ala Ile Ser Ala Glu |
| 65                                                              | 70                                          | 75                  |
| Phe Pro Glu Phe Ser                                             | Asn Lys Asp Lys Thr Leu Val Phe Gln Phe Ser | 80                  |
| 85                                                              | 90                                          | 95                  |
| Val Lys His Glu Gln Lys Leu Asp Cys Gly Gly Gly Tyr Met Lys Leu | 100                                         | 110                 |
| 115                                                             | 120                                         | 125                 |
| Leu Ser Gly Asp Val Asp Gln Lys Lys Phe Gly Gly Asp Thr Pro Tyr | 130                                         | 140                 |
| 135                                                             | 145                                         | 155                 |
| Ser Ile Met Phe Gly Pro Asp Ile Cys Gly Tyr Ser Thr Lys Lys Val | 160                                         | 170                 |
| 165                                                             | 175                                         | 185                 |
| His Ala Ile Leu Thr Tyr Asn Glu Ala Asn His Leu Ile Lys Lys Asp | 190                                         | 200                 |
| 195                                                             | 205                                         | 215                 |
| Val Pro Cys Glu Thr Asp Gln Leu Thr His Val Tyr Thr Phe Ile Leu | 220                                         | 230                 |
| 235                                                             | 240                                         | 250                 |
| Arg Pro Asp Ala Thr Tyr Ser Ile Leu Ile Asp Asn Val Glu Lys Gln | 255                                         | 265                 |
| 260                                                             | 270                                         | 280                 |
| Thr Gly Ser Leu Tyr Ser Asp Trp Asp Leu Leu Pro Pro Lys Lys Ile | 285                                         | 295                 |
| 290                                                             | 300                                         | 310                 |
| Lys Asp Pro Ser Ala Lys Lys Pro Glu Asp Trp Asp Glu Gln Glu Tyr | 315                                         | 320                 |
| 325                                                             | 330                                         | 335                 |
| Ile Ser Asp Pro Glu Asp Lys Lys Pro Asp Gly Tyr Asp Asp Ile Pro | 340                                         | 345                 |
| 345                                                             | 350                                         | 355                 |
| Lys Glu Ile Pro Asp Thr Asp Ser Lys Lys Pro Glu Asp Trp Asp Asp | 360                                         | 365                 |
| 365                                                             | 370                                         | 375                 |
| Glu Glu Asp Gly Glu Trp Thr Ala Pro Thr Ile Pro Asn Pro Glu Tyr | 380                                         | 385                 |
| 385                                                             | 390                                         | 395                 |
| Met Gly Glu Trp Lys Pro Lys Gln Ile Lys Asn Pro Asn Tyr Lys Gly | 400                                         | 405                 |
| 405                                                             | 410                                         | 415                 |
| Lys Trp Glu Ala Pro Leu Ile Asp Asn Pro Asp Phe Lys Asp Asp Pro | 420                                         |                     |
| 420                                                             |                                             |                     |
| Glu Leu Tyr Val Phe Pro Lys Leu Lys Tyr Val Gly Leu Glu Leu Trp |                                             |                     |
| 305                                                             | 310                                         | 315                 |
| Gln Val Lys Ser Gly Ser Leu Phe Asp Asn Val Leu Ile Cys Asp Asp | 320                                         | 325                 |
| 325                                                             | 330                                         | 335                 |
| Pro Asp Tyr Ala Lys Lys Leu Ala Asp Glu Thr Trp Gly Lys Leu Lys | 340                                         | 345                 |
| 345                                                             | 350                                         | 355                 |
| Asp Ala Glu Lys Ala Ala Phe Asp Glu Ala Glu Lys Lys Asn Glu Glu | 360                                         | 365                 |
| 365                                                             | 370                                         | 375                 |
| Glu Glu Ser Lys Asp Ala Pro Ala Glu Ser Asp Ala Glu Asp Glu Pro | 380                                         | 385                 |
| 385                                                             | 390                                         | 395                 |
| Glu Asp Asp Glu Gly Gly Asp Asp Ser Asp Ser Glu Ser Lys Ala Glu | 400                                         | 405                 |
| 405                                                             | 410                                         | 415                 |
| Glu Thr Lys Ser Glu Asp Ser Glu Glu Thr Ser Glu Lys Asp Ala Thr | 420                                         |                     |
| 420                                                             |                                             |                     |
| Ala His Asp Glu Leu                                             |                                             |                     |

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Leu | Ser | Gly | Asp | Val | Asp | Gln | Lys | Lys | Phe | Gly | Gly | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Tyr | Ser | Ile | Met | Phe | Gly | Pro | Asp | Ile | Cys | Gly | Tyr | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Val | His | Ala | Ile | Leu | Thr | Tyr | Asn | Glu | Ala | Asn | His | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Asp | Val | Pro | Cys | Glu | Thr | Asp | Gln | Leu | Thr | His | Val | Tyr | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ile | Leu | Arg | Pro | Asp | Ala | Thr | Tyr | Ser | Ile | Leu | Ile | Asp | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Lys | Gln | Thr | Gly | Ser | Leu | Tyr | Ser | Asp | Trp | Asp | Leu | Leu | Pro | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Lys | Ile | Lys | Asp | Pro | Ser | Ala | Lys | Lys | Pro | Glu | Asp | Trp | Asp | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Glu | Tyr | Ile | Ser | Asp | Pro | Glu | Asp | Lys | Lys | Pro | Asp | Gly | Tyr | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ile | Pro | Lys | Glu | Ile | Pro | Asp | Thr | Asp | Ser | Lys | Lys | Pro | Glu | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Trp | Asp | Asp | Glu | Glu | Asp | Gly | Glu | Trp | Thr | Ala | Pro | Thr | Ile | Pro | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Glu | Tyr | Met | Gly | Glu | Trp | Lys | Pro | Lys | Gln | Ile | Lys | Asn | Pro | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Lys | Gly | Lys | Trp | Glu | Ala | Pro | Leu | Ile | Asp | Asn | Pro | Asp | Phe | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Asp | Pro | Glu | Leu | Tyr | Val | Phe | Pro | Lys | Leu | Lys | Tyr | Val | Gly | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Leu | Trp | Gln | Val | Lys | Ser | Gly | Ser | Leu | Phe | Asp | Asn | Val | Leu | Ile |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Asp | Asp | Pro | Asp | Tyr | Ala | Lys | Lys | Leu | Ala | Asp | Glu | Thr | Trp | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Leu | Lys | Asp | Ala | Glu | Lys | Ala | Ala | Phe | Asp | Glu | Ala | Glu | Lys | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Glu | Glu | Glu | Glu | Ser | Lys | Asp | Ala | Pro | Ala | Glu | Ser | Asp | Ala | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Glu | Pro | Glu | Asp | Asp | Glu | Gly | Gly | Asp | Asp | Ser | Asp | Ser | Glu | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ala | Glu | Glu | Thr | Lys | Ser | Glu | Asp | Ser | Glu | Glu | Thr | Ser | Glu | Lys |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Ala | Thr | Ala | His | Asp | Glu | Leu |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| acactcgtct | taccaaactc | tctctacac   | aaccaaacc  | atctctttgc | aacaaaactt | 60  |
| gttgtaactc | atcttcttct | tcttcttctc  | catcacagac | tcataacaaa | tgggagaagt | 120 |
| ttcagtggtg | gagaacaaga | aagtgatact  | aaagaattat | gtagatggta | ttcctacaga | 180 |
| aacagacatg | gaagtgaaac | tccggagaaac | aattgagcta | aaagcaccaa | aaggatcttc | 240 |
| ttgtttcttc | gtcaaaaatc | tatacttgtc  | ttgtgatctc | tacatgagag | gtcgtatgcg | 300 |
| tgattttcac | ggttcctatc | tcccgccctt  | tgttctctgc | caacgtatcg | aagggtttgg | 360 |
| tttagcaaga | gtgatagatt | ctgatgatac  | taattataag | cccggcgata | tagtctctgg | 420 |
| tatcattggt | tgggaagaat | acagtttgct  | acgtaGttca | gataacctac | agttgagaaa | 480 |
| tattcaatta | gacgacgaca | ttccgctttc  | ttatcatctc | ggacttctcg | ggatggctgg | 540 |
| atttacagca | tatgcagggt | ttaatgagat  | atgttgctct | aagaaagggg | acagtgtttt | 600 |
| tgtctctgca | gcatgtggag | cagttggaca  | acttggttgg | cagctagcta | agttgcacgg | 660 |

```
ctgctatggt gttggttagcg ccggtagtaa gcaaaagggt gagatcctta aaaacgagct 720
tgatgatgat gaagccttta actacaagga agaggctgat cttgatactg ctttgaagag 780
gtacttccca gaggggatcg atatctactt cgataacgtg ggtggatcca tgcttgatgc 840
agcactcctc aacatgaagg ttcgtggaag aatcgcgctc tgtggaatgg tgtctttaca 900
aagcctctca acttcatcac aaggaatcaa gaacctatac agcgctatct acaaacgttt 960
aaggctagaa gggttcttgc agagtgatta ccttcatact tccccacagt ttcttgaaaa 1020
tgtcaagaga tattacaaag aaggcaagat tgtctacatc gaagatatat ctgaaggcct 1080
cgaccAtcgc tcNccgctgc acttggtggg ctgttttccg ggaaaaatat cggtaaacag 1140
gttggttcggg ttgctaaaga gtgattgttt ctaaaaagta tattgtaagt gacttaaaac 1200
agacattata tgaataaag ccgccataag tctcttatgg aaaaacgtta gttaatc
```

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1571313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

```
Met Gly Glu Val Ser Val Val Glu Asn Lys Lys Val Ile Leu Lys Asn
1 5 10 15
Tyr Val Asp Gly Ile Pro Thr Glu Thr Asp Met Glu Val Lys Leu Gly
20 25 30
Glu Thr Ile Glu Leu Lys Ala Pro Lys Gly Ser Ser Cys Phe Leu Val
35 40 45
Lys Asn Leu Tyr Leu Ser Cys Asp Pro Tyr Met Arg Gly Arg Met Arg
50 55 60
Asp Phe His Gly Ser Tyr Leu Pro Pro Phe Val Pro Gly Gln Arg Ile
65 70 75 80
Glu Gly Phe Gly Leu Ala Arg Val Ile Asp Ser Asp Asp Thr Asn Tyr
85 90 95
Lys Pro Gly Asp Ile Val Ser Gly Ile Ile Gly Trp Glu Glu Tyr Ser
100 105 110
Leu Leu Arg Ser Ser Asp Asn Leu Gln Leu Arg Asn Ile Gln Leu Asp
115 120 125
Asp Asp Ile Pro Leu Ser Tyr His Leu Gly Leu Leu Gly Met Ala Gly
130 135 140
Phe Thr Ala Tyr Ala Gly Phe Asn Glu Ile Cys Cys Pro Lys Lys Gly
145 150 155 160
Asp Ser Val Phe Val Ser Ala Ala Cys Gly Ala Val Gly Gln Leu Val
165 170 175
Gly Gln Leu Ala Lys Leu His Gly Cys Tyr Val Val Gly Ser Ala Gly
180 185 190
Ser Lys Gln Lys Val Glu Ile Leu Lys Asn Glu Leu Gly Tyr Asp Glu
195 200 205
Ala Phe Asn Tyr Lys Glu Glu Ala Asp Leu Asp Thr Ala Leu Lys Arg
210 215 220
Tyr Phe Pro Glu Gly Ile Asp Ile Tyr Phe Asp Asn Val Gly Gly Ser
225 230 235 240
Met Leu Asp Ala Ala Leu Leu Asn Met Lys Val Arg Gly Arg Ile Ala
245 250 255
Leu Cys Gly Met Val Ser Leu Gln Ser Leu Ser Thr Ser Ser Gln Gly
260 265 270
Ile Lys Asn Leu Tyr Ser Ala Ile Tyr Lys Arg Leu Arg Leu Glu Gly
275 280 285
Phe Leu Gln Ser Asp Tyr Leu His Ile Phe Pro Gln Phe Leu Glu Asn
290 295 300
Val Lys Arg Tyr Tyr Lys Glu Gly Lys Ile Val Tyr Ile Glu Asp Ile
```

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(2) INFORMATION FOR SEQ ID NO:1898:

(A) LENGTH: 328 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1571314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1571315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1766 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1766

(D) OTHER INFORMATION: / Ceres Seq. ID 1571333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ctaacattgg attcgagctc tctagtgaag aatccgccat ggctgttcca tttctaagct   | 60   |
| cttctctaca actcacacc acccttccga ttctcttcac taaagtaaca ccaacaccaa    | 120  |
| taatccacaa ccacagatca acatgcacta taccacacaa gcctcgtcta cgtctcctcc   | 180  |
| gccgctccgc cgtcgtgga accgccgtat ctgatcaaac agaaggagggt ggagatgttc   | 240  |
| ttttaaaccc tgaagaagag aaacgtgttg aggtggcgga ttatgattgg acagaggaat   | 300  |
| ggatattcatt gtacttaact aaaaacgtcc ctgaagatgc gcctcttggc ctcaccgtct  | 360  |
| acgatcgtca aattgttttg tataaagacg gYgaaggaac acttcgttgt tacgaagatc   | 420  |
| gggtgcctca tcggttggct aagtgtctg aaggacaatt gattgatggg agattggaat    | 480  |
| gtttgtatca tggttggcaa tttgaaggag agggcaaatg tgtcaagatt cctcagcttc   | 540  |
| ctgcaagtgc taagattcca aaggctgctt gtgtgaagac gtatgagggtg aaggattcac  | 600  |
| aaggagttgt gtgggtgtgg atgtcaacaa agacacctcc aaacctgag aagcttcctt    | 660  |
| ggtttgagaa tttcgtaga cccggtttt tcgacatttc gactactcat gagcttcctt     | 720  |
| atgaccattc cattctttta gagaatctga tggatcctgc tcatgttctt atctctcatg   | 780  |
| atagaacgga tttcactgct aaaagaaaag atgctcagcc tttggttttc gaggtcacag   | 840  |
| agcgaagtaa tcgggggtttc gcagggactt ggggccgaga gagagaagggt gggaaaggga | 900  |
| gtaatttact tcggtttgat gctccttggt ttctgcagaa caatcgagag ttcgagggga   | 960  |
| aggatggagt gaagaactat ttttcagggc tgtttctttg tagacctaca gggcaaggga   | 1020 |
| agtctatgct tattgttagg tttgggttca caaaaagatc gcctttgggt tcggtgttac   | 1080 |
| ctcaatgggt ctggcatcag aatgctgca aggtttttga acaagacatg gggtttctat    | 1140 |
| cgtctcaaaa acgaggttct gatgaaggag aaagtaccaa ctaaggactt gtatttgaat   | 1200 |
| ctaaagtcac cggacacatg ggtcgctgaa tagaaagtgg atggacaaaag ttggtcatgg  | 1260 |
| gatgccttac catttcgggc ataggacct atctctccc aaagtccctc ctgtcgtgga     | 1320 |
| acatgccccg gcagggctca ttgcagctct ctctgcttct taccctgcaa aaggcggaat   | 1380 |
| tgggactatg catgtctcca atttggttaa ccggtacttc agacatatta ttcattgtag   | 1440 |
| aagctgcagc aatgtgatca aatcttttga gctctgaaa aatatcctct ctgccacggc    | 1500 |
| agtggctttg acggcttttg ccattctggt ggtagtaga cagtggaagg ctgtcctgtt    | 1560 |
| aggttcagca gcattgtgct cagccgcagc ttatacctgc ttaagagcta taaatctaaa   | 1620 |
| caccaataac ttcattagaa cacacagaag actatgaaaa tgtatagtgt catgtttcct   | 1680 |
| cttcttccaa caatatgtat ttcatgaaat aaatttttgc ttgtaaacgc aattatataa   | 1740 |
| ttcagaaggt tccaatgttt gccagc                                        |      |

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asn Ile Gly Phe Glu Leu Ser Ser Glu Glu Ser Ala Met Ala Val Pro |  |
| 1 5 10 15                                                       |  |
| Phe Leu Ser Ser Leu Gln Leu Thr Pro Thr Ser Pro Ile Leu Phe     |  |
| 20 25 30                                                        |  |
| Thr Lys Val Thr Pro Thr Pro Ile Ile His Asn His Arg Ser Thr Cys |  |
| 35 40 45                                                        |  |
| Thr Ile Pro Thr Lys Pro Arg Leu Arg Leu Leu Arg Arg Ser Ala Val |  |
| 50 55 60                                                        |  |
| Ala Gly Thr Ala Val Ser Asp Gln Thr Glu Gly Gly Gly Asp Val Leu |  |
| 65 70 75 80                                                     |  |
| Leu Asn Pro Glu Glu Lys Arg Val Glu Val Ala Asp Tyr Asp Trp     |  |
| 85 90 95                                                        |  |
| Thr Glu Glu Trp Tyr Pro Leu Tyr Leu Thr Lys Asn Val Pro Glu Asp |  |
| 100 105 110                                                     |  |
| Ala Pro Leu Gly Leu Thr Val Tyr Asp Arg Gln Ile Val Leu Tyr Lys |  |
| 115 120 125                                                     |  |
| Asp Xaa Glu Gly Thr Leu Arg Cys Tyr Glu Asp Arg Cys Pro His Arg |  |
| 130 135 140                                                     |  |

```

Leu Ala Lys Leu Ser Glu Gly Gln Leu Ile Asp Gly Arg Leu Glu Cys
145 150 155 160
Leu Tyr His Gly Trp Gln Phe Glu Gly Glu Gly Lys Cys Val Lys Ile
 165 170 175
Pro Gln Leu Pro Ala Ser Ala Lys Ile Pro Lys Ala Ala Cys Val Lys
 180 185 190
Thr Tyr Glu Val Lys Asp Ser Gln Gly Val Val Trp Val Trp Met Ser
 195 200 205
Thr Lys Thr Pro Pro Asn Pro Glu Lys Leu Pro Trp Phe Glu Asn Phe
 210 215 220
Ala Arg Pro Gly Phe Phe Asp Ile Ser Thr Thr His Glu Leu Pro Tyr
225 230 235 240
Asp His Ser Ile Leu Leu Glu Asn Leu Met Asp Pro Ala His Val Pro
 245 250 255
Ile Ser His Asp Arg Thr Asp Phe Thr Ala Lys Arg Lys Asp Ala Gln
 260 265 270
Pro Leu Val Phe Glu Val Thr Glu Arg Ser Asn Arg Gly Phe Ala Gly
 275 280 285
Thr Trp Gly Arg Glu Arg Glu Gly Gly Lys Gly Ser Asn Leu Leu Arg
 290 295 300
Phe Asp Ala Pro Cys Val Leu Gln Asn Asn Arg Glu Phe Glu Gly Lys
305 310 315 320
Asp Gly Val Lys Asn Tyr Phe Ser Gly Leu Phe Leu Cys Arg Pro Thr
 325 330 335
Gly Gln Gly Lys Ser Met Leu Ile Val Arg Phe Gly Val Thr Lys Arg
 340 345 350
Ser Pro Leu Val Ser Val Leu Pro Gln Trp Phe Trp His Gln Asn Ala
 355 360 365
Cys Lys Val Phe Glu Gln Asp Met Gly Phe Leu Ser Ser Gln Lys Arg
 370 375 380
Gly Ser Asp Glu Gly Glu Ser Thr Asn
385 390

```

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1571335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

```

Met Ala Val Pro Phe Leu Ser Ser Ser Leu Gln Leu Thr Pro Thr Ser
1 5 10 15
Pro Ile Leu Phe Thr Lys Val Thr Pro Thr Pro Ile Ile His Asn His
 20 25 30
Arg Ser Thr Cys Thr Ile Pro Thr Lys Pro Arg Leu Arg Leu Leu Arg
 35 40 45
Arg Ser Ala Val Ala Gly Thr Ala Val Ser Asp Gln Thr Glu Gly Gly
 50 55 60
Gly Asp Val Leu Leu Asn Pro Glu Glu Glu Lys Arg Val Glu Val Ala
65 70 75 80
Asp Tyr Asp Trp Thr Glu Glu Trp Tyr Pro Leu Tyr Leu Thr Lys Asn
 85 90 95
Val Pro Glu Asp Ala Pro Leu Gly Leu Thr Val Tyr Asp Arg Gln Ile
 100 105 110
Val Leu Tyr Lys Asp Xaa Glu Gly Thr Leu Arg Cys Tyr Glu Asp Arg
 115 120 125
Cys Pro His Arg Leu Ala Lys Leu Ser Glu Gly Gln Leu Ile Asp Gly

```

CERES - 1571335



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Arg Leu Glu Cys Leu Tyr His Gly Trp Gln Phe Glu Gly Glu Gly Lys |     |     |
| 145                                                             | 150 | 155 |
| Cys Val Lys Ile Pro Gln Leu Pro Ala Ser Ala Lys Ile Pro Lys Ala |     | 160 |
|                                                                 | 165 | 170 |
| Ala Cys Val Lys Thr Tyr Glu Val Lys Asp Ser Gln Gly Val Val Trp |     | 175 |
|                                                                 | 180 | 185 |
| Val Trp Met Ser Thr Lys Thr Pro Pro Asn Pro Glu Lys Leu Pro Trp |     | 190 |
|                                                                 | 195 | 200 |
| Phe Glu Asn Phe Ala Arg Pro Gly Phe Phe Asp Ile Ser Thr Thr His |     | 205 |
|                                                                 | 210 | 215 |
| Glu Leu Pro Tyr Asp His Ser Ile Leu Leu Glu Asn Leu Met Asp Pro |     | 220 |
| 225                                                             | 230 | 235 |
| Ala His Val Pro Ile Ser His Asp Arg Thr Asp Phe Thr Ala Lys Arg |     | 240 |
|                                                                 | 245 | 250 |
| Lys Asp Ala Gln Pro Leu Val Phe Glu Val Thr Glu Arg Ser Asn Arg |     | 255 |
|                                                                 | 260 | 265 |
| Gly Phe Ala Gly Thr Trp Gly Arg Glu Arg Glu Gly Gly Lys Gly Ser |     | 270 |
|                                                                 | 275 | 280 |
| Asn Leu Leu Arg Phe Asp Ala Pro Cys Val Leu Gln Asn Asn Arg Glu |     | 285 |
|                                                                 | 290 | 295 |
| Phe Glu Gly Lys Asp Gly Val Lys Asn Tyr Phe Ser Gly Leu Phe Leu |     | 300 |
| 305                                                             | 310 | 315 |
| Cys Arg Pro Thr Gly Gln Gly Lys Ser Met Leu Ile Val Arg Phe Gly |     | 320 |
|                                                                 | 325 | 330 |
| Val Thr Lys Arg Ser Pro Leu Val Ser Val Leu Pro Gln Trp Phe Trp |     | 335 |
|                                                                 | 340 | 345 |
| His Gln Asn Ala Cys Lys Val Phe Glu Gln Asp Met Gly Phe Leu Ser |     | 350 |
|                                                                 | 355 | 360 |
| Ser Gln Lys Arg Gly Ser Asp Glu Gly Glu Ser Thr Asn             |     | 365 |
|                                                                 | 370 | 375 |
|                                                                 |     | 380 |

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

|             |            |            |             |            |             |      |
|-------------|------------|------------|-------------|------------|-------------|------|
| atcacaattt  | ttctacggtc | agagattcaa | aagagttctt  | tctctctatc | ttatttctccg | 60   |
| atcatcatga  | tgcagcagcc | accacccgga | ggtatccttc  | cacatcacgc | tctcctcct   | 120  |
| tctgcgcaac  | aacagtacgg | ttaccaacaa | ccttacggga  | ttgctggagc | tgctccacca  | 180  |
| ccaccacaga  | tgtggaatcc | tcaagcggcg | gcgcgcCat   | cagttcagcc | tacgaccgct  | 240  |
| gacgagatcc  | ggactctttg | gatcggggac | ttacagtatt  | ggatggatga | gaatttcttc  | 300  |
| tacggttgct  | ttgctcatat | cggagagatg | gtttctgcta  | aagtgattcg | taacaagcaa  | 360  |
| accggtcaag  | ttgaaggata | cggtttcatt | gaattcgcat  | ctcatgctgc | tgctgaaaga  | 420  |
| gttctacaaa  | cattcaacaa | cgctcctatc | ccgagctttc  | ctgatcagct | ctttagactg  | 480  |
| mactgggcat  | cattgagttc | aggagataaa | cgagacgatt  | caccggacta | cacgatattt  | 540  |
| gtcgggtgatc | tggctgctga | tgttacggat | tatatcttac  | ttgagacgtt | cagagcctct  | 600  |
| tatccgctcag | tgaagggtgc | aaagggttgt | attaacagag  | tcactggagc | tacaaaagga  | 660  |
| tatgggtttg  | ttaggttttc | tgatgaaagt | gaacagatcc  | gtgctatgac | ggagatgaat  | 720  |
| ggcgttcctt  | gttctactag | acctatgaga | attgggtccc  | ctgctagcaa | gaaagggtga  | 780  |
| actggtcaaa  | gagattcata | ccagagctct | gctgcagggg  | taacaactga | taatgatcca  | 840  |
| aataacacaa  | ctgtttttgt | tggtggatta | gatgcatctg  | tcacggatga | tcattctgaag | 900  |
| aatgtcttta  | gccaatatgg | tgagattgtg | catgtgaaaa  | tacccgctgg | aaagcgctgt  | 960  |
| ggattcggtc  | agttttccga | gaagagctgt | gcagaggaag  | ctcttagaat | gctgaatgga  | 1020 |
| gtgcaattag  | gcggaacaac | cgtcaggctc | tcattggggcc | gaagtccttc | gaacaaacag  | 1080 |

tcggggggtac cgagccagtt ttactacggt ggggtatggac aaggacagga gcagtatggg 1140  
tacacgatgc ctcaagaccc taatgcata tacggaggct actctggtgg aggatacagc 1200  
gggtggttacc agcagacacc acaggcagga cagcaaccac cacaacagcc accacagcag 1260  
caacaagtgc ggttttagcta ctaaccccgga gagtattgct tgagttaatg tcaactctgct 1320  
tgttgtttgc gtactttggt atgaacttgt ttctgctgct cttgttatga atattttccc 1380  
aaacacagtt tatttgtctt tgcttttctc taggtgtgtg ttgagttttt aactcttaat 1440  
aatgtttctg cgatgcttct gtttttaatg ttttcatcac cttttg

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:

Ile Thr Ile Phe Leu Arg Ser Glu Ile Gln Lys Ser Ser Phe Ser Leu  
1 5 10 15  
Ser Tyr Ser Pro Ile Ile Met Met Gln Gln Pro Pro Pro Gly Gly Ile  
20 25 30  
Leu Pro His His Ala Pro Pro Pro Ser Ala Gln Gln Gln Tyr Gly Tyr  
35 40 45  
Gln Gln Pro Tyr Gly Ile Ala Gly Ala Ala Pro Pro Pro Pro Gln Met  
50 55 60  
Trp Asn Pro Gln Ala Ala Ala Pro Pro Ser Val Gln Pro Thr Thr Ala  
65 70 75 80  
Asp Glu Ile Arg Thr Leu Trp Ile Gly Asp Leu Gln Tyr Trp Met Asp  
85 90 95  
Glu Asn Phe Leu Tyr Gly Cys Phe Ala His Thr Gly Glu Met Val Ser  
100 105 110  
Ala Lys Val Ile Arg Asn Lys Gln Thr Gly Gln Val Glu Gly Tyr Gly  
115 120 125  
Phe Ile Glu Phe Ala Ser His Ala Ala Ala Glu Arg Val Leu Gln Thr  
130 135 140  
Phe Asn Asn Ala Pro Ile Pro Ser Phe Pro Asp Gln Leu Phe Arg Leu  
145 150 155 160  
Xaa Trp Ala Ser Leu Ser Ser Gly Asp Lys Arg Asp Asp Ser Pro Asp  
165 170 175  
Tyr Thr Ile Phe Val Gly Asp Leu Ala Ala Asp Val Thr Asp Tyr Ile  
180 185 190  
Leu Leu Glu Thr Phe Arg Ala Ser Tyr Pro Ser Val Lys Gly Ala Lys  
195 200 205  
Val Val Ile Asn Arg Val Thr Gly Arg Thr Lys Gly Tyr Gly Phe Val  
210 215 220  
Arg Phe Ser Asp Glu Ser Glu Gln Ile Arg Ala Met Thr Glu Met Asn  
225 230 235 240  
Gly Val Pro Cys Ser Thr Arg Pro Met Arg Ile Gly Pro Ala Ala Ser  
245 250 255  
Lys Lys Gly Val Thr Gly Gln Arg Asp Ser Tyr Gln Ser Ser Ala Ala  
260 265 270  
Gly Val Thr Thr Asp Asn Asp Pro Asn Asn Thr Thr Val Phe Val Gly  
275 280 285  
Gly Leu Asp Ala Ser Val Thr Asp Asp His Leu Lys Asn Val Phe Ser  
290 295 300  
Gln Tyr Gly Glu Ile Val His Val Lys Ile Pro Ala Gly Lys Arg Cys  
305 310 315 320  
Gly Phe Val Gln Phe Ser Glu Lys Ser Cys Ala Glu Glu Ala Leu Arg  
325 330 335

SEQUENCE INFORMATION

Met Leu Asn Gly Val Gln Leu Gly Gly Thr Thr Val Arg Leu Ser Trp  
340 345 350  
Gly Arg Ser Pro Ser Asn Lys Gln Ser Gly Asp Pro Ser Gln Phe Tyr  
355 360 365  
Tyr Gly Gly Tyr Gly Gln Gly Gln Glu Gln Tyr Gly Tyr Thr Met Pro  
370 375 380  
Gln Asp Pro Asn Ala Tyr Tyr Gly Gly Tyr Ser Gly Gly Gly Tyr Ser  
385 390 395 400  
Gly Gly Tyr Gln Gln Thr Pro Gln Ala Gly Gln Gln Pro Pro Gln Gln  
405 410 415  
Pro Pro Gln Gln Gln Val Gly Phe Ser Tyr  
420 425

(2) INFORMATION FOR SEQ ID NO:1905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:

Met Met Gln Gln Pro Pro Pro Gly Gly Ile Leu Pro His His Ala Pro  
1 5 10 15  
Pro Pro Ser Ala Gln Gln Gln Tyr Gly Tyr Gln Gln Pro Tyr Gly Ile  
20 25 30  
Ala Gly Ala Ala Pro Pro Pro Pro Gln Met Trp Asn Pro Gln Ala Ala  
35 40 45  
Ala Pro Pro Ser Val Gln Pro Thr Thr Ala Asp Glu Ile Arg Thr Leu  
50 55 60  
Trp Ile Gly Asp Leu Gln Tyr Trp Met Asp Glu Asn Phe Leu Tyr Gly  
65 70 75 80  
Cys Phe Ala His Thr Gly Glu Met Val Ser Ala Lys Val Ile Arg Asn  
85 90 95  
Lys Gln Thr Gly Gln Val Glu Gly Tyr Gly Phe Ile Glu Phe Ala Ser  
100 105 110  
His Ala Ala Ala Glu Arg Val Leu Gln Thr Phe Asn Asn Ala Pro Ile  
115 120 125  
Pro Ser Phe Pro Asp Gln Leu Phe Arg Leu Xaa Trp Ala Ser Leu Ser  
130 135 140  
Ser Gly Asp Lys Arg Asp Asp Ser Pro Asp Tyr Thr Ile Phe Val Gly  
145 150 155 160  
Asp Leu Ala Ala Asp Val Thr Asp Tyr Ile Leu Leu Glu Thr Phe Arg  
165 170 175  
Ala Ser Tyr Pro Ser Val Lys Gly Ala Lys Val Val Ile Asn Arg Val  
180 185 190  
Thr Gly Arg Thr Lys Gly Tyr Gly Phe Val Arg Phe Ser Asp Glu Ser  
195 200 205  
Glu Gln Ile Arg Ala Met Thr Glu Met Asn Gly Val Pro Cys Ser Thr  
210 215 220  
Arg Pro Met Arg Ile Gly Pro Ala Ala Ser Lys Lys Gly Val Thr Gly  
225 230 235 240  
Gln Arg Asp Ser Tyr Gln Ser Ser Ala Ala Gly Val Thr Thr Asp Asn  
245 250 255  
Asp Pro Asn Asn Thr Thr Val Phe Val Gly Gly Leu Asp Ala Ser Val  
260 265 270  
Thr Asp Asp His Leu Lys Asn Val Phe Ser Gln Tyr Gly Glu Ile Val  
275 280 285  
His Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Phe Ser

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290 295 300  
Glu Lys Ser Cys Ala Glu Glu Ala Leu Arg Met Leu Asn Gly Val Gln  
305 310 315 320  
Leu Gly Gly Thr Thr Val Arg Leu Ser Trp Gly Arg Ser Pro Ser Asn  
325 330 335  
Lys Gln Ser Gly Asp Pro Ser Gln Phe Tyr Tyr Gly Gly Tyr Gly Gln  
340 345 350  
Gly Gln Glu Gln Tyr Gly Tyr Thr Met Pro Gln Asp Pro Asn Ala Tyr  
355 360 365  
Tyr Gly Gly Tyr Ser Gly Gly Tyr Ser Gly Gly Tyr Gln Gln Thr  
370 375 380  
Pro Gln Ala Gly Gln Gln Pro Pro Gln Gln Pro Pro Gln Gln Gln Gln  
385 390 395 400  
Val Gly Phe Ser Tyr  
405

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1571343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

Met Gln Gln Pro Pro Gly Gly Ile Leu Pro His His Ala Pro Pro  
1 5 10 15  
Pro Ser Ala Gln Gln Tyr Gly Tyr Gln Gln Pro Tyr Gly Ile Ala  
20 25 30  
Gly Ala Ala Pro Pro Pro Pro Gln Met Trp Asn Pro Gln Ala Ala Ala  
35 40 45  
Pro Pro Ser Val Gln Pro Thr Thr Ala Asp Glu Ile Arg Thr Leu Trp  
50 55 60  
Ile Gly Asp Leu Gln Tyr Trp Met Asp Glu Asn Phe Leu Tyr Gly Cys  
65 70 75 80  
Phe Ala His Thr Gly Glu Met Val Ser Ala Lys Val Ile Arg Asn Lys  
85 90 95  
Gln Thr Gly Gln Val Glu Gly Tyr Gly Phe Ile Glu Phe Ala Ser His  
100 105 110  
Ala Ala Ala Glu Arg Val Leu Gln Thr Phe Asn Asn Ala Pro Ile Pro  
115 120 125  
Ser Phe Pro Asp Gln Leu Phe Arg Leu Xaa Trp Ala Ser Leu Ser Ser  
130 135 140  
Gly Asp Lys Arg Asp Asp Ser Pro Asp Tyr Thr Ile Phe Val Gly Asp  
145 150 155 160  
Leu Ala Ala Asp Val Thr Asp Tyr Ile Leu Leu Glu Thr Phe Arg Ala  
165 170 175  
Ser Tyr Pro Ser Val Lys Gly Ala Lys Val Val Ile Asn Arg Val Thr  
180 185 190  
Gly Arg Thr Lys Gly Tyr Gly Phe Val Arg Phe Ser Asp Glu Ser Glu  
195 200 205  
Gln Ile Arg Ala Met Thr Glu Met Asn Gly Val Pro Cys Ser Thr Arg  
210 215 220  
Pro Met Arg Ile Gly Pro Ala Ala Ser Lys Lys Gly Val Thr Gly Gln  
225 230 235 240  
Arg Asp Ser Tyr Gln Ser Ser Ala Ala Gly Val Thr Thr Asp Asn Asp  
245 250 255  
Pro Asn Asn Thr Thr Val Phe Val Gly Gly Leu Asp Ala Ser Val Thr  
260 265 270

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Asp Asp His Leu Lys Asn Val Phe Ser Gln Tyr Gly Glu Ile Val His  
275 280 285  
Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Phe Ser Glu  
290 295 300  
Lys Ser Cys Ala Glu Glu Ala Leu Arg Met Leu Asn Gly Val Gln Leu  
305 310 315 320  
Gly Gly Thr Thr Val Arg Leu Ser Trp Gly Arg Ser Pro Ser Asn Lys  
325 330 335  
Gln Ser Gly Asp Pro Ser Gln Phe Tyr Tyr Gly Gly Tyr Gly Gln Gly  
340 345 350  
Gln Glu Gln Tyr Gly Tyr Thr Met Pro Gln Asp Pro Asn Ala Tyr Tyr  
355 360 365  
Gly Gly Tyr Ser Gly Gly Gly Tyr Ser Gly Gly Tyr Gln Gln Thr Pro  
370 375 380  
Gln Ala Gly Gln Gln Pro Pro Gln Gln Pro Pro Gln Gln Gln Gln Val  
385 390 395 400  
Gly Phe Ser Tyr

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atcttctctt | cttttgcctt | tcctttcttt  | gagtcgcttc | acttctcttg | catccttcaa | 60  |
| actcatccac | agcaaggaat | ggcgacagCa  | gcagcaccag | cagtgatttc | atggacaaga | 120 |
| tcaggcattg | tgtccaaatc | cggacaaacc  | cagaagaaat | ctgagatgaa | agtttcttac | 180 |
| ataactggac | ttaactcata | tgggtggtctc | aaggcacaga | acaacaaggt | tgtctcaatg | 240 |
| ggatcaccac | tctgcacaga | acagtgtttt  | gctaacgttg | tgatgtctct | caaaggaaga | 300 |
| agagttggat | togttcttct | togaatcgaa  | acttctgttg | aagaagctga | agcagagtaa | 360 |
| atagagtaaa | ttgctgctct | tataattata  | tatttttggt | tattgttggt | gtcaagcttt | 420 |
| ggtaaaactt | gatggataca | tgttacattt  | gtttatgaag | aagctctttt | cttggtagat | 480 |

g

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Ile Phe Ser Ser Phe Ala Ser Pro Phe Phe Glu Ser Leu His Phe Ser  
1 5 10 15  
Cys Ile Leu Gln Thr His Pro Gln Gln Gly Met Ala Thr Ala Ala Ala  
20 25 30  
Pro Ala Val Ile Ser Trp Thr Arg Ser Gly Ile Val Ser Lys Ser Gly  
35 40 45  
Gln Thr Gln Lys Lys Ser Glu Met Lys Val Ser Tyr Ile Thr Gly Leu  
50 55 60  
Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn Asn Lys Val Val Ser Met  
65 70 75 80

Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe Ala Asn Val Val Met Ser  
85 90 95  
Leu Lys Gly Arg Arg Val Gly Phe Val Leu Leu Arg Ile Glu Thr Ser  
100 105 110  
Val Glu Glu Ala Glu Ala Glu  
115

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

Met Ala Thr Ala Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly  
1 5 10 15  
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val  
20 25 30  
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn  
35 40 45  
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe  
50 55 60  
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Val Gly Phe Val Leu  
65 70 75 80  
Leu Arg Ile Glu Thr Ser Val Glu Glu Ala Glu Ala Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys  
1 5 10 15  
Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu  
20 25 30  
Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Val Gly  
35 40 45  
Phe Val Leu Leu Arg Ile Glu Thr Ser Val Glu Glu Ala Glu Ala Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

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(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1571360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aattctctac | tttcattaaa | gcttagtaag | caaatgtgtt | atgtgtgagt | gagattgtgt | 60  |
| gagagaaaag | aagaagataa | gtgagagaga | aagagagaaa | gagagaaaat | gaagttcttg | 120 |
| ttccagtgtc | catgttgctc | ttgcttctgc | ttcatgaaac | caaagccggg | caaaccaaaa | 180 |
| gctgttggag | atacaaaacc | aaaggaggag | aagaagaaag | aggtgaagaa | agaagagatc | 240 |
| aagaaagagg | agaagaaaga | agagaagaaa | gaagagaaga | aggaaaccaa | agcagagaag | 300 |
| gctgagttaa | aactctactt | tgagaaaatg | taattaatta | tcccattAtt | tattattatt | 360 |
| tatctgctat | ttgatgatta | tgcaagtaat | aacatgttat | ttttatgggt | ggtaaccttt | 420 |
| ttaggc     |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1571361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Leu | Phe | Gln | Cys | Pro | Cys | Cys | Ser | Cys | Phe | Cys | Phe | Met |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Pro | Lys | Pro | Gly | Lys | Pro | Lys | Ala | Val | Gly | Asp | Thr | Lys | Pro | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Lys | Lys | Lys | Glu | Val | Lys | Lys | Glu | Glu | Ile | Lys | Lys | Glu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Glu | Glu | Lys | Lys | Glu | Glu | Lys | Lys | Glu | Thr | Lys | Ala | Glu | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1913:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1571362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Leu | Leu | Leu | His | Glu | Thr | Lys | Ala | Gly | Gln | Thr | Lys |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Cys | Trp | Arg | Tyr | Lys | Thr | Lys | Gly | Gly | Glu | Glu | Glu | Arg | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Arg | Arg | Asp | Gln | Glu | Arg | Gly | Glu | Glu | Arg | Arg | Glu | Glu | Arg | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Gly | Asn | Gln | Ser | Arg | Glu | Gly |     |     |     |     |     |     |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:

Met Lys Pro Lys Pro Gly Lys Pro Lys Ala Val Gly Asp Thr Lys Pro  
1 5 10 15  
Lys Glu Glu Lys Lys Lys Glu Val Lys Lys Glu Glu Ile Lys Lys Glu  
20 25 30  
Glu Lys Lys Glu Glu Lys Lys Glu Glu Lys Lys Glu Thr Lys Ala Glu  
35 40 45  
Lys Ala Glu  
50

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..754  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

aagtgaactgc gacgccggaa aatcgcaatg ggtgcgtaca aatacgtgtc ggagctatgg 60  
aggagaagc agtcggatgt gatgaggttt cttcagaggg ttaggtgttg ggagtatcgc 120  
cagcagcctt ccattgttcg tcttggttcgt cccactcgtc ccgacaaggc tcgtcgtctc 180  
ggctacaagg ccaagcaggg gtttggttgc taccgtgttc gagtcagacg tgggtggacgc 240  
aagaggccag tgcctaaggg tatcgtgtac ggtaaaccga ccaaccaggg agtgacacag 300  
ctcaaattcc agcgtagtaa gagatctggt gctgaggaac gtgctggtcg caaactggga 360  
ggccttaggg ttgttaactc ctactggctc aatgaggact ctacctaca gtactacgag 420  
attatccttg tagaccctgc acacaatgcc gtccgaaatg atccaaggat caactggatc 480  
tgcaaccctg tgcacaagca cagagaactc agaggtctca cctccgaaGg aaagaagaat 540  
cgtggtcttc gtggaaaggg tcacaacaac cacaagaaca gaccttcccg cagggcaacc 600  
tggaagaaga acaacagtat ctctctccgt cgttaccggg gatcagtttt atgttttgtt 660  
ttttctcgaa ctggtatatc ttcagtgtgg attgtgtttc ggaattctgg aattacattg 720  
ggatggaaga ctttcacatt caagagtttg tttc

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..204  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp Arg Lys Lys Gln Ser  
1 5 10 15  
Asp Val Met Arg Phe Leu Gln Arg Val Arg Cys Trp Glu Tyr Arg Gln  
20 25 30  
Gln Pro Ser Ile Val Arg Leu Val Arg Pro Thr Arg Pro Asp Lys Ala  
35 40 45  
Arg Arg Leu Gly Tyr Lys Ala Lys Gln Gly Phe Val Val Tyr Arg Val  
50 55 60  
Arg Val Arg Arg Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ile Val  
65 70 75 80  
Tyr Gly Lys Pro Thr Asn Gln Gly Val Thr Gln Leu Lys Phe Gln Arg  
85 90 95



(D) OTHER INFORMATION: / Ceres Seq. ID 1571367



85 90 95  
Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met  
100 105 110  
Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly  
115 120 125  
Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

Met Ile Arg Asn Lys Pro Gly Met Ala Ser Val Lys Asp Met Pro Leu  
1 5 10 15  
Leu Gln Asp Gly Pro Pro Pro Gly Gly Phe Ala Pro Val Arg Tyr Ala  
20 25 30  
Arg Arg Ile Ser Asn Thr Gly Pro Ser Ala Met Ala Met Phe Leu Ala  
35 40 45  
Val Ser Gly Ala Phe Ala Trp Gly Met Tyr Gln Val Gly Gln Gly Asn  
50 55 60  
Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala Ala Arg Arg Thr  
65 70 75 80  
Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Glu Arg Phe Val Ser Glu  
85 90 95  
Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met Lys Asp Val Pro  
100 105 110  
Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly Arg Trp Met Pro  
115 120 125  
Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp  
130 135

(2) INFORMATION FOR SEQ ID NO:1922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

Met Ala Ser Val Lys Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro  
1 5 10 15  
Gly Gly Phe Ala Pro Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly  
20 25 30  
Pro Ser Ala Met Ala Met Phe Leu Ala Val Ser Gly Ala Phe Ala Trp  
35 40 45  
Gly Met Tyr Gln Val Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys  
50 55 60  
Glu Glu Lys Tyr Ala Ala Arg Arg Thr Ile Leu Pro Ile Leu Gln Ala  
65 70 75 80  
Glu Glu Asp Glu Arg Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr  
85 90 95

Glu Ala Asp Val Met Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn  
100 105 110  
Val Tyr Asn Ser Gly Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg  
115 120 125  
Pro Asp Val Trp  
130

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| acatctatct  | ctttctctct | ctttccttgc  | aaattttcag  | ctctcaaaga  | gttaagagtt  | 60   |
| agagagagag  | aggatggcca | ttagggaaat  | caaagatgta  | gagaggggtg  | aaatagttaa  | 120  |
| taaggtagaa  | gatcttggga | aaccattttt  | gactcatgaa  | gatgatgaaa  | aagagagtga  | 180  |
| gaataatgaa  | tcataattga | tggttctctt  | cagtactttt  | gttgctgtct  | gtggctcctt  | 240  |
| tgagtttggc  | tcttgtgttg | gatactcagc  | gcctactcag  | tcactataaa  | gacaagatct  | 300  |
| caatctctcc  | cttgcagagt | tctccatggt  | tggatccatc  | ttaaactatcg | gtgcaatgct  | 360  |
| tgggtgctgtt | atgagtgagg | aaattttcaga | tttctccggc  | cgaaaagggg  | caatgaggac  | 420  |
| gtcagcttgc  | ttctgcatta | cagggttggt  | cgctgtcttc  | ttcaccaagg  | gggcattggt  | 480  |
| acttgatgta  | ggaaggttct | ttacaggata  | tgggaattgga | gttttttctt  | atgtggtccc  | 540  |
| tgtgtacatt  | gctgagatat | ctcccaagaa  | tctccgaggt  | ggactcacaa  | cactgaacca  | 600  |
| actcatgatt  | gtgatcggt  | catcggtttc  | tttcttgatc  | ggatctctca  | tttcttgtaa  | 660  |
| aactcttgcc  | ctaaccgtac | ttgctccctg  | cattgttttg  | ctctttggct  | tgtgcttcat  | 720  |
| acccgaatct  | cctcgatggc | tggcaaaaagc | aggccatgag  | aaagagtttc  | gcgtagccct  | 780  |
| gcaaaaagctg | cgaggaaaag | atgcagatat  | cacaaatgaa  | gcagacggta  | ttcaagtctc  | 840  |
| gattcaagct  | ctagagattc | ttccaaaagc  | aagaatccaa  | gaccttgtgt  | ccaagaaata  | 900  |
| tggtcgatct  | gtcatcattg | gtgtttccct  | gatggtattc  | caacagtttg  | ttggaatcaa  | 960  |
| tgggatcgga  | ttctacgcaa | gtgaaaagct  | tgtaaaagcc  | ggatttacct  | ctgggaaact  | 1020 |
| aggaacaatc  | gctatcgctt | gttcagggtg  | caataactgt  | tcttggaaca  | atcttgatag  | 1080 |
| ataaatctgg  | acgaaggcca | ctaattatga  | tttcagctgg  | tggatcttct  | ttgggatgca  | 1140 |
| tactcacagg  | cacatctttc | ttactcaagg  | gacagagctt  | gttgcttgaa  | tgggtccctt  | 1200 |
| ccttagccgt  | tggaggtgta | cttatctatg  | tagctgcttt  | ctccatcgga  | atgggacctg  | 1260 |
| ttccttgggt  | gataatgtct | gagatatctc  | cgataaacgt  | aaagggaatc  | gcagggaagct | 1320 |
| tagtggtact  | agtgaattgg | tctggtgctt  | gggctgtttc  | ttacactttc  | aacttcctca  | 1380 |
| tgagctggag  | ctctccaggt | acattctatt  | tgtactcggc  | ttttgcagct  | gcgacgataa  | 1440 |
| tatttgtggc  | gaagatggtg | ccagagacga  | aagggaagac  | actggaagag  | atccaagctt  | 1500 |
| gtattcgaag  | agaaacataa | gaagaaagat  | acaatcaatg  | ttatgggaat  | gttatcaaat  | 1560 |
| gaaaagactc  | gaactattcc | cgttggtgag  | ctcaaagtgg  | agtagagtaa  | aaattatcgc  | 1620 |
| cgggagataa  | cgttgaaaag | ccgatgatga  | ggcataaggg  | ttttgcatga  | atgttatgag  | 1680 |
| aataggttta  | cttttatgta | tttgttcacg  | ttttTaagtt  | ttcatcaaat  | aggtttttga  | 1740 |
| wtggtaaaaa  | aaacc      |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

Met Ala Ile Arg Glu Ile Lys Asp Val Glu Arg Gly Glu Ile Val Asn

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1 5 10 15  
Lys Val Glu Asp Leu Gly Lys Pro Phe Leu Thr His Glu Asp Asp Glu  
20 25 30  
Lys Glu Ser Glu Asn Asn Glu Ser Tyr Leu Met Val Leu Phe Ser Thr  
35 40 45  
Phe Val Ala Val Cys Gly Ser Phe Glu Phe Gly Ser Cys Val Gly Tyr  
50 55 60  
Ser Ala Pro Thr Gln Ser Ser Ile Arg Gln Asp Leu Asn Leu Ser Leu  
65 70 75 80  
Ala Glu Phe Ser Met Phe Gly Ser Ile Leu Thr Ile Gly Ala Met Leu  
85 90 95  
Gly Ala Val Met Ser Gly Lys Ile Ser Asp Phe Ser Gly Arg Lys Gly  
100 105 110  
Ala Met Arg Thr Ser Ala Cys Phe Cys Ile Thr Gly Trp Leu Ala Val  
115 120 125  
Phe Phe Thr Lys Gly Ala Leu Leu Leu Asp Val Gly Arg Phe Phe Thr  
130 135 140  
Gly Tyr Gly Ile Gly Val Phe Ser Tyr Val Val Pro Val Tyr Ile Ala  
145 150 155 160  
Glu Ile Ser Pro Lys Asn Leu Arg Gly Gly Leu Thr Thr Leu Asn Gln  
165 170 175  
Leu Met Ile Val Ile Gly Ser Ser Val Ser Phe Leu Ile Gly Ser Leu  
180 185 190  
Ile Ser Trp Lys Thr Leu Ala Leu Thr Val Leu Ala Pro Cys Ile Val  
195 200 205  
Leu Leu Phe Gly Leu Cys Phe Ile Pro Glu Ser Pro Arg Trp Leu Ala  
210 215 220  
Lys Ala Gly His Glu Lys Glu Phe Arg Val Ala Leu Gln Lys Leu Arg  
225 230 235 240  
Gly Lys Asp Ala Asp Ile Thr Asn Glu Ala Asp Gly Ile Gln Val Ser  
245 250 255  
Ile Gln Ala Leu Glu Ile Leu Pro Lys Ala Arg Ile Gln Asp Leu Val  
260 265 270  
Ser Lys Lys Tyr Gly Arg Ser Val Ile Ile Gly Val Ser Leu Met Val  
275 280 285  
Phe Gln Gln Phe Val Gly Ile Asn Gly Ile Gly Phe Tyr Ala Ser Glu  
290 295 300  
Thr Phe Val Lys Ala Gly Phe Thr Ser Gly Lys Leu Gly Thr Ile Ala  
305 310 315 320  
Ile Ala Cys Ser Gly Ala Asn Asn Cys Ser Trp Asn Asn Leu Asp Arg  
325 330 335

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1571378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

Met Val Leu Phe Ser Thr Phe Val Ala Val Cys Gly Ser Phe Glu Phe  
1 5 10 15  
Gly Ser Cys Val Gly Tyr Ser Ala Pro Thr Gln Ser Ser Ile Arg Gln  
20 25 30  
Asp Leu Asn Leu Ser Leu Ala Glu Phe Ser Met Phe Gly Ser Ile Leu  
35 40 45

Thr Ile Gly Ala Met Leu Gly Ala Val Met Ser Gly Lys Ile Ser Asp  
50 55 60  
Phe Ser Gly Arg Lys Gly Ala Met Arg Thr Ser Ala Cys Phe Cys Ile  
65 70 75 80  
Thr Gly Trp Leu Ala Val Phe Phe Thr Lys Gly Ala Leu Leu Leu Asp  
85 90 95  
Val Gly Arg Phe Phe Thr Gly Tyr Gly Ile Gly Val Phe Ser Tyr Val  
100 105 110  
Val Pro Val Tyr Ile Ala Glu Ile Ser Pro Lys Asn Leu Arg Gly Gly  
115 120 125  
Leu Thr Thr Leu Asn Gln Leu Met Ile Val Ile Gly Ser Ser Val Ser  
130 135 140  
Phe Leu Ile Gly Ser Leu Ile Ser Trp Lys Thr Leu Ala Leu Thr Val  
145 150 155 160  
Leu Ala Pro Cys Ile Val Leu Leu Phe Gly Leu Cys Phe Ile Pro Glu  
165 170 175  
Ser Pro Arg Trp Leu Ala Lys Ala Gly His Glu Lys Glu Phe Arg Val  
180 185 190  
Ala Leu Gln Lys Leu Arg Gly Lys Asp Ala Asp Ile Thr Asn Glu Ala  
195 200 205  
Asp Gly Ile Gln Val Ser Ile Gln Ala Leu Glu Ile Leu Pro Lys Ala  
210 215 220  
Arg Ile Gln Asp Leu Val Ser Lys Lys Tyr Gly Arg Ser Val Ile Ile  
225 230 235 240  
Gly Val Ser Leu Met Val Phe Gln Gln Phe Val Gly Ile Asn Gly Ile  
245 250 255  
Gly Phe Tyr Ala Ser Glu Thr Phe Val Lys Ala Gly Phe Thr Ser Gly  
260 265 270  
Lys Leu Gly Thr Ile Ala Ile Ala Cys Ser Gly Ala Asn Asn Cys Ser  
275 280 285  
Trp Asn Asn Leu Asp Arg  
290

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1571379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

Met Phe Gly Ser Ile Leu Thr Ile Gly Ala Met Leu Gly Ala Val Met  
1 5 10 15  
Ser Gly Lys Ile Ser Asp Phe Ser Gly Arg Lys Gly Ala Met Arg Thr  
20 25 30  
Ser Ala Cys Phe Cys Ile Thr Gly Trp Leu Ala Val Phe Phe Thr Lys  
35 40 45  
Gly Ala Leu Leu Leu Asp Val Gly Arg Phe Phe Thr Gly Tyr Gly Ile  
50 55 60  
Gly Val Phe Ser Tyr Val Val Pro Val Tyr Ile Ala Glu Ile Ser Pro  
65 70 75 80  
Lys Asn Leu Arg Gly Gly Leu Thr Thr Leu Asn Gln Leu Met Ile Val  
85 90 95  
Ile Gly Ser Ser Val Ser Phe Leu Ile Gly Ser Leu Ile Ser Trp Lys  
100 105 110  
Thr Leu Ala Leu Thr Val Leu Ala Pro Cys Ile Val Leu Leu Phe Gly  
115 120 125  
Leu Cys Phe Ile Pro Glu Ser Pro Arg Trp Leu Ala Lys Ala Gly His

SEQUENCE - 1926

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Glu Lys Glu Phe Arg Val Ala Leu Gln Lys Leu Arg Gly Lys Asp Ala |     |     |
| 145                                                             | 150 | 155 |
| Asp Ile Thr Asn Glu Ala Asp Gly Ile Gln Val Ser Ile Gln Ala Leu |     | 160 |
|                                                                 | 165 | 170 |
| Glu Ile Leu Pro Lys Ala Arg Ile Gln Asp Leu Val Ser Lys Lys Tyr |     | 175 |
|                                                                 | 180 | 185 |
| Gly Arg Ser Val Ile Ile Gly Val Ser Leu Met Val Phe Gln Gln Phe |     | 190 |
|                                                                 | 195 | 200 |
| Val Gly Ile Asn Gly Ile Gly Phe Tyr Ala Ser Glu Thr Phe Val Lys |     | 205 |
|                                                                 | 210 | 215 |
| Ala Gly Phe Thr Ser Gly Lys Leu Gly Thr Ile Ala Ile Ala Cys Ser |     | 220 |
| 225                                                             | 230 | 235 |
| Gly Ala Asn Asn Cys Ser Trp Asn Asn Leu Asp Arg                 |     | 240 |
|                                                                 | 245 | 250 |

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..580
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ctgggtggtc ttactctctt tatccgcttg actaaagaaa attggcgctcg agtgatagag | 60  |
| acgaagaaga agaagaaaaat gccgtgcctc aacctctcca ccaacgttaa ccttgacggc | 120 |
| gtcgatacat cttccattct ctcggaagct tcctccaccg tcgcgaaaat catcggaag   | 180 |
| cctgagaact atgtgatgat tgtcttgaaa ggctcagtgc ctatgtcatt tggcgggacc  | 240 |
| gaggatcctg cagcttatgg tgaattagtt tctatcggtg gccttaatgc ggatgtgaac  | 300 |
| aagaagctaa gcgctgctgt ttccgccatt cttgagacta agctatcggt gcccaagtct  | 360 |
| cgattcttcc tcaagtttta tgacaccaag ggatccttct ttggttgaa cggggcgact   | 420 |
| ctttaattcc gtggtagggtg attagtgatg ttgtcttaaa atgtatgatc tactctcatc | 480 |
| gatcaagtaa ctttgaactA cttcgtattg taaacatatc taaggtttga tggagttgca  | 540 |
| ttaagaaata acatttatgc tatatatgat gctacaactc                        |     |

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Leu Gly Gly Leu Thr Leu Phe Ile Arg Leu Thr Lys Glu Asn Trp Arg |    |
| 1                                                               | 5  |
| Arg Val Ile Glu Thr Lys Lys Lys Lys Lys Met Pro Cys Leu Asn Leu | 10 |
|                                                                 | 15 |
|                                                                 | 20 |
| Ser Thr Asn Val Asn Leu Asp Gly Val Asp Thr Ser Ser Ile Leu Ser | 25 |
|                                                                 | 30 |
|                                                                 | 35 |
|                                                                 | 40 |
|                                                                 | 45 |
| Glu Ala Ser Ser Thr Val Ala Lys Ile Ile Gly Lys Pro Glu Asn Tyr | 50 |
|                                                                 | 55 |
|                                                                 | 60 |
| Val Met Ile Val Leu Lys Gly Ser Val Pro Met Ser Phe Gly Gly Thr | 65 |
|                                                                 | 70 |
|                                                                 | 75 |
|                                                                 | 80 |
| Glu Asp Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn | 85 |
|                                                                 | 90 |
|                                                                 | 95 |

Ala Asp Val Asn Lys Lys Leu Ser Ala Ala Val Ser Ala Ile Leu Glu  
100 105 110  
Thr Lys Leu Ser Val Pro Lys Ser Arg Phe Phe Leu Lys Phe Tyr Asp  
115 120 125  
Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly Ala Thr Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1571389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met Pro Cys Leu Asn Leu Ser Thr Asn Val Asn Leu Asp Gly Val Asp  
1 5 10 15  
Thr Ser Ser Ile Leu Ser Glu Ala Ser Ser Thr Val Ala Lys Ile Ile  
20 25 30  
Gly Lys Pro Glu Asn Tyr Val Met Ile Val Leu Lys Gly Ser Val Pro  
35 40 45  
Met Ser Phe Gly Gly Thr Glu Asp Pro Ala Ala Tyr Gly Glu Leu Val  
50 55 60  
Ser Ile Gly Gly Leu Asn Ala Asp Val Asn Lys Lys Leu Ser Ala Ala  
65 70 75 80  
Val Ser Ala Ile Leu Glu Thr Lys Leu Ser Val Pro Lys Ser Arg Phe  
85 90 95  
Phe Leu Lys Phe Tyr Asp Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly  
100 105 110  
Ala Thr Leu  
115

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1571390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met Ile Val Leu Lys Gly Ser Val Pro Met Ser Phe Gly Gly Thr Glu  
1 5 10 15  
Asp Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Ala  
20 25 30  
Asp Val Asn Lys Lys Leu Ser Ala Ala Val Ser Ala Ile Leu Glu Thr  
35 40 45  
Lys Leu Ser Val Pro Lys Ser Arg Phe Phe Leu Lys Phe Tyr Asp Thr  
50 55 60  
Lys Gly Ser Phe Phe Gly Trp Asn Gly Ala Thr Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1332  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| acgacctttt  | gtttctctct | tctctattaa | tactatagtt | tctctcaaac  | tctctgatta  | 60   |
| gctcataatt  | actaaaccag | ttgaccattt | ttttctgata | aacaatcaat  | ggcaagggtca | 120  |
| ccttggttgcg | agaagaacgg | actcaagaaa | gggccatgga | catctgaaga  | agaccagaag  | 180  |
| cttggttgact | atatccagaa | acatggttat | ggtaactgga | gaaccctccc  | caaaaatgcc  | 240  |
| ggtttgcaaa  | gatgtggcaa | aagttgtagg | ttaagggtga | ctaattatct  | cgcaccagat  | 300  |
| ataaagcgag  | gaaggttctc | ttttgaggaa | gaagaaacca | ttattcagct  | tcatagcttc  | 360  |
| ttaggaaaca  | agtggtctgc | gattgcggcg | cgtttaccag | gaagaacaga  | taatgagatc  | 420  |
| aagaactttt  | ggaacactca | tataagaaag | aagctactta | gaatggggat  | tgatccagtg  | 480  |
| actcacagtc  | cacgactcga | tctcctcgat | atctcatcca | tcttagcttc  | atctctatac  | 540  |
| aattcatctt  | cacatcacat | gaacatgtca | agactcatga | tggatactaa  | tcgtcgatcat | 600  |
| caccagcaac  | atccattggg | taaccccgag | atactcaagc | tcgctacctc  | tctcttctct  | 660  |
| caaaatcaaa  | accaaGaacc | ttgtggtgga | tcatgactcg | agaactcaag  | agaagcaaac  | 720  |
| agtttatagc  | caaaccggag | taaaccaata | ccaaaccgac | caatatttcg  | agaacacgat  | 780  |
| tactcaagaa  | ctccaatctt | ccatgccacc | attccccaat | gaagtcacat  | agtttaacaa  | 840  |
| catggatcat  | cacttcaatg | gttttgagaa | acaaaatctt | gtttcaactt  | ctactacgtc  | 900  |
| agtccaagat  | tgctataatc | cgctattcaa | cgattattca | agttcaaat   | ttgtcttgga  | 960  |
| tccttcttat  | tcggatcaga | gcttcaactt | cgcaaattcg | gtcttaaaaca | cgccatcctc  | 1020 |
| gagcccgagc  | ccgactacgt | taaactcgag | ttacatcaat | agtagcagtt  | gcagcactga  | 1080 |
| ggatgaaata  | gaaagctatt | gcagtaatct | catgaagttt | gatattcccg  | atttcttgga  | 1140 |
| cgttaatggg  | tttattatat | aattccaaga | aacaaaataa | aactcgagtg  | ggatacagtt  | 1200 |
| ttctttttat  | tctttgttgt | aatcttaaga | cttttttttt | tgtttttccg  | atttgtttac  | 1260 |
| ttgtaaaata  | ctgttttcgt | tttggttgta | atttggtata | tttctctaga  | gtttatagct  | 1320 |
| aataccattt  | tt         |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1932:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 195 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..195  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571392

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Ser | Pro | Cys | Cys | Glu | Lys | Asn | Gly | Leu | Lys | Lys | Gly | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Thr | Ser | Glu | Glu | Asp | Gln | Lys | Leu | Val | Asp | Tyr | Ile | Gln | Lys | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Tyr | Gly | Asn | Trp | Arg | Thr | Leu | Pro | Lys | Asn | Ala | Gly | Leu | Gln | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Gly | Lys | Ser | Cys | Arg | Leu | Arg | Trp | Thr | Asn | Tyr | Leu | Arg | Pro | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Lys | Arg | Gly | Arg | Phe | Ser | Phe | Glu | Glu | Glu | Glu | Thr | Ile | Ile | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | His | Ser | Phe | Leu | Gly | Asn | Lys | Trp | Ser | Ala | Ile | Ala | Ala | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Gly | Arg | Thr | Asp | Asn | Glu | Ile | Lys | Asn | Phe | Trp | Asn | Thr | His | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Lys | Lys | Leu | Leu | Arg | Met | Gly | Ile | Asp | Pro | Val | Thr | His | Ser | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Leu | Asp | Leu | Leu | Asp | Ile | Ser | Ser | Ile | Leu | Ala | Ser | Ser | Leu | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Ser | Ser | Ser | His | His | Met | Asn | Met | Ser | Arg | Leu | Met | Met | Asp | Thr |

(2) INFORMATION FOR SEQ ID NO:1933:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1571393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

(2) INFORMATION FOR SEQ ID NO:1934:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1571394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

|           |           |           |            |           |     |           |           |            |           |     |           |           |           |           |     |
|-----------|-----------|-----------|------------|-----------|-----|-----------|-----------|------------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Met<br>1  | Asp       | His       | His        | Phe<br>5  | Asn | Gly       | Phe       | Gly        | Glu<br>10 | Gln | Asn       | Leu       | Val       | Ser<br>15 | Thr |
| Ser       | Thr       | Thr       | Ser<br>20  | Val       | Gln | Asp       | Cys       | Tyr<br>25  | Asn       | Pro | Ser       | Phe       | Asn       | Asp       | Tyr |
| Ser       | Ser       | Ser<br>35 | Asn        | Phe       | Val | Leu       | Asp<br>40 | Pro        | Ser       | Tyr | Ser       | Asp<br>45 | Gln       | Ser       | Phe |
| Asn       | Phe<br>50 | Ala       | Asn        | Ser       | Val | Leu<br>55 | Asn       | Thr        | Pro       | Ser | Ser<br>60 | Ser       | Pro       | Ser       | Pro |
| Thr<br>65 | Thr       | Leu       | Asn        | Ser<br>70 | Ser | Tyr       | Ile       | Asn        | Ser<br>75 | Ser | Ser       | Cys       | Ser       | Thr<br>80 | Glu |
| Asp       | Glu       | Ile       | Glu<br>85  | Ser       | Tyr | Cys       | Ser       | Asn<br>90  | Leu       | Met | Lys       | Phe       | Asp<br>95 | Ile       | Pro |
| Asp       | Phe       | Leu       | Asp<br>100 | Val       | Asn | Gly       | Phe       | Ile<br>105 | Ile       |     |           |           |           |           |     |

(2) INFORMATION FOR SEQ ID NO:1935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| actcaactct  | ctttcgaaac  | tcaatcctta  | tataacacat | cccatGttaa | gcctataagc  | 60   |
| tacacatatc  | agctctctca  | caaaaataaa  | atggagggaa | gccagtgac  | cagtgtcagg  | 120  |
| ctctcttcgg  | tgggtgcctgc | ttctgtggta  | ggtgagaaca | agccacgaca | gctcacaccc  | 180  |
| atggacttag  | ccatgaagct  | ccactacgtc  | cgagccgtct | acttcttcaa | gggtgcacgt  | 240  |
| gacttcactg  | tcgccgacgt  | gaagaacacc  | atgtttactc | tacagtctct | actccaatct  | 300  |
| tatcaccacg  | tctcaggctg  | gatccggatg  | tccgacaacg | acaacgacac | ttcagctgca  | 360  |
| gccatacctt  | acattcgctg  | caacgacagt  | ggcatacgcg | tggtcgaggc | caacgtcgaa  | 420  |
| gagttcacag  | tggagaagtg  | gctcgagttg  | gaagaccgtt | ccattgacca | ccgattccct  | 480  |
| gtctacgata  | acgttcttgg  | tcctgatctt  | accttctcgc | cactcgtttt | cctccagata  | 540  |
| actcagttta  | aatgtgggtg  | gctctgtatt  | gggttgagtt | gggcccata  | tcttgagagc  | 600  |
| gtgttttcag  | catcaacggt  | catgaaaaca  | cttgacagc  | tggatcggg  | tcattgcccc  | 660  |
| acaaaaccgg  | tttaccggaa  | aacccccgaa  | ctaacctctc | atgctcgtaa | tgatggtgaa  | 720  |
| gctattttcca | ttgaaaagat  | agattcggtt  | ggcgagtatt | ggttacttac | caataaatgc  | 780  |
| aagatgggga  | gacacatttt  | taatttttagc | ctcaaccaca | ttgatagctt | gatggccaag  | 840  |
| tacaccacgc  | gagaccaacc  | tttctcggag  | gttgatattt | tgtatgcatt | gatatggaag  | 900  |
| tcgctactga  | atatccgcgg  | cgaaacaaac  | acgaatgtta | taacaatttg | tgaccgtaaa  | 960  |
| aagtcttcaa  | cctgttgtaa  | cgaggacttg  | gtaataagcg | tagtggaata | gaatgacgaa  | 1020 |
| atggttgagg  | tatccgaact  | agctgcactg  | attgctggtg | aaaaaagaga | agaaaacggg  | 1080 |
| gcgatcaaga  | ggatgataga  | acaagataaa  | ggctcttcgg | attttttcac | gtacgggtgca | 1140 |
| aatttaacgt  | ttgtgaatct  | tgatgaaata  | gatattgatg | aacttgagat | caacggaggg  | 1200 |
| aagccggatt  | tcgtaaaacta | cacgattcat  | ggggtcggag | acaaagggtg | tgttttgggt  | 1260 |
| tttcccaagc  | aaaactttgc  | aaggattgta  | agtgtagtga | tgctgaaga  | agaccttgca  | 1320 |
| aaactcaagg  | aggaggtgac  | taatatgatt  | atataacttt | gtatcttctt | cttggttgta  | 1380 |
| tacataaatg  | ctgtttttta  | ctctttgtaa  | tttcattatc | gaattgttgg | gaagcctatc  | 1440 |
| aataaattgt  | ttgaactgtt  | t           |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gln | Leu | Ser | Phe | Glu | Thr | Gln | Ser | Leu | Tyr | Asn | Thr | Ser | His | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Pro | Ile | Ser | Tyr | Thr | Tyr | Gln | Leu | Ser | His | Lys | Asn | Lys | Met | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Gly | Ser | Pro | Val | Thr | Ser | Val | Arg | Leu | Ser | Ser | Val | Val | Pro | Ala | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Val | Val | Gly | Glu | Asn | Lys | Pro | Arg | Gln | Leu | Thr | Pro | Met | Asp | Leu | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Met | Lys | Leu | His | Tyr | Val | Arg | Ala | Val | Tyr | Phe | Phe | Lys | Gly | Ala | Arg |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     | 80  |     |
| Asp | Phe | Thr | Val | Ala | Asp | Val | Lys | Asn | Thr | Met | Phe | Thr | Leu | Gln | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Leu Leu Gln Ser Tyr His His Val Ser Gly Arg Ile Arg Met Ser Asp  
100 105 110  
Asn Asp Asn Asp Thr Ser Ala Ala Ile Pro Tyr Ile Arg Cys Asn  
115 120 125  
Asp Ser Gly Ile Arg Val Val Glu Ala Asn Val Glu Glu Phe Thr Val  
130 135 140  
Glu Lys Trp Leu Glu Leu Asp Asp Arg Ser Ile Asp His Arg Phe Leu  
145 150 155 160  
Val Tyr Asp His Val Leu Gly Pro Asp Leu Thr Phe Ser Pro Leu Val  
165 170 175  
Phe Leu Gln Ile Thr Gln Phe Lys Cys Gly Gly Leu Cys Ile Gly Leu  
180 185 190  
Ser Trp Ala His Ile Leu Gly Asp Val Phe Ser Ala Ser Thr Phe Met  
195 200 205  
Lys Thr Leu Gly Gln Leu Val Ser Gly His Ala Pro Thr Lys Pro Val  
210 215 220  
Tyr Pro Lys Thr Pro Glu Leu Thr Ser His Ala Arg Asn Asp Gly Glu  
225 230 235 240  
Ala Ile Ser Ile Glu Lys Ile Asp Ser Val Gly Glu Tyr Trp Leu Leu  
245 250 255  
Thr Asn Lys Cys Lys Met Gly Arg His Ile Phe Asn Phe Ser Leu Asn  
260 265 270  
His Ile Asp Ser Leu Met Ala Lys Tyr Thr Thr Arg Asp Gln Pro Phe  
275 280 285  
Ser Glu Val Asp Ile Leu Tyr Ala Leu Ile Trp Lys Ser Leu Leu Asn  
290 295 300  
Ile Arg Gly Glu Thr Asn Thr Asn Val Ile Thr Ile Cys Asp Arg Lys  
305 310 315 320  
Lys Ser Ser Thr Cys Trp Asn Glu Asp Leu Val Ile Ser Val Val Glu  
325 330 335  
Lys Asn Asp Glu Met Val Gly Ile Ser Glu Leu Ala Ala Leu Ile Ala  
340 345 350  
Gly Glu Lys Arg Glu Glu Asn Gly Ala Ile Lys Arg Met Ile Glu Gln  
355 360 365  
Asp Lys Gly Ser Ser Asp Phe Phe Thr Tyr Gly Ala Asn Leu Thr Phe  
370 375 380  
Val Asn Leu Asp Glu Ile Asp Met Tyr Glu Leu Glu Ile Asn Gly Gly  
385 390 395 400  
Lys Pro Asp Phe Val Asn Tyr Thr Ile His Gly Val Gly Asp Lys Gly  
405 410 415  
Val Val Leu Val Phe Pro Lys Gln Asn Phe Ala Arg Ile Val Ser Val  
420 425 430  
Val Met Pro Glu Glu Asp Leu Ala Lys Leu Lys Glu Glu Val Thr Asn  
435 440 445  
Met Ile Ile  
450

(2) INFORMATION FOR SEQ ID NO:1937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1571397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

Met Glu Gly Ser Pro Val Thr Ser Val Arg Leu Ser Ser Val Val Pro  
1 5 10 15  
Ala Ser Val Val Gly Glu Asn Lys Pro Arg Gln Leu Thr Pro Met Asp

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1571398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

Met Asp Leu Ala Met Lys Leu His Tyr Val Arg Ala Val Tyr Phe Phe  
1 5 10 15  
Lys Gly Ala Arg Asp Phe Thr Val Ala Asp Val Lys Asn Thr Met Phe  
20 25 30  
Thr Leu Gln Ser Leu Leu Gln Ser Tyr His His Val Ser Gly Arg Ile  
35 40 45  
Arg Met Ser Asp Asn Asp Asn Asp Thr Ser Ala Ala Ala Ile Pro Tyr  
50 55 60  
Ile Arg Cys Asn Asp Ser Gly Ile Arg Val Val Glu Ala Asn Val Glu  
65 70 75 80  
Glu Phe Thr Val Glu Lys Trp Leu Glu Leu Asp Asp Arg Ser Ile Asp  
85 90 95  
His Arg Phe Leu Val Tyr Asp His Val Leu Gly Pro Asp Leu Thr Phe  
100 105 110  
Ser Pro Leu Val Phe Leu Gln Ile Thr Gln Phe Lys Cys Gly Gly Leu  
115 120 125  
Cys Ile Gly Leu Ser Trp Ala His Ile Leu Gly Asp Val Phe Ser Ala  
130 135 140  
Ser Thr Phe Met Lys Thr Leu Gly Gln Leu Val Ser Gly His Ala Pro  
145 150 155 160  
Thr Lys Pro Val Tyr Pro Lys Thr Pro Glu Leu Thr Ser His Ala Arg  
165 170 175  
Asn Asp Gly Glu Ala Ile Ser Ile Glu Lys Ile Asp Ser Val Gly Glu  
180 185 190  
Tyr Trp Leu Leu Thr Asn Lys Cys Lys Met Gly Arg His Ile Phe Asn  
195 200 205  
Phe Ser Leu Asn His Ile Asp Ser Leu Met Ala Lys Tyr Thr Thr Arg  
210 215 220  
Asp Gln Pro Phe Ser Glu Val Asp Ile Leu Tyr Ala Leu Ile Trp Lys  
225 230 235 240  
Ser Leu Leu Asn Ile Arg Gly Glu Thr Asn Thr Asn Val Ile Thr Ile  
245 250 255  
Cys Asp Arg Lys Lys Ser Ser Thr Cys Trp Asn Glu Asp Leu Val Ile  
260 265 270  
Ser Val Val Glu Lys Asn Asp Glu Met Val Gly Ile Ser Glu Leu Ala  
275 280 285  
Ala Leu Ile Ala Gly Glu Lys Arg Glu Glu Asn Gly Ala Ile Lys Arg  
290 295 300  
Met Ile Glu Gln Asp Lys Gly Ser Ser Asp Phe Phe Thr Tyr Gly Ala  
305 310 315 320  
Asn Leu Thr Phe Val Asn Leu Asp Glu Ile Asp Met Tyr Glu Leu Glu  
325 330 335  
Ile Asn Gly Gly Lys Pro Asp Phe Val Asn Tyr Thr Ile His Gly Val  
340 345 350  
Gly Asp Lys Gly Val Val Leu Val Phe Pro Lys Gln Asn Phe Ala Arg  
355 360 365  
Ile Val Ser Val Val Met Pro Glu Glu Asp Leu Ala Lys Leu Lys Glu  
370 375 380  
Glu Val Thr Asn Met Ile Ile  
385 390

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| ctcttttagca | aaaaatctca | gaactcaRaa | aaaaaaCaSR | tccaacacca | aagacaatgS | 60   |
| gagatgagtt  | tgcgtctcgc | ttcatcttca | acctcaaacc | caatttgtct | actaaaccct | 120  |
| ggaaaaaacc  | ttaatttccc | aatccgaaac | catagaatcc | ctaaaacttc | gaaacccttt | 180  |
| tgcgttaggt  | cttcaatgag | cttgtctaaa | ccaccagac  | aaaccttatc | tagtaactgg | 240  |
| gatgtatcta  | gcttctccat | tgattccggt | gctcaatctc | cttcaagact | cccaagtttc | 300  |
| gaagaactcg  | ataccaccaa | catgttgctc | cgtcaaagaa | tcgtcttttt | gggttctcag | 360  |
| gttgatgata  | tgacggcgga | tttggttata | agtcagctat | tgttactaga | tgctgaggac | 420  |
| tcagaaagag  | acattacgct | ttttatcaat | tcacccggtg | gatctattac | tgctgggatg | 480  |
| ggaatatatg  | atgcaatgaa | acaatgtaag | gcggatgtat | ctactgtttg | cttaggggta | 540  |
| gctgcactca  | tgggtgcggt | tcttcttgct | tctgggtcaa | aagggaacg  | gtattgtatg | 600  |
| cctaactcta  | aagttatgat | ccatcagcca | cttggtactg | ctggaggcaa | agcaacggaa | 660  |
| atgagcatac  | gtataagaga | aatgatgtac | cacaagatta | aacttaacaa | aatcttctct | 720  |
| agaatcactg  | ggaagcctga | atcagagatc | gaaagtgaca | cagaccgtga | taacttcttg | 780  |
| aatccatggg  | aggcgaaaga | atatggtttg | atcgacgctg | taatcgatga | tgggaaaccg | 840  |
| ggactaatcg  | ctccaattgg | agatggtact | cctcctccta | aaaccaaagt | ctgggatctt | 900  |
| tggaaagtcg  | aaggaaccaa | gaaagacaac | actaacttgc | catctgagcg | ctccatgaca | 960  |
| cagaatgggt  | atgccgccat | tgaatagaac | tggtgttgca | gcgtttacgc | cttttatatg | 1020 |
| ttattctggt  | ggtacctgta | accatataac | gttgcatctc | ctgtgtttgt | accatttctc | 1080 |
| tgatagattt  | ttggaataat | ttgaaggcaa | aagatagatt | attgttgta  | gaagaagcta | 1140 |
| caaaatttaa  | tgattaaatt | gaatcatcaa | gccatgagaa | gctttgtgtt | ttc        |      |

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1571419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Ser | Lys | Lys | Ser | Gln | Asn | Ser | Xaa | Lys | Lys | Xaa | Xaa | Gln | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Arg | Gln | Xaa | Glu | Met | Ser | Leu | Arg | Leu | Ala | Ser | Ser | Ser | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Pro | Ile | Cys | Leu | Leu | Asn | Pro | Gly | Lys | Asn | Leu | Asn | Phe | Pro | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asn | His | Arg | Ile | Pro | Lys | Thr | Ser | Lys | Pro | Phe | Cys | Val | Arg | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Met | Ser | Leu | Ser | Lys | Pro | Pro | Arg | Gln | Thr | Leu | Ser | Ser | Asn | Trp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Ser | Ser | Phe | Ser | Ile | Asp | Ser | Val | Ala | Gln | Ser | Pro | Ser | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Pro | Ser | Phe | Glu | Glu | Leu | Asp | Thr | Thr | Asn | Met | Leu | Leu | Arg | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ile | Val | Phe | Leu | Gly | Ser | Gln | Val | Asp | Asp | Met | Thr | Ala | Asp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ile | Ser | Gln | Leu | Leu | Leu | Leu | Asp | Ala | Glu | Asp | Ser | Glu | Arg | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Thr | Leu | Phe | Ile | Asn | Ser | Pro | Gly | Gly | Ser | Ile | Thr | Ala | Gly | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ile | Tyr | Asp | Ala | Met | Lys | Gln | Cys | Lys | Ala | Asp | Val | Ser | Thr | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Leu | Gly | Leu | Ala | Ala | Ser | Met | Gly | Ala | Phe | Leu | Leu | Ala | Ser | Gly |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Ser | Lys | Gly | Lys | Arg | Tyr | Cys | Met | Pro | Asn | Ser | Lys | Val | Met | Ile | His |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Gln Pro Leu Gly Thr Ala Gly Gly Lys Ala Thr Glu Met Ser Ile Arg  
210 215 220  
Ile Arg Glu Met Met Tyr His Lys Ile Lys Leu Asn Lys Ile Phe Ser  
225 230 235 240  
Arg Ile Thr Gly Lys Pro Glu Ser Glu Ile Glu Ser Asp Thr Asp Arg  
245 250 255  
Asp Asn Phe Leu Asn Pro Trp Glu Ala Lys Glu Tyr Gly Leu Ile Asp  
260 265 270  
Ala Val Ile Asp Asp Gly Lys Pro Gly Leu Ile Ala Pro Ile Gly Asp  
275 280 285  
Gly Thr Pro Pro Pro Lys Thr Lys Val Trp Asp Leu Trp Lys Val Glu  
290 295 300  
Gly Thr Lys Lys Asp Asn Thr Asn Leu Pro Ser Glu Arg Ser Met Thr  
305 310 315 320  
Gln Asn Gly Tyr Ala Ala Ile Glu  
325

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

Met Ser Leu Arg Leu Ala Ser Ser Ser Thr Ser Asn Pro Ile Cys Leu  
1 5 10 15  
Leu Asn Pro Gly Lys Asn Leu Asn Phe Pro Ile Arg Asn His Arg Ile  
20 25 30  
Pro Lys Thr Ser Lys Pro Phe Cys Val Arg Ser Ser Met Ser Leu Ser  
35 40 45  
Lys Pro Pro Arg Gln Thr Leu Ser Ser Asn Trp Asp Val Ser Ser Phe  
50 55 60  
Ser Ile Asp Ser Val Ala Gln Ser Pro Ser Arg Leu Pro Ser Phe Glu  
65 70 75 80  
Glu Leu Asp Thr Thr Asn Met Leu Leu Arg Gln Arg Ile Val Phe Leu  
85 90 95  
Gly Ser Gln Val Asp Asp Met Thr Ala Asp Leu Val Ile Ser Gln Leu  
100 105 110  
Leu Leu Leu Asp Ala Glu Asp Ser Glu Arg Asp Ile Thr Leu Phe Ile  
115 120 125  
Asn Ser Pro Gly Gly Ser Ile Thr Ala Gly Met Gly Ile Tyr Asp Ala  
130 135 140  
Met Lys Gln Cys Lys Ala Asp Val Ser Thr Val Cys Leu Gly Leu Ala  
145 150 155 160  
Ala Ser Met Gly Ala Phe Leu Leu Ala Ser Gly Ser Lys Gly Lys Arg  
165 170 175  
Tyr Cys Met Pro Asn Ser Lys Val Met Ile His Gln Pro Leu Gly Thr  
180 185 190  
Ala Gly Gly Lys Ala Thr Glu Met Ser Ile Arg Ile Arg Glu Met Met  
195 200 205  
Tyr His Lys Ile Lys Leu Asn Lys Ile Phe Ser Arg Ile Thr Gly Lys  
210 215 220  
Pro Glu Ser Glu Ile Glu Ser Asp Thr Asp Arg Asp Asn Phe Leu Asn  
225 230 235 240  
Pro Trp Glu Ala Lys Glu Tyr Gly Leu Ile Asp Ala Val Ile Asp Asp  
245 250 255  
Gly Lys Pro Gly Leu Ile Ala Pro Ile Gly Asp Gly Thr Pro Pro Pro



260 265 270  
Lys Thr Lys Val Trp Asp Leu Trp Lys Val Glu Gly Thr Lys Lys Asp  
275 280 285  
Asn Thr Asn Leu Pro Ser Glu Arg Ser Met Thr Gln Asn Gly Tyr Ala  
290 295 300  
Ala Ile Glu  
305

(2) INFORMATION FOR SEQ ID NO:1942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1571421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

Met Ser Leu Ser Lys Pro Pro Arg Gln Thr Leu Ser Ser Asn Trp Asp  
1 5 10 15  
Val Ser Ser Phe Ser Ile Asp Ser Val Ala Gln Ser Pro Ser Arg Leu  
20 25 30  
Pro Ser Phe Glu Glu Leu Asp Thr Thr Asn Met Leu Leu Arg Gln Arg  
35 40 45  
Ile Val Phe Leu Gly Ser Gln Val Asp Asp Met Thr Ala Asp Leu Val  
50 55 60  
Ile Ser Gln Leu Leu Leu Asp Ala Glu Asp Ser Glu Arg Asp Ile  
65 70 75 80  
Thr Leu Phe Ile Asn Ser Pro Gly Gly Ser Ile Thr Ala Gly Met Gly  
85 90 95  
Ile Tyr Asp Ala Met Lys Gln Cys Lys Ala Asp Val Ser Thr Val Cys  
100 105 110  
Leu Gly Leu Ala Ala Ser Met Gly Ala Phe Leu Leu Ala Ser Gly Ser  
115 120 125  
Lys Gly Lys Arg Tyr Cys Met Pro Asn Ser Lys Val Met Ile His Gln  
130 135 140  
Pro Leu Gly Thr Ala Gly Gly Lys Ala Thr Glu Met Ser Ile Arg Ile  
145 150 155 160  
Arg Glu Met Met Tyr His Lys Ile Lys Leu Asn Lys Ile Phe Ser Arg  
165 170 175  
Ile Thr Gly Lys Pro Glu Ser Glu Ile Glu Ser Asp Thr Asp Arg Asp  
180 185 190  
Asn Phe Leu Asn Pro Trp Glu Ala Lys Glu Tyr Gly Leu Ile Asp Ala  
195 200 205  
Val Ile Asp Asp Gly Lys Pro Gly Leu Ile Ala Pro Ile Gly Asp Gly  
210 215 220  
Thr Pro Pro Pro Lys Thr Lys Val Trp Asp Leu Trp Lys Val Glu Gly  
225 230 235 240  
Thr Lys Lys Asp Asn Thr Asn Leu Pro Ser Glu Arg Ser Met Thr Gln  
245 250 255  
Asn Gly Tyr Ala Ala Ile Glu  
260

(2) INFORMATION FOR SEQ ID NO:1943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1191

(D) OTHER INFORMATION: / Ceres Seq. ID 1571422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| taccattctt  | ctgaaaatga  | acacctcaga | agccctaagc  | accacaatga | ttttgggcat | 60   |
| cacactagaa  | aaccacaggc  | tgctgtgaag | cctgatgctt  | tgaaggagcc | tccatctatt | 120  |
| gatgtgcctg  | cattgtcatt  | ggatgagttg | aaagaaaaga  | ccgataactt | tggatcaaa  | 180  |
| tcattgattg  | gtgaaggatc  | ttacggcaga | gcctattatg  | caaccttgaa | agatggaaa  | 240  |
| gctgtcgagg  | tgaagaagct  | tgacaatgca | gcggaacctg  | aatcaaagt  | tgagttcttg | 300  |
| actcaggtct  | cgagggtttc  | caagctgaag | cacgataaatt | ttgttgagct | cttcggttat | 360  |
| tgcggtgaag  | ggaatttccg  | cattcttgcg | tatgagtttg  | ctactatggg | atctttacat | 420  |
| gacatcttac  | acggggaggaa | aggagtccaa | ggagcacaac  | caggtcctac | gcttgactgg | 480  |
| atccaacggg  | tcagaatagc  | agttgatgca | gctagaggac  | ttgagtattt | gcatgagaaa | 540  |
| gttcaacctg  | cagtaataca  | cagagatatt | cgatctagca  | atgtgcttct | ctttgaagat | 600  |
| tttaaagcca  | agatcgctga  | ttttaatcta | tcgaaccaat  | ctcctgatat | ggctgctcgt | 660  |
| cttcattcta  | ccagagtttt  | gggaaMcttc | ggttaccacg  | caccagagta | tgcatgact  | 720  |
| gggtcaactga | cacagaagag  | tgatgtttat | agttttgggtg | tggtgctttt | ggagctcttg | 780  |
| actggtagga  | aaccogtcga  | tcatacgatg | cctcgtggtc  | aacaaagtct | tgttacttgg | 840  |
| gctactccaa  | ggctaagtga  | agacaaagtg | aagcaatgtg  | ttgatccaaa | actaaagggg | 900  |
| gaatatcctc  | ctaaagctgt  | tgcaaagctc | gctgcagtag  | cagcattgtg | tgtgcaatat | 960  |
| gaatcagagt  | ttaggccaaa  | catgagcatt | gtggtaaaa   | ctcttcaacc | attggtgagg | 1020 |
| tcatacaacag | cagcagctgt  | accagtccag | gaagcctgat  | tcttctgtgc | aatagcaaca | 1080 |
| atggaagatt  | gggttcgggtt | tcagttgttg | ccataccgta  | taaagtgtgt | cttaaagaga | 1140 |
| gtctttttgt  | cgaggctttt  | cttcagttaa | gagctccaaa  | agcaccacac | c          |      |

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..352

(D) OTHER INFORMATION: / Ceres Seq. ID 1571423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | His | Ser | Ser | Glu | Asn | Glu | His | Leu | Arg | Ser | Pro | Lys | His | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Asp | Phe | Gly | His | His | Thr | Arg | Lys | Pro | Gln | Ala | Ala | Val | Lys | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     | Asp |
| Ala | Leu | Lys | Glu | Pro | Pro | Ser | Ile | Asp | Val | Pro | Ala | Leu | Ser | Leu |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     | Asp |
| Glu | Leu | Lys | Glu | Lys | Thr | Asp | Asn | Phe | Gly | Ser | Lys | Ser | Leu | Ile |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     | Gly |
| Glu | Gly | Ser | Tyr | Gly | Arg | Ala | Tyr | Tyr | Ala | Thr | Leu | Lys | Asp | Gly |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |
| Ala | Val | Ala | Val | Lys | Lys | Leu | Asp | Asn | Ala | Ala | Glu | Pro | Glu | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  | Asn |
| Val | Glu | Phe | Leu | Thr | Gln | Val | Ser | Arg | Val | Ser | Lys | Leu | Lys | His |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     | Asp |
| Asn | Phe | Val | Glu | Leu | Phe | Gly | Tyr | Cys | Val | Glu | Gly | Asn | Phe | Arg |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     | Ile |
| Leu | Ala | Tyr | Glu | Phe | Ala | Thr | Met | Gly | Ser | Leu | His | Asp | Ile | Leu |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     | His |
| Gly | Arg | Lys | Gly | Val | Gln | Gly | Ala | Gln | Pro | Gly | Pro | Thr | Leu | Asp |
|     |     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     | Trp |
| Ile | Gln | Arg | Val | Arg | Ile | Ala | Val | Asp | Ala | Ala | Arg | Gly | Leu | Glu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 | Tyr |
| Leu | His | Glu | Lys | Val | Gln | Pro | Ala | Val | Ile | His | Arg | Asp | Ile | Arg |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     | 190 |     | Ser |
| Ser | Asn | Val | Leu | Leu | Phe | Glu | Asp | Phe | Lys | Ala | Lys | Ile | Ala | Asp |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Asn Leu Ser Asn Gln Ser Pro Asp Met Ala Ala Arg Leu His Ser Thr |     |     |
| 210                                                             | 215 | 220 |
| Arg Val Leu Gly Xaa Phe Gly Tyr His Ala Pro Glu Tyr Ala Met Thr |     |     |
| 225                                                             | 230 | 235 |
| Gly Gln Leu Thr Gln Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu |     |     |
| 245                                                             | 250 | 255 |
| Leu Glu Leu Leu Thr Gly Arg Lys Pro Val Asp His Thr Met Pro Arg |     |     |
| 260                                                             | 265 | 270 |
| Gly Gln Gln Ser Leu Val Thr Trp Ala Thr Pro Arg Leu Ser Glu Asp |     |     |
| 275                                                             | 280 | 285 |
| Lys Val Lys Gln Cys Val Asp Pro Lys Leu Lys Gly Glu Tyr Pro Pro |     |     |
| 290                                                             | 295 | 300 |
| Lys Ala Val Ala Lys Leu Ala Ala Val Ala Ala Leu Cys Val Gln Tyr |     |     |
| 305                                                             | 310 | 315 |
| Glu Ser Glu Phe Arg Pro Asn Met Ser Ile Val Val Lys Ala Leu Gln |     |     |
| 325                                                             | 330 | 335 |
| Pro Leu Leu Arg Ser Ser Thr Ala Ala Ala Val Pro Val Gln Glu Ala |     |     |
| 340                                                             | 345 | 350 |

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1571424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gly Ser Leu His Asp Ile Leu His Gly Arg Lys Gly Val Gln Gly |     |     |
| 1                                                               | 5   | 10  |
| Ala Gln Pro Gly Pro Thr Leu Asp Trp Ile Gln Arg Val Arg Ile Ala |     |     |
| 20                                                              | 25  | 30  |
| Val Asp Ala Ala Arg Gly Leu Glu Tyr Leu His Glu Lys Val Gln Pro |     |     |
| 35                                                              | 40  | 45  |
| Ala Val Ile His Arg Asp Ile Arg Ser Ser Asn Val Leu Leu Phe Glu |     |     |
| 50                                                              | 55  | 60  |
| Asp Phe Lys Ala Lys Ile Ala Asp Phe Asn Leu Ser Asn Gln Ser Pro |     |     |
| 65                                                              | 70  | 75  |
| Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Xaa Phe Gly |     |     |
| 85                                                              | 90  | 95  |
| Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Thr Gln Lys Ser |     |     |
| 100                                                             | 105 | 110 |
| Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Leu Thr Gly Arg |     |     |
| 115                                                             | 120 | 125 |
| Lys Pro Val Asp His Thr Met Pro Arg Gly Gln Gln Ser Leu Val Thr |     |     |
| 130                                                             | 135 | 140 |
| Trp Ala Thr Pro Arg Leu Ser Glu Asp Lys Val Lys Gln Cys Val Asp |     |     |
| 145                                                             | 150 | 155 |
| Pro Lys Leu Lys Gly Glu Tyr Pro Pro Lys Ala Val Ala Lys Leu Ala |     |     |
| 165                                                             | 170 | 175 |
| Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ser Glu Phe Arg Pro Asn |     |     |
| 180                                                             | 185 | 190 |
| Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Arg Ser Ser Thr |     |     |
| 195                                                             | 200 | 205 |
| Ala Ala Ala Val Pro Val Gln Glu Ala                             |     |     |
| 210                                                             | 215 |     |

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| aacgttttca  | cagtctctac | accgtcatga  | acactgaatc | agttgtcgag | ttccttggga  | 60   |
| atgtgacctt  | gttgacgagg | ttacctagtt  | cctctctgaa | gagaatctcc | gaagtcgttg  | 120  |
| tcttcaaagg  | ttatgacaga | ggtgattatg  | tggttcgtga | aaatcaaaat | gtggatggag  | 180  |
| tttattttct  | cttgcaagga | caggctcagg  | ttctgagatc | agccgaagag | gaaaactatc  | 240  |
| aagagttccc  | tttgaaacga | tatgattttc  | tcggccatgg | tattttcggg | gatgtttact  | 300  |
| cagcagatgt  | tgttgctgtg | acagagctta  | cctgcttgct | gttgatgtct | gatcatcggtg | 360  |
| ctttacttga  | aataaagtc  | gtctcggatt  | cagataagga | acgctgtcct | gtggaagaca  | 420  |
| tactatatct  | agaaccatta | gatttgaatg  | tataccgggg | gttcacccca | cctaattgctc | 480  |
| caacctatgg  | aaaggtttat | ggagggcaat  | tagttggaca | ggcacttgcc | gcagcatcaa  | 540  |
| aaactgttga  | aactatgaag | atagtccata  | attttcattg | ctatttcctt | cttgttggag  | 600  |
| atataaatat  | tcccatcata | tatgatgtta  | accgcttacg | tgacggcaac | aactttgcca  | 660  |
| ccagaagtgt  | agatgctaga | cagaaaggaa  | aaactatatt | caccttgctc | gcgtcatttc  | 720  |
| agaaaaagca  | acaaggtttt | attcaccagg  | agtcgaccat | gcctcataca | ccagctcctg  | 780  |
| aaacgcttct  | accaagggag | gagatgcttg  | aacggcttgt | tactgagcct | ctgctaccta  | 840  |
| gggattaccg  | aaaccaagtt | gcaactgaaa  | ttagtgttcc | attccctata | gatattcgat  | 900  |
| tttgtgagcc  | aaatcgttcc | actaaacaga  | ataagtctcc | tccaagacta | aaatattggt  | 960  |
| ttagagcaaaa | gggaaaactt | tctgatgatg  | atcaagcttt | gcacagatgt | gtgggtgcat  | 1020 |
| ttgcttccga  | tttgatattc | gccactatca  | gtttaaaccc | tcaccggaga | gagggcatga  | 1080 |
| gtgtagctgc  | tcttagcctg | gaccactoga  | tgtggttcca | ccgacctgta | agagcagatg  | 1140 |
| attggttggt  | gtttgtgtga | gtccaaactgc | gacctaaagc | cgcggttttg | caactggcaa  | 1200 |
| aatgttcaac  | agaaagggag | agctgggtgg  | atcattgacg | caagaagctg | tggttaagaga | 1260 |
| agctgtgact  | attaagccat | ccttcggggc  | caagctatga | agccatagga | ttttgatagt  | 1320 |
| gagagaattg  | ctgcatctgt | tactcctcac  | ggtcacattc | caaagagtcg | tcacttatac  | 1380 |
| tacatttgca  | tatgtttttc | gatccacaat  | tattattttc | ccctctaaaa | gggtctacac  | 1440 |
| atatgtttgt  | ttgtaaccac | gataatgttt  | caacagcaat | gaaaaagcaa | acagtggttc  | 1500 |

(2) INFORMATION FOR SEQ ID NO:1947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Asp | Ser | Leu | Tyr | Thr | Val | Met | Asn | Thr | Glu | Ser | Val | Val | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Leu | Gly | Asn | Val | Thr | Leu | Leu | Gln | Arg | Leu | Pro | Ser | Ser | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Lys | Arg | Ile | Ser | Glu | Val | Val | Val | Phe | Lys | Gly | Tyr | Asp | Arg | Gly | Asp |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Tyr | Val | Val | Arg | Glu | Asn | Gln | Asn | Val | Asp | Gly | Val | Tyr | Phe | Leu | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Gln | Gly | Gln | Ala | Gln | Val | Leu | Arg | Ser | Ala | Glu | Glu | Glu | Asn | Tyr | Gln |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Glu | Phe | Pro | Leu | Lys | Arg | Tyr | Asp | Phe | Phe | Gly | His | Gly | Ile | Phe | Gly |

Val  
385

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1571427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Glu | Ser | Val | Val | Glu | Phe | Leu | Gly | Asn | Val | Thr | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Leu | Pro | Ser | Ser | Ser | Leu | Lys | Arg | Ile | Ser | Glu | Val | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Lys | Gly | Tyr | Asp | Arg | Gly | Asp | Tyr | Val | Val | Arg | Glu | Asn | Gln | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asp | Gly | Val | Tyr | Phe | Leu | Leu | Gln | Gly | Gln | Ala | Gln | Val | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Glu | Glu | Glu | Asn | Tyr | Gln | Glu | Phe | Pro | Leu | Lys | Arg | Tyr | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

```

Phe Phe Gly His Gly Ile Phe Gly Asp Val Tyr Ser Ala Asp Val Val
 85 90 95
Ala Val Thr Glu Leu Thr Cys Leu Leu Met Ser Asp His Arg Ala
 100 105 110
Leu Leu Glu Ile Lys Ser Val Ser Asp Ser Asp Lys Glu Arg Cys Leu
 115 120 125
Val Glu Asp Ile Leu Tyr Leu Glu Pro Leu Asp Leu Asn Val Tyr Arg
 130 135 140
Gly Phe Thr Pro Pro Asn Ala Pro Thr Tyr Gly Lys Val Tyr Gly Gly
145 150 155 160
Gln Leu Val Gly Gln Ala Leu Ala Ala Ser Lys Thr Val Glu Thr
 165 170 175
Met Lys Ile Val His Asn Phe His Cys Tyr Phe Leu Leu Val Gly Asp
 180 185 190
Ile Asn Ile Pro Ile Ile Tyr Asp Val Asn Arg Leu Arg Asp Gly Asn
 195 200 205
Asn Phe Ala Thr Arg Ser Val Asp Ala Arg Gln Lys Gly Lys Thr Ile
 210 215 220
Phe Thr Leu Phe Ala Ser Phe Gln Lys Lys Gln Gln Gly Phe Ile His
225 230 235 240
Gln Glu Ser Thr Met Pro His Thr Pro Ala Pro Glu Thr Leu Leu Pro
 245 250 255
Arg Glu Glu Met Leu Glu Arg Leu Val Thr Glu Pro Leu Leu Pro Arg
 260 265 270
Asp Tyr Arg Asn Gln Val Ala Thr Glu Ile Ser Val Pro Phe Pro Ile
 275 280 285
Asp Ile Arg Phe Cys Glu Pro Asn Arg Ser Thr Lys Gln Asn Lys Ser
 290 295 300
Pro Pro Arg Leu Lys Tyr Trp Phe Arg Ala Lys Gly Lys Leu Ser Asp
305 310 315 320
Asp Asp Gln Ala Leu His Arg Cys Val Val Ala Phe Ala Ser Asp Leu
 325 330 335
Ile Phe Ala Thr Ile Ser Leu Asn Pro His Arg Arg Glu Gly Met Ser
 340 345 350
Val Ala Ala Leu Ser Leu Asp His Ser Met Trp Phe His Arg Pro Val
 355 360 365
Arg Ala Asp Asp Trp Leu Leu Phe Val
 370 375

```

(2) INFORMATION FOR SEQ ID NO:1949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1571428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

```

Met Ser Asp His Arg Ala Leu Leu Glu Ile Lys Ser Val Ser Asp Ser
1 5 10 15
Asp Lys Glu Arg Cys Leu Val Glu Asp Ile Leu Tyr Leu Glu Pro Leu
 20 25 30
Asp Leu Asn Val Tyr Arg Gly Phe Thr Pro Pro Asn Ala Pro Thr Tyr
 35 40 45
Gly Lys Val Tyr Gly Gly Gln Leu Val Gly Gln Ala Leu Ala Ala Ala
 50 55 60
Ser Lys Thr Val Glu Thr Met Lys Ile Val His Asn Phe His Cys Tyr
 65 70 75 80
Phe Leu Leu Val Gly Asp Ile Asn Ile Pro Ile Ile Tyr Asp Val Asn

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 85  |     | 90  |     | 95  |     |     |     |     |     |     |     |     |     |     |
| Arg | Leu | Arg | Asp | Gly | Asn | Asn | Phe | Ala | Thr | Arg | Ser | Val | Asp | Ala | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Lys | Gly | Lys | Thr | Ile | Phe | Thr | Leu | Phe | Ala | Ser | Phe | Gln | Lys | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Gln | Gly | Phe | Ile | His | Gln | Glu | Ser | Thr | Met | Pro | His | Thr | Pro | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Glu | Thr | Leu | Leu | Pro | Arg | Glu | Glu | Met | Leu | Glu | Arg | Leu | Val | Thr |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Pro | Leu | Leu | Pro | Arg | Asp | Tyr | Arg | Asn | Gln | Val | Ala | Thr | Glu | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Val | Pro | Phe | Pro | Ile | Asp | Ile | Arg | Phe | Cys | Glu | Pro | Asn | Arg | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Lys | Gln | Asn | Lys | Ser | Pro | Pro | Arg | Leu | Lys | Tyr | Trp | Phe | Arg | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Gly | Lys | Leu | Ser | Asp | Asp | Asp | Gln | Ala | Leu | His | Arg | Cys | Val | Val |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Phe | Ala | Ser | Asp | Leu | Ile | Phe | Ala | Thr | Ile | Ser | Leu | Asn | Pro | His |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Arg | Glu | Gly | Met | Ser | Val | Ala | Ala | Leu | Ser | Leu | Asp | His | Ser | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Trp | Phe | His | Arg | Pro | Val | Arg | Ala | Asp | Asp | Trp | Leu | Leu | Phe | Val |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:1950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1974
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| aaaaaagaat | acacagacca | gtcttcgtgt  | gctcgtaatt | ggcgattctc  | aaattcgatc  | 60   |
| tccgtacaaa | caatggccga | aacctcgaag  | caagtcaacg | gcgacgatgc  | ccaggatctt  | 120  |
| cactcgcttc | tttcttctcc | ggcgagggat  | ttctctgttc | gtaatgacgg  | cgaacaggtg  | 180  |
| aaagttgaca | gcttgtagg  | gaagaagatt  | ggattgtatt | tttcagctgc  | ttggtgtgga  | 240  |
| ccgtgtcagc | ggtttactcc | acagctgggtg | gaagtctaca | acgagctctc  | ttcgaaagtt  | 300  |
| ggttttgaga | ttgtgtttgt | gtcaggtgat  | gaggatgaag | agtcatttgg  | agattatttc  | 360  |
| agtaagatgc | cctggctcgc | tgttccgttt  | actgattcgg | aaacccgtga  | ccgtttggat  | 420  |
| gagttgttta | aggttagggg | aatacctaac  | ctagtgatgg | ttgatgatca  | tggtaaactt  | 480  |
| gtgaatgaga | atggtgttgg | ggtcatacga  | agctatggag | ctgatgctta  | tccttttcaca | 540  |
| ccagagaaaa | tgaaggagat | caaagaggat  | gaagatagag | ctcggagaga  | acagacctta  | 600  |
| agatctgtct | tggtgactcc | ttcacgagac  | tttgtgattt | cgctgacgg   | aaacaaggta  | 660  |
| cccgtatcag | agcttgaggg | aaaaaccatt  | ggccttctct | tctctgtggc  | ctcttacagg  | 720  |
| aaatgcacag | agcttactcc | aaagcttggt  | gagttttata | cgaagctgaa  | ggagaataag  | 780  |
| gaggattttg | agattgtggt | gatatctctt  | gaagatgatg | aggagtcttt  | taatcaagac  | 840  |
| ttcaagacca | agccatggct | agcattgccg  | ttcaacgaca | aaagtggatc  | aaaattggct  | 900  |
| cggcatttca | tgctgtcaac | actaccgaca  | ctggtcattc | tgggcctga   | tggaaaaatc  | 960  |
| cgtcactcga | atgtcgcgtg | agctattgat  | gactatggag | ttcttgcgta  | tccttttact  | 1020 |
| ccagagaagt | ttcaagaact | caaggagcta  | gaaaaggcaa | aggtagaggc  | tcaaacgctc  | 1080 |
| gagtcacttc | ttgtctcagg | tgatctcaac  | tacgttctcg | gaaaagatgg  | ggcaaagggtg | 1140 |
| cttggttcgg | atctgggtgg | gaagactatt  | cttatgtact | tctcagctca  | ctggtgtcct  | 1200 |
| ccttgctcgc | cttttacacc | aaagcttggt  | gaagtataca | agcagataaa  | ggagcggaat  | 1260 |
| gaagcgtttg | aattgatctt | catctccagt  | gaccgtgacc | aggaatcatt  | cgatgagtac  | 1320 |
| tattcgcaaa | tgccgtggct | ggctcttcca  | tttggtgatc | ctaggaaagc  | atccttggca  | 1380 |
| aaaaccttta | aggttggtgg | atcccaatgc  | tagcagctct | gggaccaact  | Gggcaaaccg  | 1440 |
| taacaaaaga | agcaagggac | cttgctgtag  | cccatggagc | cgatgcttaC  | Cccctttttac | 1500 |
| tgaggaacgt | ttgaaggaga | ttgaagctaa  | gtacgatgag | atagcaaaaag | attggcctaa  | 1560 |

```
gaaggtgaaa catgttctcc atgaagaaca tgagctagaa ctaactcgtg ttcaggttta 1620
cacatgcgat aagtgtgagg aagaaggac aatatggtga ccattgcgac gaatgcgact 1680
ttgatcttca cgccaagtgt gctttaaacg agtacacaaa agaaaacggc gatgaggctg 1740
tgaaagttgg tggcAgacga gtccaaagat ggttgggttt gtgaaggaaa cgtatgcacc 1800
aaggcctgat aggtagcttc aggcacagtt atgtcactat gtgtatgcaa agctattttcc 1860
tttctttgta taattgctaa tagtgagaat gtgtgggttac aatctgatat ctgattaaga 1920
ccttgagat aaactctgtt aatctaaagt agtaataaaa gaatcttctt attt
```

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1571433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:

```
Lys Lys Glu Tyr Thr Asp Gln Ser Ser Cys Ala Arg Asn Trp Arg Phe
1 5 10 15
Ser Asn Ser Ile Ser Val Gln Thr Met Ala Glu Thr Ser Lys Gln Val
20 25 30
Asn Gly Asp Asp Ala Gln Asp Leu His Ser Leu Leu Ser Ser Pro Ala
35 40 45
Arg Asp Phe Leu Val Arg Asn Asp Gly Glu Gln Val Lys Val Asp Ser
50 55 60
Leu Leu Gly Lys Lys Ile Gly Leu Tyr Phe Ser Ala Ala Trp Cys Gly
65 70 75 80
Pro Cys Gln Arg Phe Thr Pro Gln Leu Val Glu Val Tyr Asn Glu Leu
85 90 95
Ser Ser Lys Val Gly Phe Glu Ile Val Phe Val Ser Gly Asp Glu Asp
100 105 110
Glu Glu Ser Phe Gly Asp Tyr Phe Ser Lys Met Pro Trp Leu Ala Val
115 120 125
Pro Phe Thr Asp Ser Glu Thr Arg Asp Arg Leu Asp Glu Leu Phe Lys
130 135 140
Val Arg Gly Ile Pro Asn Leu Val Met Val Asp Asp His Gly Lys Leu
145 150 155 160
Val Asn Glu Asn Gly Val Gly Val Ile Arg Ser Tyr Gly Ala Asp Ala
165 170 175
Tyr Pro Phe Thr Pro Glu Lys Met Lys Glu Ile Lys Glu Asp Glu Asp
180 185 190
Arg Ala Arg Arg Glu Gln Thr Leu Arg Ser Val Leu Val Thr Pro Ser
195 200 205
Arg Asp Phe Val Ile Ser Pro Asp Gly Asn Lys Val Pro Val Ser Glu
210 215 220
Leu Glu Gly Lys Thr Ile Gly Leu Leu Phe Ser Val Ala Ser Tyr Arg
225 230 235 240
Lys Cys Thr Glu Leu Thr Pro Lys Leu Val Glu Phe Tyr Thr Lys Leu
245 250 255
Lys Glu Asn Lys Glu Asp Phe Glu Ile Val Leu Ile Ser Leu Glu Asp
260 265 270
Asp Glu Glu Ser Phe Asn Gln Asp Phe Lys Thr Lys Pro Trp Leu Ala
275 280 285
Leu Pro Phe Asn Asp Lys Ser Gly Ser Lys Leu Ala Arg His Phe Met
290 295 300
Leu Ser Thr Leu Pro Thr Leu Val Ile Leu Gly Pro Asp Gly Lys Ile
305 310 315 320
Arg His Ser Asn Val Ala Glu Ala Ile Asp Asp Tyr Gly Val Leu Ala
325 330 335
```

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Tyr Pro Phe Thr Pro Glu Lys Phe Gln Glu Leu Lys Glu Leu Glu Lys  
340 345 350  
Ala Lys Val Glu Ala Gln Thr Leu Glu Ser Leu Leu Val Ser Gly Asp  
355 360 365  
Leu Asn Tyr Val Leu Gly Lys Asp Gly Ala Lys Val Leu Val Ser Asp  
370 375 380  
Leu Val Gly Lys Thr Ile Leu Met Tyr Phe Ser Ala His Trp Cys Pro  
385 390 395 400  
Pro Cys Arg Ala Phe Thr Pro Lys Leu Val Glu Val Tyr Lys Gln Ile  
405 410 415  
Lys Glu Arg Asn Glu Ala Phe Glu Leu Ile Phe Ile Ser Ser Asp Arg  
420 425 430  
Asp Gln Glu Ser Phe Asp Glu Tyr Ser Gln Met Pro Trp Leu Ala  
435 440 445  
Leu Pro Phe Gly Asp Pro Arg Lys Ala Ser Leu Ala Lys Thr Phe Lys  
450 455 460  
Val Gly Gly Ser Gln Cys  
465 470

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1571434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

Met Ala Glu Thr Ser Lys Gln Val Asn Gly Asp Asp Ala Gln Asp Leu  
1 5 10 15  
His Ser Leu Leu Ser Ser Pro Ala Arg Asp Phe Leu Val Arg Asn Asp  
20 25 30  
Gly Glu Gln Val Lys Val Asp Ser Leu Leu Gly Lys Lys Ile Gly Leu  
35 40 45  
Tyr Phe Ser Ala Ala Trp Cys Gly Pro Cys Gln Arg Phe Thr Pro Gln  
50 55 60  
Leu Val Glu Val Tyr Asn Glu Leu Ser Ser Lys Val Gly Phe Glu Ile  
65 70 75 80  
Val Phe Val Ser Gly Asp Glu Asp Glu Glu Ser Phe Gly Asp Tyr Phe  
85 90 95  
Ser Lys Met Pro Trp Leu Ala Val Pro Phe Thr Asp Ser Glu Thr Arg  
100 105 110  
Asp Arg Leu Asp Glu Leu Phe Lys Val Arg Gly Ile Pro Asn Leu Val  
115 120 125  
Met Val Asp Asp His Gly Lys Leu Val Asn Glu Asn Gly Val Gly Val  
130 135 140  
Ile Arg Ser Tyr Gly Ala Asp Ala Tyr Pro Phe Thr Pro Glu Lys Met  
145 150 155 160  
Lys Glu Ile Lys Glu Asp Glu Asp Arg Ala Arg Arg Glu Gln Thr Leu  
165 170 175  
Arg Ser Val Leu Val Thr Pro Ser Arg Asp Phe Val Ile Ser Pro Asp  
180 185 190  
Gly Asn Lys Val Pro Val Ser Glu Leu Glu Gly Lys Thr Ile Gly Leu  
195 200 205  
Leu Phe Ser Val Ala Ser Tyr Arg Lys Cys Thr Glu Leu Thr Pro Lys  
210 215 220  
Leu Val Glu Phe Tyr Thr Lys Leu Lys Glu Asn Lys Glu Asp Phe Glu  
225 230 235 240  
Ile Val Leu Ile Ser Leu Glu Asp Asp Glu Glu Ser Phe Asn Gln Asp

SEQUENCE - 1952

245 250 255  
Phe Lys Thr Lys Pro Trp Leu Ala Leu Pro Phe Asn Asp Lys Ser Gly  
260 265 270  
Ser Lys Leu Ala Arg His Phe Met Leu Ser Thr Leu Pro Thr Leu Val  
275 280 285  
Ile Leu Gly Pro Asp Gly Lys Ile Arg His Ser Asn Val Ala Glu Ala  
290 295 300  
Ile Asp Asp Tyr Gly Val Leu Ala Tyr Pro Phe Thr Pro Glu Lys Phe  
305 310 315 320  
Gln Glu Leu Lys Glu Leu Glu Lys Ala Lys Val Glu Ala Gln Thr Leu  
325 330 335  
Glu Ser Leu Leu Val Ser Gly Asp Leu Asn Tyr Val Leu Gly Lys Asp  
340 345 350  
Gly Ala Lys Val Leu Val Ser Asp Leu Val Gly Lys Thr Ile Leu Met  
355 360 365  
Tyr Phe Ser Ala His Trp Cys Pro Pro Cys Arg Ala Phe Thr Pro Lys  
370 375 380  
Leu Val Glu Val Tyr Lys Gln Ile Lys Glu Arg Asn Glu Ala Phe Glu  
385 390 395 400  
Leu Ile Phe Ile Ser Ser Asp Arg Asp Gln Glu Ser Phe Asp Glu Tyr  
405 410 415  
Tyr Ser Gln Met Pro Trp Leu Ala Leu Pro Phe Gly Asp Pro Arg Lys  
420 425 430  
Ala Ser Leu Ala Lys Thr Phe Lys Val Gly Gly Ser Gln Cys  
435 440 445

(2) INFORMATION FOR SEQ ID NO:1953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1571435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:

Met Pro Trp Leu Ala Val Pro Phe Thr Asp Ser Glu Thr Arg Asp Arg  
1 5 10 15  
Leu Asp Glu Leu Phe Lys Val Arg Gly Ile Pro Asn Leu Val Met Val  
20 25 30  
Asp Asp His Gly Lys Leu Val Asn Glu Asn Gly Val Gly Val Ile Arg  
35 40 45  
Ser Tyr Gly Ala Asp Ala Tyr Pro Phe Thr Pro Glu Lys Met Lys Glu  
50 55 60  
Ile Lys Glu Asp Glu Asp Arg Ala Arg Arg Glu Gln Thr Leu Arg Ser  
65 70 75 80  
Val Leu Val Thr Pro Ser Arg Asp Phe Val Ile Ser Pro Asp Gly Asn  
85 90 95  
Lys Val Pro Val Ser Glu Leu Glu Gly Lys Thr Ile Gly Leu Leu Phe  
100 105 110  
Ser Val Ala Ser Tyr Arg Lys Cys Thr Glu Leu Thr Pro Lys Leu Val  
115 120 125  
Glu Phe Tyr Thr Lys Leu Lys Glu Asn Lys Glu Asp Phe Glu Ile Val  
130 135 140  
Leu Ile Ser Leu Glu Asp Glu Glu Ser Phe Asn Gln Asp Phe Lys  
145 150 155 160  
Thr Lys Pro Trp Leu Ala Leu Pro Phe Asn Asp Lys Ser Gly Ser Lys  
165 170 175  
Leu Ala Arg His Phe Met Leu Ser Thr Leu Pro Thr Leu Val Ile Leu  
180 185 190

Gly Pro Asp Gly Lys Ile Arg His Ser Asn Val Ala Glu Ala Ile Asp  
195 200 205  
Asp Tyr Gly Val Leu Ala Tyr Pro Phe Thr Pro Glu Lys Phe Gln Glu  
210 215 220  
Leu Lys Glu Leu Glu Lys Ala Lys Val Glu Ala Gln Thr Leu Glu Ser  
225 230 235 240  
Leu Leu Val Ser Gly Asp Leu Asn Tyr Val Leu Gly Lys Asp Gly Ala  
245 250 255  
Lys Val Leu Val Ser Asp Leu Val Gly Lys Thr Ile Leu Met Tyr Phe  
260 265 270  
Ser Ala His Trp Cys Pro Pro Cys Arg Ala Phe Thr Pro Lys Leu Val  
275 280 285  
Glu Val Tyr Lys Gln Ile Lys Glu Arg Asn Glu Ala Phe Glu Leu Ile  
290 295 300  
Phe Ile Ser Ser Asp Arg Asp Gln Glu Ser Phe Asp Glu Tyr Tyr Ser  
305 310 315 320  
Gln Met Pro Trp Leu Ala Leu Pro Phe Gly Asp Pro Arg Lys Ala Ser  
325 330 335  
Leu Ala Lys Thr Phe Lys Val Gly Gly Ser Gln Cys  
340 345

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| ctctgctaaa  | ttctgtctga | tctaaaaaat | caacgaacac | aaaactcatc  | aaagctcctc | 60   |
| aaaaccctaa  | acacagtctc | tccatcttct | tcaatctctc | tctcgttcgg  | attctcatct | 120  |
| cttcttctgg  | tttcagattg | agtcttggtt | ctgtgtttca | taagactatt  | gaagttaaga | 180  |
| tgtctggagc  | attgaatatg | actcttgatg | agattgttaa | gaggggtaaa  | actgcaaggt | 240  |
| ctgggggaag  | agggatttct | cgtgggcgtg | gtcgtggaag | tggtgggtgt  | ggaagaggag | 300  |
| ctggacctgc  | tagaagaggt | cctcttgctg | gtgaatgctc | gtccatcatc  | tttcaccatt | 360  |
| aacaagcctg  | tccgtaSggt | caggagcttg | ccatggcaaa | gcggtttggt  | tgaagatggc | 420  |
| ctaagagctg  | ccggggcatc | aggagttgaa | ggttgaacca | ggctccatgt  | tacaaatctg | 480  |
| gaccagggtg  | tgacaaatga | agatataagg | gaactcttct | ctgagattgg  | ggaggtagag | 540  |
| cgttatgcca  | ttcattatga | caaaaatggg | cgtccaagtg | gcacagctga  | agtgggtgat | 600  |
| ccaagaagaa  | gtgatgcatt | tcaagctctg | aagaaatata | acaatgtgct  | attggatgga | 660  |
| aggccaatga  | gacttgagat | tttggttggt | aacaattctt | ccgaggctcc  | tttatctggt | 720  |
| cgtgtgaatg  | tgaatgtcac | tggactcaat | ggaaggtctg | agaggacggt  | tggtatccaa | 780  |
| caaggaggag  | gagggagagg | aggaagaggt | ccagctccta | ctgtcagtcg  | ccgccttcca | 840  |
| attcataacc  | agcagggagg | agggatgaga | ggaggaagag | gcgggtttcg  | tgctagaggg | 900  |
| cgtggtaatg  | gtggccgtgg | tcgtggtggt | ggaagaggaa | atggaaagaa  | gccagtggag | 960  |
| aagtacagctg | ctgatcttga | caaagatctt | gagagctatc | acgctgatgc  | catgaacacc | 1020 |
| tcttaaactg  | tggtgtgttg | ttcttactaa | actagtttca | gatgaaatca  | tgcttctctt | 1080 |
| tttttcatgc  | tcttcgttgg | ttttgttgga | tggtgattgt | aaagtaaattg | gaagcctttt | 1140 |

agaatc

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1571441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Met Arg Leu Leu Arg Gly Val Lys Leu Gln Gly Leu Gly Glu Glu Gly  
1 5 10 15  
Phe Leu Val Gly Val Val Val Asp Val Val Val Val Glu Glu Glu Leu  
20 25 30  
Asp Leu Leu Glu Glu Val Leu Leu Leu Val Asn Ala Arg Pro Ser Ser  
35 40 45  
Phe Thr Ile Asn Lys Pro Val Arg Xaa Val Arg Ser Leu Pro Trp Gln  
50 55 60  
Ser Gly Leu Phe Glu Asp Gly Leu Arg Ala Ala Gly Ala Ser Gly Val  
65 70 75 80  
Glu Val Gly Thr Arg Leu His Val Thr Asn Leu Asp Gln Gly Val Thr  
85 90 95  
Asn Glu Asp Ile Arg Glu Leu Phe Ser Glu Ile Gly Glu Val Glu Arg  
100 105 110  
Tyr Ala Ile His Tyr Asp Lys Asn Gly Arg Pro Ser Gly Thr Ala Glu  
115 120 125  
Val Val Tyr Pro Arg Arg Ser Asp Ala Phe Gln Ala Leu Lys Lys Tyr  
130 135 140  
Asn Asn Val Leu Leu Asp Gly Arg Pro Met Arg Leu Glu Ile Leu Gly  
145 150 155 160  
Gly Asn Asn Ser Ser Glu Ala Pro Leu Ser Gly Arg Val Asn Val Asn  
165 170 175  
Val Thr Gly Leu Asn Gly Arg Leu Lys Arg Thr Val Val Ile Gln Gln  
180 185 190  
Gly Gly Gly Gly Arg Gly Gly Arg Gly Pro Ala Pro Thr Val Ser Arg  
195 200 205  
Arg Leu Pro Ile His Asn Gln Gly Gly Gly Met Arg Gly Gly Arg  
210 215 220  
Gly Gly Phe Arg Ala Arg Gly Arg Gly Asn Gly Gly Arg Gly Arg Gly  
225 230 235 240  
Gly Gly Arg Gly Asn Gly Lys Lys Pro Val Glu Lys Ser Ala Ala Asp  
245 250 255  
Leu Asp Lys Asp Leu Glu Ser Tyr His Ala Asp Ala Met Asn Thr Ser  
260 265 270

(2) INFORMATION FOR SEQ ID NO:1956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1569

(D) OTHER INFORMATION: / Ceres Seq. ID 1571445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

aaaaaaacaa aaacagagcc aggaataatg tcagtcttcc tctgtttcct ctgcctctta 60  
ccccttatct taatcttctt gaaaaatctc aaaccatcga aatggaagct tcctccaggc 120  
ccaaagaagc ttccgcatcat cggaactta caccaacgcc gggaattaca tcccaggaac 180  
agtcggaatc tttccgaaaa gtacggacca atcgtgttcc tccgatacgg attcgtcccc 240  
gtggtcgtga tctcgtcaaa agaagcagca gaggaagtcc tcaagaccac gatcttgagt 300  
gttgtagccg accagagacg gttgggacca gagcaatctc ttacaacttt aaagacatcg 360  
gattcgcacc gtgcggtgaa gattggagaa cgatgcggaa gctctcgggtg gtcgagctct 420  
tcagctcgaa aaagcttcaa tctttcaggt atatcagaga ggaagagAAC gacttggtgtg 480  
tcaagaaact ctctgattta gttcagagac gatctttggt gaatcttgag aaaacccttt 540  
ttacttttagt cggaagtata gtgtgtagga taggggttgg gataaatctc cgtgagtgtg 600

(2) INFORMATION FOR SEQ ID NO:1957:

(A) LENGTH: 498 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..498

(D) OTHER INFORMATION: / Ceres Seq. ID 1571446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

|            |           |            |            |            |     |            |            |            |            |            |            |            |     |            |     |
|------------|-----------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|-----|------------|-----|
| Lys<br>1   | Asn       | Lys        | Asn        | Arg<br>5   | Ala | Arg        | Asn        | Asn        | Val<br>10  | Ser        | Leu        | Pro        | Leu | Phe<br>15  | Pro |
| Leu        | Pro       | Leu        | Thr<br>20  | Pro        | Tyr | Leu        | Asn<br>25  | Leu        | Leu        | Glu        | Lys        | Ser<br>30  | Gln | Thr        | Ile |
| Glu        | Met       | Glu<br>35  | Ala        | Ser        | Ser | Arg        | Pro<br>40  | Lys        | Glu        | Ala        | Ser<br>45  | Asp        | His | Arg        | Glu |
| Leu        | Thr<br>50 | Pro        | Thr        | Pro        | Gly | Ile<br>55  | Thr        | Ser        | Gln        | Glu        | Gln<br>60  | Ser        | Glu | Ser        | Phe |
| Arg<br>65  | Lys       | Val        | Arg        | Thr<br>70  | Asn | Arg        | Val        | Ser        | Pro        | Ile<br>75  | Arg        | Ile        | Arg | Pro<br>80  | Arg |
| Gly        | Arg       | Asp        | Leu<br>85  | Val        | Lys | Arg        | Ser        | Ser        | Arg<br>90  | Gly        | Ser        | Ser        | Gln | Asp<br>95  | His |
| Asp        | Leu       | Glu        | Cys<br>100 | Cys        | Ser | Arg        | Pro        | Glu<br>105 | Thr        | Val        | Gly        | Thr<br>110 | Arg | Ala        | Ile |
| Ser        | Tyr       | Asn<br>115 | Phe        | Lys        | Asp | Ile        | Gly<br>120 | Phe        | Ala        | Pro        | Cys        | Gly<br>125 | Glu | Asp        | Trp |
| Arg<br>130 | Thr       | Met        | Arg        | Lys        | Leu | Ser<br>135 | Val        | Val        | Glu        | Leu        | Phe<br>140 | Ser        | Ser | Lys        | Lys |
| Leu<br>145 | Gln       | Ser        | Phe        | Arg<br>150 | Tyr | Ile        | Arg        | Glu        | Glu        | Glu<br>155 | Asn        | Asp        | Leu | Cys<br>160 | Val |
| Lys        | Lys       | Leu        | Ser<br>165 | Asp        | Leu | Ala        | Ser        | Arg<br>170 | Ser        | Leu        | Val        | Asn<br>175 | Leu | Glu        |     |
| Lys        | Thr       | Leu<br>180 | Phe        | Thr        | Leu | Val        | Gly<br>185 | Ser        | Ile        | Val        | Cys        | Arg<br>190 | Ile | Gly        | Phe |
| Gly        | Ile       | Asn<br>195 | Leu        | Arg        | Glu | Cys        | Glu<br>200 | Phe        | Val        | Asp        | Glu        | Asp<br>205 | Ser | Ile        | Asp |
| Asp<br>210 | Leu       | Val        | His        | Lys        | Ser | Glu<br>215 | Asp        | Val        | Ile        | Arg        | Asn<br>220 | Ser        | Ile | Phe        | Ser |
| Asp<br>225 | Phe       | Phe        | Pro        | Gly<br>230 | Leu | Met        | Gly        | Arg        | Leu        | Ile<br>235 | Glu        | Trp        | Ile | Phe        | Ser |
| Glu        | Arg       | Lys        | Arg<br>245 | Leu        | Asn | Arg        | Leu        | Tyr        | Ser<br>250 | Glu        | Val        | Asp        | Thr | Phe<br>255 | Phe |

|      | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |      |

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Gln Asn Ile Leu Asp Asp His Leu Lys Pro Gly Arg Glu Ser Ser Asp
 260 265 270
Ile Ile Asp Val Met Ile Asp Met Lys Lys Gln Glu Lys Glu Gly
 275 280 285
Asp Ser Phe Lys Phe Thr Thr Asp His Leu Lys Gly Met Ile Ser Asp
 290 295 300
Ile Phe Leu Ala Gly Val Gly Thr Ser Ser Thr Thr Leu Ile Trp Ala
305 310 315 320
Met Thr Glu Leu Ile Arg Asn Pro Arg Val Met Lys Lys Val Gln Asp
 325 330 335
Glu Ile Arg Thr Thr Leu Gly Asp Lys Lys Glu Arg Ile Thr Glu Glu
 340 345 350
Asp Leu Asn Gln Leu His Tyr Phe Lys Leu Met Val Lys Glu Ile Phe
 355 360 365
Arg Leu His Pro Ala Ala Pro Leu Leu Leu Pro Arg Glu Thr Leu Ser
 370 375 380
His Val Lys Ile Gln Gly Tyr Asp Ile Pro Ala Lys Thr Gln Ile Met
385 390 395 400
Ile Asn Ala Tyr Ala Ile Ala Arg Asp Pro Lys Leu Trp Thr Asn Pro
 405 410 415
Asp Glu Phe Asn Pro Asp Arg Phe Leu Asp Ser Ser Ile Asp Tyr Arg
 420 425 430
Gly Leu Asn Phe Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys
 435 440 445
Pro Gly Met Thr Met Gly Ile Ala Ile Val Glu Leu Gly Leu Leu Asn
 450 455 460
Leu Leu Tyr Phe Phe Asp Trp Gly Leu Pro Glu Lys Glu Glu Ala Lys
465 470 475 480
Glu Ile Ile Thr Gly Asn Glu Val Ala Leu Asp Leu Val Gln Val Phe
 485 490 495
Leu His

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(2) INFORMATION FOR SEQ ID NO:1958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1571447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

```

Met Glu Ala Ser Ser Arg Pro Lys Glu Ala Ser Asp His Arg Glu Leu
1 5 10 15
Thr Pro Thr Pro Gly Ile Thr Ser Gln Glu Gln Ser Glu Ser Phe Arg
 20 25 30
Lys Val Arg Thr Asn Arg Val Ser Pro Ile Arg Ile Arg Pro Arg Gly
 35 40 45
Arg Asp Leu Val Lys Arg Ser Ser Arg Gly Ser Ser Gln Asp His Asp
 50 55 60
Leu Glu Cys Cys Ser Arg Pro Glu Thr Val Gly Thr Arg Ala Ile Ser
 65 70 75 80
Tyr Asn Phe Lys Asp Ile Gly Phe Ala Pro Cys Gly Glu Asp Trp Arg
 85 90 95
Thr Met Arg Lys Leu Ser Val Val Glu Leu Phe Ser Ser Lys Lys Leu
 100 105 110
Gln Ser Phe Arg Tyr Ile Arg Glu Glu Glu Asn Asp Leu Cys Val Lys
 115 120 125
Lys Leu Ser Asp Leu Ala Ser Arg Arg Ser Leu Val Asn Leu Glu Lys

```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Thr Leu Phe Thr Leu Val Gly Ser Ile Val Cys Arg Ile Gly Phe Gly |     |     |
| 145                                                             | 150 | 155 |
| Ile Asn Leu Arg Glu Cys Glu Phe Val Asp Glu Asp Ser Ile Asp Asp |     | 160 |
|                                                                 | 165 | 170 |
| Leu Val His Lys Ser Glu Asp Val Ile Arg Asn Ser Ile Phe Ser Asp |     | 175 |
|                                                                 | 180 | 185 |
| Phe Phe Pro Gly Leu Met Gly Arg Leu Ile Glu Trp Ile Phe Ser Glu |     | 190 |
|                                                                 | 195 | 200 |
| Arg Lys Arg Leu Asn Arg Leu Tyr Ser Glu Val Asp Thr Phe Phe Gln |     | 205 |
| 210                                                             | 215 | 220 |
| Asn Ile Leu Asp Asp His Leu Lys Pro Gly Arg Glu Ser Ser Asp Ile |     | 225 |
| 225                                                             | 230 | 235 |
| Ile Asp Val Met Ile Asp Met Met Lys Lys Gln Glu Lys Glu Gly Asp |     | 240 |
|                                                                 | 245 | 250 |
| Ser Phe Lys Phe Thr Thr Asp His Leu Lys Gly Met Ile Ser Asp Ile |     | 255 |
|                                                                 | 260 | 265 |
| Phe Leu Ala Gly Val Gly Thr Ser Ser Thr Thr Leu Ile Trp Ala Met |     | 270 |
|                                                                 | 275 | 280 |
| Thr Glu Leu Ile Arg Asn Pro Arg Val Met Lys Lys Val Gln Asp Glu |     | 285 |
| 290                                                             | 295 | 300 |
| Ile Arg Thr Thr Leu Gly Asp Lys Lys Glu Arg Ile Thr Glu Glu Asp |     | 305 |
| 305                                                             | 310 | 315 |
| Leu Asn Gln Leu His Tyr Phe Lys Leu Met Val Lys Glu Ile Phe Arg |     | 320 |
|                                                                 | 325 | 330 |
| Leu His Pro Ala Ala Pro Leu Leu Leu Pro Arg Glu Thr Leu Ser His |     | 335 |
|                                                                 | 340 | 345 |
| Val Lys Ile Gln Gly Tyr Asp Ile Pro Ala Lys Thr Gln Ile Met Ile |     | 350 |
|                                                                 | 355 | 360 |
| Asn Ala Tyr Ala Ile Ala Arg Asp Pro Lys Leu Trp Thr Asn Pro Asp |     | 365 |
| 370                                                             | 375 | 380 |
| Glu Phe Asn Pro Asp Arg Phe Leu Asp Ser Ser Ile Asp Tyr Arg Gly |     | 385 |
| 385                                                             | 390 | 395 |
| Leu Asn Phe Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro |     | 400 |
|                                                                 | 405 | 410 |
| Gly Met Thr Met Gly Ile Ala Ile Val Glu Leu Gly Leu Leu Asn Leu |     | 415 |
|                                                                 | 420 | 425 |
| Leu Tyr Phe Phe Asp Trp Gly Leu Pro Glu Lys Glu Glu Ala Lys Glu |     | 430 |
|                                                                 | 435 | 440 |
| Ile Ile Thr Gly Asn Glu Val Ala Leu Asp Leu Val Gln Val Phe Leu |     | 445 |
| 450                                                             | 455 | 460 |
| His                                                             |     |     |
| 465                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:1959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1571448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Arg Lys Leu Ser Val Val Glu Leu Phe Ser Ser Lys Lys Leu Gln |    |    |
| 1                                                               | 5  | 10 |
| Ser Phe Arg Tyr Ile Arg Glu Glu Glu Asn Asp Leu Cys Val Lys Lys |    | 15 |
|                                                                 | 20 | 25 |
| Leu Ser Asp Leu Ala Ser Arg Arg Ser Leu Val Asn Leu Glu Lys Thr |    | 30 |
|                                                                 | 35 | 40 |
|                                                                 |    | 45 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Thr | Leu | Val | Gly | Ser | Ile | Val | Cys | Arg | Ile | Gly | Phe | Gly | Ile |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Arg | Glu | Cys | Glu | Phe | Val | Asp | Glu | Asp | Ser | Ile | Asp | Asp | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | His | Lys | Ser | Glu | Asp | Val | Ile | Arg | Asn | Ser | Ile | Phe | Ser | Asp | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Pro | Gly | Leu | Met | Gly | Arg | Leu | Ile | Glu | Trp | Ile | Phe | Ser | Glu | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Lys | Arg | Leu | Asn | Arg | Leu | Tyr | Ser | Glu | Val | Asp | Thr | Phe | Phe | Gln | Asn |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Ile | Leu | Asp | Asp | His | Leu | Lys | Pro | Gly | Arg | Glu | Ser | Ser | Asp | Ile | Ile |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Asp | Val | Met | Ile | Asp | Met | Lys | Lys | Gln | Glu | Lys | Glu | Gly | Asp | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Phe | Lys | Phe | Thr | Thr | Asp | His | Leu | Lys | Gly | Met | Ile | Ser | Asp | Ile | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ala | Gly | Val | Gly | Thr | Ser | Ser | Thr | Thr | Leu | Ile | Trp | Ala | Met | Thr |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Glu | Leu | Ile | Arg | Asn | Pro | Arg | Val | Met | Lys | Lys | Val | Gln | Asp | Glu | Ile |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Arg | Thr | Thr | Leu | Gly | Asp | Lys | Lys | Glu | Arg | Ile | Thr | Glu | Glu | Asp | Leu |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |
| Asn | Gln | Leu | His | Tyr | Phe | Lys | Leu | Met | Val | Lys | Glu | Ile | Phe | Arg | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Pro | Ala | Ala | Pro | Leu | Leu | Leu | Pro | Arg | Glu | Thr | Leu | Ser | His | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Ile | Gln | Gly | Tyr | Asp | Ile | Pro | Ala | Lys | Thr | Gln | Ile | Met | Ile | Asn |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ala | Tyr | Ala | Ile | Ala | Arg | Asp | Pro | Lys | Leu | Trp | Thr | Asn | Pro | Asp | Glu |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |
| Phe | Asn | Pro | Asp | Arg | Phe | Leu | Asp | Ser | Ser | Ile | Asp | Tyr | Arg | Gly | Leu |
|     |     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Asn | Phe | Glu | Leu | Leu | Pro | Phe | Gly | Ser | Gly | Arg | Arg | Ile | Cys | Pro | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Met | Thr | Met | Gly | Ile | Ala | Ile | Val | Glu | Leu | Gly | Leu | Leu | Asn | Leu | Leu |
|     |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |
| Tyr | Phe | Phe | Asp | Trp | Gly | Leu | Pro | Glu | Lys | Glu | Glu | Ala | Lys | Glu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Thr | Gly | Asn | Glu | Val | Ala | Leu | Asp | Leu | Val | Gln | Val | Phe | Leu | His |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| attttttcttc | ttctcttcaa | tttacagttc | tctgcacott | ttactttccc | ctgttttttg | 60  |
| atcctcaatc  | accaaaccct | agcttggttc | tctgttgatt | atttcgaaaa | gggggtttgt | 120 |
| ttgttttctg  | ggaatcagca | aaaatcacga | aatgggtggc | ttaatatctc | aatcgggata | 180 |
| aaatcgatcg  | aaaatgagtc | agccttctgt | gattcttgct | acggctagct | atgatcacac | 240 |
| catccgattc  | tgggaagccg | aamctggtcg | ctgttaccgt | accattcagt | atcctgattc | 300 |
| gcatgtaaat  | aggcttgaga | taaccccaga | taagcattat | ctagctgcag | cttgcaatcc | 360 |
| tcatattcga  | ctctttgatg | tcaattccaa | tagtcctcaa | cctgtgatga | cttacgattc | 420 |



acacaccaac aatgttatgg cagtaggatt tcaatgtgat gcaaaatgga tgtattcagg 480  
atcagaagat ggcacagtta agatctggga ctttaagggct ccgggttgcc aaaaggagta 540  
tgaaagtgtt gcagcggtta atacagttgt tttacaccca aatcagactg aattgatatc 600  
tggagaccaa aatggaaata tacgtgtatg ggatctcaga gcaaattcgt gtagctgtga 660  
actgggtacca gaagttgata cagctgtacg gtctttaact gttatgtggg atgggacaat 720  
ggtagtcgct gctaacaacc gtggCaacat gttatgtatg gcgcttggtg cgtggghaaac 780  
agacaatgac agagtttgag ccccttcata agctgcaagc tcataatggc cacatcctta 840  
aatgtctcct ctctcctgca aacaaatatc tagcgactgc atcatctgat aaaactgtca 900  
aaatatggaa cgtcgatggt ttcaaactag agaaagtttt aacaggacat caaagatggg 960  
tttGggactg cgtcttctca gtggatggag aatttcttgt aacagcatca tcggacatga 1020  
cggctagatt gtggctgatg ccagcaggca aagaagtga agtataccaa ggcatcaca 1080  
aagccactgt gtgctgtgca ctccacgact aaaaccttaa taagaatgaa agctaaatta 1140  
tgaacaaact acgattgtgt tatttgtgtt ttagtaaact cttgtacatt tcaatcgaat 1200  
tcgttcaaat tgctcttatg t

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1571461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Pro | Ser | Val | Ile | Leu | Ala | Thr | Ala | Ser | Tyr | Asp | His | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Arg | Phe | Trp | Glu | Ala | Glu | Xaa | Gly | Arg | Cys | Tyr | Arg | Thr | Ile | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Pro | Asp | Ser | His | Val | Asn | Arg | Leu | Glu | Ile | Thr | Pro | Asp | Lys | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Tyr | Leu | Ala | Ala | Ala | Cys | Asn | Pro | His | Ile | Arg | Leu | Phe | Asp | Val | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |
| Ser | Asn | Ser | Pro | Gln | Pro | Val | Met | Thr | Tyr | Asp | Ser | His | Thr | Asn | Asn |
|     |     |     |     |     |     |     | 70  |     |     |     |     |     | 75  |     | 80  |
| Val | Met | Ala | Val | Gly | Phe | Gln | Cys | Asp | Ala | Lys | Trp | Met | Tyr | Ser | Gly |
|     |     |     |     |     |     |     | 85  |     |     |     |     |     | 90  |     | 95  |
| Ser | Glu | Asp | Gly | Thr | Val | Lys | Ile | Trp | Asp | Leu | Arg | Ala | Pro | Gly | Cys |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 100 |     |     |
| Gln | Lys | Glu | Tyr | Glu | Ser | Val | Ala | Ala | Val | Asn | Thr | Val | Val | Leu | His |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 105 |     |     |
| Pro | Asn | Gln | Thr | Glu | Leu | Ile | Ser | Gly | Asp | Gln | Asn | Gly | Asn | Ile | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |     |
| Val | Trp | Asp | Leu | Arg | Ala | Asn | Ser | Cys | Ser | Cys | Glu | Leu | Val | Pro | Glu |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 115 |     |     |
| Val | Asp | Thr | Ala | Val | Arg | Ser | Leu | Thr | Val | Met | Trp | Asp | Gly | Thr | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 120 |     |     |
| Val | Val | Ala | Ala | Asn | Asn | Arg | Gly | Asn | Met | Leu | Cys | Met | Ala | Leu | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |     |     |
| Ala | Trp | Xaa | Thr | Asp | Asn | Asp | Arg | Val |     |     |     |     | 130 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     | 135 |     |     |

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1571462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

```
Met Thr Tyr Asp Ser His Thr Asn Asn Val Met Ala Val Gly Phe Gln
1 5 10 15
Cys Asp Ala Lys Trp Met Tyr Ser Gly Ser Glu Asp Gly Thr Val Lys
 20 25 30
Ile Trp Asp Leu Arg Ala Pro Gly Cys Gln Lys Glu Tyr Glu Ser Val
 35 40 45
Ala Ala Val Asn Thr Val Val Leu His Pro Asn Gln Thr Glu Leu Ile
 50 55 60
Ser Gly Asp Gln Asn Gly Asn Ile Arg Val Trp Asp Leu Arg Ala Asn
 65 70 75 80
Ser Cys Ser Cys Glu Leu Val Pro Glu Val Asp Thr Ala Val Arg Ser
 85 90 95
Leu Thr Val Met Trp Asp Gly Thr Met Val Val Ala Ala Asn Asn Arg
 100 105 110
Gly Asn Met Leu Cys Met Ala Leu Val Ala Trp Xaa Thr Asp Asn Asp
 115 120 125
Arg Val
130
```

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1571463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

```
Met Ala Val Gly Phe Gln Cys Asp Ala Lys Trp Met Tyr Ser Gly Ser
1 5 10 15
Glu Asp Gly Thr Val Lys Ile Trp Asp Leu Arg Ala Pro Gly Cys Gln
 20 25 30
Lys Glu Tyr Glu Ser Val Ala Ala Val Asn Thr Val Val Leu His Pro
 35 40 45
Asn Gln Thr Glu Leu Ile Ser Gly Asp Gln Asn Gly Asn Ile Arg Val
 50 55 60
Trp Asp Leu Arg Ala Asn Ser Cys Ser Cys Glu Leu Val Pro Glu Val
 65 70 75 80
Asp Thr Ala Val Arg Ser Leu Thr Val Met Trp Asp Gly Thr Met Val
 85 90 95
Val Ala Ala Asn Asn Arg Gly Asn Met Leu Cys Met Ala Leu Val Ala
 100 105 110
Trp Xaa Thr Asp Asn Asp Arg Val
 115 120
```

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1636

(D) OTHER INFORMATION: / Ceres Seq. ID 1571464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| acttcctttt  | gttccccaaa  | ttctcgaaat  | cgaaacacga | cttaaaacga  | aaaagacgag  | 60   |
| acttttaaca  | ctcagaccta  | aaccaacact  | cttcctcttt | ctatctctct  | ctcgccgatc  | 120  |
| ggaagcagat  | ttttctcaaa  | aggatggatt  | caacgaagct | tagtgagcta  | aaggtcttca  | 180  |
| tcgatcaatg  | caagtctgac  | ccttcccttc  | tcactactcc | ttcactctcc  | ttcttccgtg  | 240  |
| actatctcga  | gagtccttgg  | gctaagatac  | ctactggtgt | ccatgaagaa  | gacaaagaca  | 300  |
| ctaagccgag  | gagtttctgt  | gtggaagaga  | gtgatgatga | tatggatgaa  | actgaagaag  | 360  |
| taaaaccgaa  | agtggaggaa  | gaagaagaag  | aggatgagat | tggtgaatct  | gatgtagagc  | 420  |
| ttgaaggaga  | cactgttgag  | cctgataatg  | atcctcctca | gaagatgggg  | gattcatcag  | 480  |
| tggaggtgac  | tgatgagaat  | cgtgaagctg  | ctcaagaagc | taagggcaaa  | gcCatggagg  | 540  |
| ccctttctga  | aggaaacttt  | gatgaagcaa  | ttgagcattt | aactcgggca  | ataacgttga  | 600  |
| acccgacttc  | agctattatg  | tatggaaaca  | gagctagtgt | ctacattaag  | ttgaagaagc  | 660  |
| caaacgctgc  | tattcgagat  | gcaaacgcag  | cattggagat | taaccctgat  | tctgccaagg  | 720  |
| gatacaagtc  | acgaggtatg  | gctcgtgcc   | tgcttgagag | atgggcagag  | gctgcaaaaag | 780  |
| accttcacct  | tgcactctacg | atagactatg  | atgaggaaat | tagtgctgtt  | ctcaaaaagg  | 840  |
| ttgaacctaa  | tgcacataag  | cttggaggagc | accgtagaaa | gtatgacaga  | ttacgtaagg  | 900  |
| aaagagagga  | caaaaaggct  | gaacgggata  | gattacgtcg | ccgtgctgaa  | gcacaggctg  | 960  |
| cctatgataa  | agctaagaaa  | gaagaacagt  | catcatctag | cagaccatca  | ggaggcgggt  | 1020 |
| tcccaggagg  | tatgcccggt  | ggtttcccg   | gaggtatgcc | cggtggaattc | ccaggaggaa  | 1080 |
| tgggaggcat  | gcccggcgga  | ttcccgggag  | gaatgggtgg | tatggcggtg  | atgcccggtg  | 1140 |
| gattcccagg  | aggaatgggc  | ggtggtatgc  | ctgcaggaa  | gggcggtggt  | atgcccgga   | 1200 |
| tgggcggtgg  | tatgcctgct  | ggaatgggtg  | gtggcggtat | gccagtgca   | ggcggtggtg  | 1260 |
| tgcoctggtg  | tggcggtatg  | cctggtggta  | tggacttcag | caaaatattg  | aatgatcctg  | 1320 |
| agctaattgac | ggcatttagc  | gaccctgaag  | tcattgctgc | tcttcaagat  | gtgatgaaga  | 1380 |
| accctgcgaa  | tctagcgaag  | catcaggcga  | atccgaaggt | ggctcccgtg  | attgcaaaga  | 1440 |
| tgatgggcaa  | atttgcagga  | cctcagtaaa  | caaaacaaga | agcttgcttt  | tctttgccaa  | 1500 |
| tttctgtgtt  | taattgcgtg  | agataagaga  | tatgttgag  | aacttttgtt  | ttcttttatg  | 1560 |
| ttgtcgttgc  | agaggaactt  | taacaggaac  | aaaactcttt | tctcttcggt  | agtaatctac  | 1620 |
| cctcttctcg  | tttttc      |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..441
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Thr | Lys | Leu | Ser | Glu | Leu | Lys | Val | Phe | Ile | Asp | Gln | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Asp | Pro | Ser | Leu | Leu | Thr | Thr | Pro | Ser | Leu | Ser | Phe | Phe | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Tyr | Leu | Glu | Ser | Leu | Gly | Ala | Lys | Ile | Pro | Thr | Gly | Val | His | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Asp | Lys | Asp | Thr | Lys | Pro | Arg | Ser | Phe | Val | Val | Glu | Glu | Ser | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Asp | Met | Asp | Glu | Thr | Glu | Glu | Val | Lys | Pro | Lys | Val | Glu | Glu | Glu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Glu | Glu | Glu | Asp | Glu | Ile | Val | Glu | Ser | Asp | Val | Glu | Leu | Glu | Gly | Asp |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Thr | Val | Glu | Pro | Asp | Asn | Asp | Pro | Pro | Gln | Lys | Met | Gly | Asp | Ser | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Glu | Val | Thr | Asp | Glu | Asn | Arg | Glu | Ala | Ala | Gln | Glu | Ala | Lys | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Lys | Ala | Met | Glu | Ala | Leu | Ser | Glu | Gly | Asn | Phe | Asp | Glu | Ala | Ile | Glu |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| His | Leu | Thr | Arg | Ala | Ile | Thr | Leu | Asn | Pro | Thr | Ser | Ala | Ile | Met | Tyr |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |     |
| Gly | Asn | Arg | Ala | Ser | Val | Tyr | Ile | Lys | Leu | Lys | Lys | Pro | Asn | Ala | Ala |

(2) INFORMATION FOR SEQ ID NO:1966:

(A) LENGTH: 375 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1571466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Glu | Thr | Glu | Glu | Val | Lys | Pro | Lys | Val | Glu | Glu | Glu | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Glu | Ile | Val | Glu | Ser | Asp | Val | Glu | Leu | Glu | Gly | Asp | Thr | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Pro | Asp | Asn | Asp | Pro | Pro | Gln | Lys | Met | Gly | Asp | Ser | Ser | Val | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Thr | Asp | Glu | Asn | Arg | Glu | Ala | Ala | Gln | Glu | Ala | Lys | Gly | Lys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Glu | Ala | Leu | Ser | Glu | Gly | Asn | Phe | Asp | Glu | Ala | Ile | Glu | His | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Arg | Ala | Ile | Thr | Leu | Asn | Pro | Thr | Ser | Ala | Ile | Met | Tyr | Gly | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Ala | Ser | Val | Tyr | Ile | Lys | Leu | Lys | Lys | Pro | Asn | Ala | Ala | Ile | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

```

Asp Ala Asn Ala Ala Leu Glu Ile Asn Pro Asp Ser Ala Lys Gly Tyr
 115 120 125
Lys Ser Arg Gly Met Ala Arg Ala Met Leu Gly Glu Trp Ala Glu Ala
 130 135 140
Ala Lys Asp Leu His Leu Ala Ser Thr Ile Asp Tyr Asp Glu Glu Ile
 145 150 155 160
Ser Ala Val Leu Lys Lys Val Glu Pro Asn Ala His Lys Leu Glu Glu
 165 170 175
His Arg Arg Lys Tyr Asp Arg Leu Arg Lys Glu Arg Glu Asp Lys Lys
 180 185 190
Ala Glu Arg Asp Arg Leu Arg Arg Arg Ala Glu Ala Gln Ala Ala Tyr
 195 200 205
Asp Lys Ala Lys Lys Glu Glu Gln Ser Ser Ser Ser Arg Pro Ser Gly
 210 215 220
Gly Gly Phe Pro Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met Pro
 225 230 235 240
Gly Gly Phe Pro Gly Gly Met Gly Gly Met Pro Gly Gly Phe Pro Gly
 245 250 255
Gly Met Gly Gly Met Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met
 260 265 270
Gly Gly Gly Met Pro Ala Gly Met Gly Gly Gly Met Pro Gly Met Gly
 275 280 285
Gly Gly Met Pro Ala Gly Met Gly Gly Gly Gly Met Pro Gly Ala Gly
 290 295 300
Gly Gly Met Pro Gly Gly Gly Gly Met Pro Gly Gly Met Asp Phe Ser
 305 310 315 320
Lys Ile Leu Asn Asp Pro Glu Leu Met Thr Ala Phe Ser Asp Pro Glu
 325 330 335
Val Met Ala Ala Leu Gln Asp Val Met Lys Asn Pro Ala Asn Leu Ala
 340 345 350
Lys His Gln Ala Asn Pro Lys Val Ala Pro Val Ile Ala Lys Met Met
 355 360 365
Gly Lys Phe Ala Gly Pro Gln
 370 375

```

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

```

Met Gly Asp Ser Ser Val Glu Val Thr Asp Glu Asn Arg Glu Ala Ala
1 5 10 15
Gln Glu Ala Lys Gly Lys Ala Met Glu Ala Leu Ser Glu Gly Asn Phe
 20 25 30
Asp Glu Ala Ile Glu His Leu Thr Arg Ala Ile Thr Leu Asn Pro Thr
 35 40 45
Ser Ala Ile Met Tyr Gly Asn Arg Ala Ser Val Tyr Ile Lys Leu Lys
 50 55 60
Lys Pro Asn Ala Ala Ile Arg Asp Ala Asn Ala Leu Glu Ile Asn
 65 70 75 80
Pro Asp Ser Ala Lys Gly Tyr Lys Ser Arg Gly Met Ala Arg Ala Met
 85 90 95
Leu Gly Glu Trp Ala Glu Ala Ala Lys Asp Leu His Leu Ala Ser Thr
 100 105 110
Ile Asp Tyr Asp Glu Glu Ile Ser Ala Val Leu Lys Lys Val Glu Pro

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115 120 125  
Asn Ala His Lys Leu Glu Glu His Arg Arg Lys Tyr Asp Arg Leu Arg  
130 135 140  
Lys Glu Arg Glu Asp Lys Lys Ala Glu Arg Asp Arg Leu Arg Arg Arg  
145 150 155 160  
Ala Glu Ala Gln Ala Ala Tyr Asp Lys Ala Lys Lys Glu Glu Gln Ser  
165 170 175  
Ser Ser Ser Arg Pro Ser Gly Gly Gly Phe Pro Gly Gly Met Pro Gly  
180 185 190  
Gly Phe Pro Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met Gly Gly  
195 200 205  
Met Pro Gly Gly Phe Pro Gly Gly Met Gly Gly Met Gly Gly Met Pro  
210 215 220  
Gly Gly Phe Pro Gly Gly Met Gly Gly Gly Met Pro Ala Gly Met Gly  
225 230 235 240  
Gly Gly Met Pro Gly Met Gly Gly Gly Met Pro Ala Gly Met Gly Gly  
245 250 255  
Gly Gly Met Pro Gly Ala Gly Gly Gly Met Pro Gly Gly Gly Gly Met  
260 265 270  
Pro Gly Gly Met Asp Phe Ser Lys Ile Leu Asn Asp Pro Glu Leu Met  
275 280 285  
Thr Ala Phe Ser Asp Pro Glu Val Met Ala Ala Leu Gln Asp Val Met  
290 295 300  
Lys Asn Pro Ala Asn Leu Ala Lys His Gln Ala Asn Pro Lys Val Ala  
305 310 315 320  
Pro Val Ile Ala Lys Met Met Gly Lys Phe Ala Gly Pro Gln  
325 330

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acattcctca ccaaaccctc tccaaaacac acccacacgt acgcacacac acaaagacaa  | 60   |
| tgtctccttt caaaatattc ttcttcacga ctcttctcgt ggccggcggtt tcagtgtcgg | 120  |
| ctgctgattt caacactgac gtcaacgtag cttggggaaa tggccgtggg aagatactca  | 180  |
| acaacggcca gtttcttact ctctccttag acaaatcctc tggttccggt tttcaatcca  | 240  |
| aaacagagta tttgtttgga aagattgata tgcagattaa gcttggttct ggtaactctg  | 300  |
| caggaacagt cacaactttt tacgtgagtt tatatatattw ctttaggagt tttaagtgat | 360  |
| tttgatttg gtttttatat tgagacttca tcttgacatt tttgtgtatt tgcagctaaa   | 420  |
| atccgaagga tccacttggg atgagattga ttttgagttc ttgggtaata tgagtggaga  | 480  |
| tccttatact ttacacacta atgtttacac tcaaggtaaa ggtgacaaag agcaacaatt  | 540  |
| ccatctcttg ttcgacccaa ccgccaattt ccacacttac tcaatcctct ggaaccctca  | 600  |
| aagaatcata ttgaccgtcg atgacacacc cattagagag tttaaaaact atgagtctct  | 660  |
| cggtgtcttg tttccaaaga acaagccgat gaggatgtac gcgagtttat ggaacgcaga  | 720  |
| cgattgggca acaagaggcg gtcttggttaa aactgattgg tctaaagctc cattcatggc | 780  |
| ttcttacaga aacattaaga ttgactcgaa accaaactcc aattggtaca ctcaagaaat  | 840  |
| ggattcaaca agccaagcta gactcaaatt gggttcagaag aattacatga tctacaatta | 900  |
| ttgtactgac cataggaggt ttccacaggg agctoctaag gaatgcacaa caagtcata   | 960  |
| gaatctcaaa ttatatctta tttattttat tacacttctt ctcttttctt tatgtgaaaa  | 1020 |
| ttgtgaatgc tctgttttct gcttgcttat tatgtccgag aattttcttt tctgtttttg  | 1080 |
| attcttttctg ttgtakatct ttgTccarta aaggaaatga tgtgtcttta cc         |      |

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..118
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571469
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

Ile Pro His Gln Thr Leu Ser Lys Thr His Pro His Val Arg Thr His  
1 5 10 15  
Thr Lys Thr Met Ser Pro Phe Lys Ile Phe Phe Phe Thr Thr Leu Leu  
20 25 30  
Val Ala Ala Phe Ser Val Ser Ala Ala Asp Phe Asn Thr Asp Val Asn  
35 40 45  
Val Ala Trp Gly Asn Gly Arg Gly Lys Ile Leu Asn Asn Gly Gln Leu  
50 55 60  
Leu Thr Leu Ser Leu Asp Lys Ser Ser Gly Ser Gly Phe Gln Ser Lys  
65 70 75 80  
Thr Glu Tyr Leu Phe Gly Lys Ile Asp Met Gln Ile Lys Leu Val Pro  
85 90 95  
Gly Asn Ser Ala Gly Thr Val Thr Thr Phe Tyr Val Ser Leu Tyr Ile  
100 105 110  
Xaa Phe Arg Ser Phe Lys  
115

(2) INFORMATION FOR SEQ ID NO:1970:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..99
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571470
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

Met Ser Pro Phe Lys Ile Phe Phe Phe Thr Thr Leu Leu Val Ala Ala  
1 5 10 15  
Phe Ser Val Ser Ala Ala Asp Phe Asn Thr Asp Val Asn Val Ala Trp  
20 25 30  
Gly Asn Gly Arg Gly Lys Ile Leu Asn Asn Gly Gln Leu Leu Thr Leu  
35 40 45  
Ser Leu Asp Lys Ser Ser Gly Ser Gly Phe Gln Ser Lys Thr Glu Tyr  
50 55 60  
Leu Phe Gly Lys Ile Asp Met Gln Ile Lys Leu Val Pro Gly Asn Ser  
65 70 75 80  
Ala Gly Thr Val Thr Thr Phe Tyr Val Ser Leu Tyr Ile Xaa Phe Arg  
85 90 95  
Ser Phe Lys

(2) INFORMATION FOR SEQ ID NO:1971:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 163 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1571471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

Met Ser Gly Asp Pro Tyr Thr Leu His Thr Asn Val Tyr Thr Gln Gly  
1 5 10 15  
Lys Gly Asp Lys Glu Gln Gln Phe His Leu Trp Phe Asp Pro Thr Ala  
20 25 30  
Asn Phe His Thr Tyr Ser Ile Leu Trp Asn Pro Gln Arg Ile Ile Leu  
35 40 45  
Thr Val Asp Asp Thr Pro Ile Arg Glu Phe Lys Asn Tyr Glu Ser Leu  
50 55 60  
Gly Val Leu Phe Pro Lys Asn Lys Pro Met Arg Met Tyr Ala Ser Leu  
65 70 75 80  
Trp Asn Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Val Lys Thr Asp  
85 90 95  
Trp Ser Lys Ala Pro Phe Met Ala Ser Tyr Arg Asn Ile Lys Ile Asp  
100 105 110  
Ser Lys Pro Asn Ser Asn Trp Tyr Thr Gln Glu Met Asp Ser Thr Ser  
115 120 125  
Gln Ala Arg Leu Lys Trp Val Gln Lys Asn Tyr Met Ile Tyr Asn Tyr  
130 135 140  
Cys Thr Asp His Arg Arg Phe Pro Gln Gly Ala Pro Lys Glu Cys Thr  
145 150 155 160  
Thr Ser Ser

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..733

(D) OTHER INFORMATION: / Ceres Seq. ID 1571472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

cccggttcaa aaacccaaaa ttctagagat agaggacggc aatgcgatgg ggtcatcttt 60  
ctccgcctcc tttactaaact ccaccaccgc cgccgcggtt cctcctccgt cgccaccttc 120  
atcgccgtca cgttccaatg taaaatctaa cggagaagag agacctcggt tcttcgatgg 180  
aaaggcgaag aacaagtgtc gggctaattgc tgacatcgta cctgggtcgac atcccgagag 240  
gtggcgtaaa gacgtcgccg gtaacatagt ctgcaaacgc ttcggaaatt gcaatggttg 300  
tctctgtttc gagtatgatc acattgttcc ttattccaaa ggtggagagt cgatagcgga 360  
gaattgtcag attcttcaaa caagagttaa cagattcaaa tcagctcaag aaaatggtga 420  
tgccaccact cttaagagtgt gtGgcggaag ctacggtggt ggaagacgtg arggaggagg 480  
atacgggtggt ggtgaaggag gaggttacgg aggaagcggg ggtggtggag gatggttaatt 540  
cctttaatta ggTtttgga ttaccaatga atgttctctc tctcgcttgt tatgcttcta 600  
cttggttttg tgtgttctct attttgttct ggttctgctt tagatttgat gtaacagttc 660  
gtgattaggt attttggtat ctggaaacgt aattttaagt cacttgatcat tctctaaata 720  
acaaatttct tcg

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

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Pro Val Gln Lys Pro Lys Ile Leu Glu Ile Glu Asp Gly Asn Ala Met  
1 5 10 15  
Gly Ser Ser Phe Ser Ala Ser Phe Thr Asn Ser Thr Thr Ala Ala Ala  
20 25 30  
Val Pro Pro Pro Ser Pro Pro Ser Ser Pro Ser Arg Ser Asn Val Lys  
35 40 45  
Ser Asn Gly Glu Glu Arg Pro Arg Phe Phe Asp Gly Lys Ala Lys Asn  
50 55 60  
Lys Cys Trp Ala Asn Ala Asp Ile Val Pro Gly Arg His Pro Glu Arg  
65 70 75 80  
Trp Arg Lys Asp Val Ala Gly Asn Ile Val Cys Lys Arg Phe Gly Asn  
85 90 95  
Cys Asn Gly Cys Leu Cys Phe Glu Tyr Asp His Ile Val Pro Tyr Ser  
100 105 110  
Lys Gly Gly Glu Ser Ile Ala Glu Asn Cys Gln Ile Leu Gln Thr Arg  
115 120 125  
Val Asn Arg Phe Lys Ser Ala Gln Glu Asn Val Asp Ala Thr Thr Leu  
130 135 140  
Lys Ser Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Xaa Gly Gly Gly  
145 150 155 160  
Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly  
165 170 175  
Gly Trp

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1571474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Met Gly Ser Ser Phe Ser Ala Ser Phe Thr Asn Ser Thr Thr Ala Ala  
1 5 10 15  
Ala Val Pro Pro Pro Ser Pro Pro Ser Ser Pro Ser Arg Ser Asn Val  
20 25 30  
Lys Ser Asn Gly Glu Glu Arg Pro Arg Phe Phe Asp Gly Lys Ala Lys  
35 40 45  
Asn Lys Cys Trp Ala Asn Ala Asp Ile Val Pro Gly Arg His Pro Glu  
50 55 60  
Arg Trp Arg Lys Asp Val Ala Gly Asn Ile Val Cys Lys Arg Phe Gly  
65 70 75 80  
Asn Cys Asn Gly Cys Leu Cys Phe Glu Tyr Asp His Ile Val Pro Tyr  
85 90 95  
Ser Lys Gly Gly Glu Ser Ile Ala Glu Asn Cys Gln Ile Leu Gln Thr  
100 105 110  
Arg Val Asn Arg Phe Lys Ser Ala Gln Glu Asn Val Asp Ala Thr Thr  
115 120 125  
Leu Lys Ser Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Xaa Gly Gly  
130 135 140  
Gly Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly  
145 150 155 160  
Gly Gly Trp

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1406  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| aatttttttga | gttttgttct  | cgcaaaccgg | tttaacccaa  | gaacccaaag  | atctctctct  | 60   |
| atttgtttgc  | cttcttcttt  | ctttctgact | caaaccctta  | aatcaattct  | cgcgattaag  | 120  |
| caaaacccta  | gatttattct  | actcttcgaa | gtcgatttca  | atggaagggt  | cctcgtcagc  | 180  |
| catcgcgagg  | aagacatggg  | agctagagaa | caacattctc  | cgagtggaaac | caaccgattc  | 240  |
| agcctccgac  | agtatattcc  | actacgacga | cgcttcacaa  | gccaaaatcc  | agcaggagaa  | 300  |
| gccatggggc  | tccgatccta  | actacttcaa | gcgcgttcac  | atctcagccc  | ttgctcttct  | 360  |
| caagatgggtg | gttcacgctc  | gctccgggtg | cacaatcgag  | atcatgggtc  | ttatgcaggg  | 420  |
| taaaaccgag  | gggtgatacaa | tcacgttatt | ggatgctttt  | gctttgcttg  | ttgaaggtag  | 480  |
| tgagactagg  | gttaatgctc  | agtctgatgc | ctatgagtat  | atggttgaat  | actctcagac  | 540  |
| cagcaagctg  | gctgggaggt  | tggagaacgt | tgttggatgg  | tatcaactctc | accctgggta  | 600  |
| tggatgttgg  | ctctcgggta  | ttgatgtttc | gacacagatg  | cttaaccaac  | agtatcagga  | 660  |
| gccattctta  | gctgttggtta | ttgatccaac | aaggactggt  | tcggctggta  | agggttgagat | 720  |
| tggggcattc  | agaacatata  | cagagggaca | taagatctcg  | gatgatcatg  | tttctgagta  | 780  |
| tcagactatac | cctcttaaca  | agattgagga | ctttggtgta  | cattgcaaac  | agtactactc  | 840  |
| attggacatac | acttattttca | agtcactctc | cgatagtcac  | cttctggatc  | tcctttggaa  | 900  |
| caagtactgg  | gtgaacactc  | tttcttcttc | cccactgttg  | ggcaatggag  | actatgttgc  | 960  |
| cgggcaaata  | tcagacttgg  | ctgagaagct | cgagcaagcg  | gagagtcagc  | tcgctaactc  | 1020 |
| ccggtatggA  | aggaattgcg  | Cccagccggt | caccAaaagg  | aggaaagagg  | atgagcctcA  | 1080 |
| aactcgcgaa  | gataactcgg  | gatagtgcaa | agataactgt  | cgagcagggtc | catggactaa  | 1140 |
| tgtcacaggt  | tatcaaagac  | atcttgttca | attccgctcg  | tcagtccaag  | aagtctgctg  | 1200 |
| acgactcatc  | agatccagag  | cccatgatta | catcgtagaag | ttggtctatt  | cttttgtttt  | 1260 |
| ttggctgcgg  | aaattgacta  | tcggtttgac | ccggtttatg  | aggcaatgcc  | cattgttccc  | 1320 |
| tatatctcta  | gtgtagtata  | tgcttcagac | aaagatcttt  | gggttattaa  | atgacattaa  | 1380 |
| cataaatoga  | tcattatggt  | tttgcg     |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..314  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Ser | Ser | Ser | Ala | Ile | Ala | Arg | Lys | Thr | Trp | Glu | Leu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asn | Ile | Leu | Arg | Val | Glu | Pro | Thr | Asp | Ser | Ala | Ser | Asp | Ser | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | His | Tyr | Asp | Asp | Ala | Ser | Gln | Ala | Lys | Ile | Gln | Gln | Glu | Lys | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Trp | Ala | Ser | Asp | Pro | Asn | Tyr | Phe | Lys | Arg | Val | His | Ile | Ser | Ala | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Leu | Lys | Met | Val | Val | His | Ala | Arg | Ser | Gly | Gly | Thr | Ile | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Met | Gly | Leu | Met | Gln | Gly | Lys | Thr | Glu | Gly | Asp | Thr | Ile | Ile | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Asp | Ala | Phe | Ala | Leu | Pro | Val | Glu | Gly | Thr | Glu | Thr | Arg | Val | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Gln | Ser | Asp | Ala | Tyr | Glu | Tyr | Met | Val | Glu | Tyr | Ser | Gln | Thr | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His  
130 135 140  
Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met  
145 150 155 160  
Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro  
165 170 175  
Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr  
180 185 190  
Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln  
195 200 205  
Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln  
210 215 220  
Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His  
225 230 235 240  
Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser  
245 250 255  
Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp  
260 265 270  
Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg  
275 280 285  
Tyr Gly Arg Asn Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp  
290 295 300  
Glu Pro Gln Thr Arg Glu Asp Asn Ser Gly  
305 310

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1571481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu  
1 5 10 15  
Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met Asp Ala Phe  
20 25 30  
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ser Asp  
35 40 45  
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys Leu Ala Gly  
50 55 60  
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly  
65 70 75 80  
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln  
85 90 95  
Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val  
100 105 110  
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Pro Glu Gly  
115 120 125  
His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr Ile Pro Leu  
130 135 140  
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu  
145 150 155 160  
Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu  
165 170 175  
Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu  
180 185 190  
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys

195 200 205  
Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr Gly Arg Asn  
210 215 220  
Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp Glu Pro Gln Thr  
225 230 235 240  
Arg Glu Asp Asn Ser Gly  
245

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1571482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met  
1 5 10 15  
Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala  
20 25 30  
Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys  
35 40 45  
Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro  
50 55 60  
Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu  
65 70 75 80  
Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr  
85 90 95  
Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr  
100 105 110  
Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr  
115 120 125  
Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr  
130 135 140  
Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu  
145 150 155 160  
Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser  
165 170 175  
Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu  
180 185 190  
Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr  
195 200 205  
Gly Arg Asn Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp Glu  
210 215 220  
Pro Gln Thr Arg Glu Asp Asn Ser Gly  
225 230

(2) INFORMATION FOR SEQ ID NO:1979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1654

(D) OTHER INFORMATION: / Ceres Seq. ID 1571483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| acmatwacyt | agaacatcct  | aatcaaaaact | gcttccgcca  | ttgctcgaaa | atcgcgctctt | 60   |
| ctgacaatgt | gctgaaaactg | agtcacgcgc  | cgagtttagca | aagtgaact  | tcgaagtttc  | 120  |
| tcttacacta | atctcaggtt  | tgggattttg  | taagaaaccg  | cgtttacaaa | atgttcaagt  | 180  |
| tgaagcaatg | gttgatttat  | ttgggtgtatt | cgtttagtaat | aatgaacaca | gaaggactgt  | 240  |
| ttgtcaatat | tacatttggt  | cgaaacgcag  | tcgctaaagg  | ggccgtttgt | ttagatggaa  | 300  |
| gtccaccagc | ttatcatttg  | gatagagggt  | ctggaactgg  | aatcaatagt | tgggtgatac  | 360  |
| agcttgaggg | aggaggatgg  | tgcaataatg  | taacaaattg  | cgttagtcgg | atgcatactc  | 420  |
| gattaggttc | atcgaagaaa  | atgggtggaga | accttgcttt  | ctcagctatt | cttagcaata  | 480  |
| agaaacaata | taatcctgat  | ttttacaatt  | ggaatagagt  | gaaagttaga | tactgtgacg  | 540  |
| gggcatcatt | cacaggagat  | gtagaagcag  | tgaaccctgc  | tactaatctt | cacttcagag  | 600  |
| gtgctcgagt | ttgggttagcc | gttatgcaag  | agctgctagc  | taaaggcatg | ataaacgccg  | 660  |
| agaatgctgt | tttgtctggc  | tgttctgctg  | gcggttagtc  | ttcgctgatg | cattgtgata  | 720  |
| gtttccgtgc | tctattaccg  | atgggaacca  | aagtaaaatg  | tctttcagat | gctgggtttt  | 780  |
| ttctcaacac | aagagacgtc  | tcaggagttc  | aatacattaa  | aacatacttc | gaagatgttg  | 840  |
| ttactcttca | tggatcagca  | aagaacttgc  | cgaggctcatg | cacatcaaga | ttactcctg   | 900  |
| caatgtgttt | ctttccgcaa  | tatgtggctc  | gccagattag  | aactcctctg | ttcattctta  | 960  |
| atgccgctta | tgactcttgg  | cagataaaga  | acattttggc  | tccgcgagca | gctgatcctt  | 1020 |
| acggaaaatg | gcaaagttgt  | caactagaca  | tcaagaattg  | ccatccaagt | cagatcaaag  | 1080 |
| ttatgcaaga | tttcagggtta | gagttcttga  | gtgcagtgat  | aggtttaggg | agatcttcat  | 1140 |
| caagagggat | gttcatagat  | tcttgctaca  | ctcactgcc   | aaccgagaca | caaacttcat  | 1200 |
| ggttctggca | agattctcca  | attctaaacc  | gaacgacaat  | agcaaaagct | gttgagatt   | 1260 |
| gggtttatga | cagaacattg  | tttcagaaga  | tagattgtcc  | ttacccttgt | aaccctactt  | 1320 |
| gccaccacag | ggTttttcac  | tcctctagat  | gctcctccaa  | tttaagtgt  | tctaccatat  | 1380 |
| acagtataga | tttattatta  | ttttgaaaag  | aaaatttgct  | tataaatgat | tcatttggtta | 1440 |
| gatacatata | gtgaaatatt  | cctagggttt  | agctatagaa  | gatgaaaaag | aaaaagagtg  | 1500 |
| tgattaattc | ttgagtgttg  | agaataagca  | ataggagtaa  | ttttcttcag | cacttgctct  | 1560 |
| gtgtgctgtt | taaattgctc  | tgtttctctt  | ctattctgat  | gtaaaatgca | aattgttacc  | 1620 |
| tttatcctat | caaataaagt  | ataattcttt  | tctc        |            |             |      |

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1571484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Lys | Leu | Lys | Gln | Trp | Leu | Ile | Tyr | Leu | Val | Tyr | Ser | Leu | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Asn | Thr | Glu | Gly | Leu | Phe | Val | Asn | Ile | Thr | Phe | Val | Arg | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Ala | Lys | Gly | Ala | Val | Cys | Leu | Asp | Gly | Ser | Pro | Pro | Ala | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Leu | Asp | Arg | Gly | Ser | Gly | Thr | Gly | Ile | Asn | Ser | Trp | Leu | Ile | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Gly | Gly | Gly | Trp | Cys | Asn | Asn | Val | Thr | Asn | Cys | Val | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | His | Thr | Arg | Leu | Gly | Ser | Ser | Lys | Lys | Met | Val | Glu | Asn | Leu | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Ser | Ala | Ile | Leu | Ser | Asn | Lys | Lys | Gln | Tyr | Asn | Pro | Asp | Phe | Tyr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | Trp | Asn | Arg | Val | Lys | Val | Arg | Tyr | Cys | Asp | Gly | Ala | Ser | Phe | Thr |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Gly | Asp | Val | Glu | Ala | Val | Asn | Pro | Ala | Thr | Asn | Leu | His | Phe | Arg | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Arg | Val | Trp | Leu | Ala | Val | Met | Gln | Glu | Leu | Leu | Ala | Lys | Gly | Met |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Asn | Ala | Glu | Asn | Ala | Val | Leu | Ser | Gly | Cys | Ser | Ala | Gly | Gly | Leu |

```
(2) INFORMATION FOR SEQ ID NO:1981:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..394
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571485
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | Glu | Gly | Leu | Phe | Val | Asn | Ile | Thr | Phe | Val | Arg | Asn | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Lys | Gly | Ala | Val | Cys | Leu | Asp | Gly | Ser | Pro | Pro | Ala | Tyr | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Arg | Gly | Ser | Gly | Thr | Gly | Ile | Asn | Ser | Trp | Leu | Ile | Gln | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Gly | Gly | Gly | Trp | Cys | Asn | Asn | Val | Thr | Asn | Cys | Val | Ser | Arg | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Thr | Arg | Leu | Gly | Ser | Ser | Lys | Lys | Met | Val | Glu | Asn | Leu | Ala | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ala | Ile | Leu | Ser | Asn | Lys | Lys | Gln | Tyr | Asn | Pro | Asp | Phe | Tyr | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | Asn | Arg | Val | Lys | Val | Arg | Tyr | Cys | Asp | Gly | Ala | Ser | Phe | Thr | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Val | Glu | Ala | Val | Asn | Pro | Ala | Thr | Asn | Leu | His | Phe | Arg | Gly | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Val | Trp | Leu | Ala | Val | Met | Gln | Glu | Leu | Leu | Ala | Lys | Gly | Met | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

```

Asn Ala Glu Asn Ala Val Leu Ser Gly Cys Ser Ala Gly Gly Leu Ala
145 150 155 160
Ser Leu Met His Cys Asp Ser Phe Arg Ala Leu Leu Pro Met Gly Thr
 165 170 175
Lys Val Lys Cys Leu Ser Asp Ala Gly Phe Phe Leu Asn Thr Arg Asp
 180 185 190
Val Ser Gly Val Gln Tyr Ile Lys Thr Tyr Phe Glu Asp Val Val Thr
 195 200 205
Leu His Gly Ser Ala Lys Asn Leu Pro Arg Ser Cys Thr Ser Arg Leu
 210 215 220
Thr Pro Ala Met Cys Phe Phe Pro Gln Tyr Val Ala Arg Gln Ile Arg
225 230 235 240
Thr Pro Leu Phe Ile Leu Asn Ala Ala Tyr Asp Ser Trp Gln Ile Lys
 245 250 255
Asn Ile Leu Ala Pro Arg Ala Ala Asp Pro Tyr Gly Lys Trp Gln Ser
 260 265 270
Cys Gln Leu Asp Ile Lys Asn Cys His Pro Ser Gln Ile Lys Val Met
 275 280 285
Gln Asp Phe Arg Leu Glu Phe Leu Ser Ala Val Ile Gly Leu Gly Arg
290 295 300
Ser Ser Ser Arg Gly Met Phe Ile Asp Ser Cys Tyr Thr His Cys Gln
305 310 315 320
Thr Glu Thr Gln Thr Ser Trp Phe Trp Gln Asp Ser Pro Ile Leu Asn
 325 330 335
Arg Thr Thr Ile Ala Lys Ala Val Gly Asp Trp Val Tyr Asp Arg Thr
 340 345 350
Leu Phe Gln Lys Ile Asp Cys Pro Tyr Pro Cys Asn Pro Thr Cys His
 355 360 365
His Arg Val Phe His Ser Ser Arg Cys Ser Ser Asn Leu Ser Asp Ser
370 375 380
Thr Ile Tyr Ser Ile Asp Leu Leu Leu Phe
385 390

```

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1571486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

```

Met His Thr Arg Leu Gly Ser Ser Lys Lys Met Val Glu Asn Leu Ala
1 5 10 15
Phe Ser Ala Ile Leu Ser Asn Lys Lys Gln Tyr Asn Pro Asp Phe Tyr
 20 25 30
Asn Trp Asn Arg Val Lys Val Arg Tyr Cys Asp Gly Ala Ser Phe Thr
 35 40 45
Gly Asp Val Glu Ala Val Asn Pro Ala Thr Asn Leu His Phe Arg Gly
50 55 60
Ala Arg Val Trp Leu Ala Val Met Gln Glu Leu Leu Ala Lys Gly Met
65 70 75 80
Ile Asn Ala Glu Asn Ala Val Leu Ser Gly Cys Ser Ala Gly Gly Leu
 85 90 95
Ala Ser Leu Met His Cys Asp Ser Phe Arg Ala Leu Leu Pro Met Gly
100 105 110
Thr Lys Val Lys Cys Leu Ser Asp Ala Gly Phe Phe Leu Asn Thr Arg
115 120 125
Asp Val Ser Gly Val Gln Tyr Ile Lys Thr Tyr Phe Glu Asp Val Val

```

130 135 140  
Thr Leu His Gly Ser Ala Lys Asn Leu Pro Arg Ser Cys Thr Ser Arg  
145 150 155 160  
Leu Thr Pro Ala Met Cys Phe Phe Pro Gln Tyr Val Ala Arg Gln Ile  
165 170 175  
Arg Thr Pro Leu Phe Ile Leu Asn Ala Ala Tyr Asp Ser Trp Gln Ile  
180 185 190  
Lys Asn Ile Leu Ala Pro Arg Ala Ala Asp Pro Tyr Gly Lys Trp Gln  
195 200 205  
Ser Cys Gln Leu Asp Ile Lys Asn Cys His Pro Ser Gln Ile Lys Val  
210 215 220  
Met Gln Asp Phe Arg Leu Glu Phe Leu Ser Ala Val Ile Gly Leu Gly  
225 230 235 240  
Arg Ser Ser Ser Arg Gly Met Phe Ile Asp Ser Cys Tyr Thr His Cys  
245 250 255  
Gln Thr Glu Thr Gln Thr Ser Trp Phe Trp Gln Asp Ser Pro Ile Leu  
260 265 270  
Asn Arg Thr Thr Ile Ala Lys Ala Val Gly Asp Trp Val Tyr Asp Arg  
275 280 285  
Thr Leu Phe Gln Lys Ile Asp Cys Pro Tyr Pro Cys Asn Pro Thr Cys  
290 295 300  
His His Arg Val Phe His Ser Ser Arg Cys Ser Ser Asn Leu Ser Asp  
305 310 315 320  
Ser Thr Ile Tyr Ser Ile Asp Leu Leu Leu Phe  
325 330

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1649
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| tccattaata  | ctctctctcc | ctcatcctct | cttcttctct | catcatcatc | ttctttcttca | 60   |
| atggccttca  | cgcgttttct | cctcctcctc | tcttccatcg | ccgccggcgt | cctcctccta  | 120  |
| ctccgcogta  | caagttaccg | tcggatgggt | cttccctcgg | gaagccttgg | tctccctctg  | 180  |
| ataggagaga  | cttttcagct | gatcgagct  | tacaaaacag | agaaccttga | gcctttcatc  | 240  |
| gacgagagag  | tagcccggtg | cGgttcggtt | ttcatgacgc | atcttttttg | tgaaccgacg  | 300  |
| attttctcag  | ctgacccgga | aacgaaccgg | ttgttctctc | agaacgaagg | gaagcttttt  | 360  |
| gagtgttctt  | atcctgcttc | catttgtaac | cttttgggga | aacactctct | gcttcttatg  | 420  |
| aaagggttctt | tgcataaacg | tatgcactct | ctcaccatga | gctttgctaa | ttcttcaatc  | 480  |
| attaaagacc  | atctcatgct | tgatattgac | cggttagtc  | ggtttaatct | tgattcttgg  | 540  |
| tctctctgtg  | ttctctcat  | ggaagaagcc | aaaaagataa | cgtttgagct | aacggtgaag  | 600  |
| cagttgatga  | gctttgatcc | aggggaatgg | agtgagagtt | taaggaaaga | gtatcttctt  | 660  |
| gtcatcgaag  | gcttcttctc | tcttctctc  | cctctcttct | ccaccactta | ccgcaaagcc  | 720  |
| atccaagcgc  | ggaggaaggt | ggcggaggcg | ttgacgggtg | tggtgatgaa | aaggaggagg  | 780  |
| gaggaggaag  | aaggagcgga | gagaaagaaa | gatatgcttg | cggcgttgct | tgccgcggtg  | 840  |
| gatggatttt  | cogatgaaga | gattgttgac | ttcttggttg | ctttacttgt | cgccggttat  | 900  |
| gaaacaacct  | ccacgatcat | gactctcgcc | gtcaaatttc | tcaccgagac | tcctttagct  | 960  |
| cttgctcaac  | tcaaggaaga | gcatgaaaag | attagggcaa | tgaagagtga | ttcgtatagt  | 1020 |
| cttgaatgga  | gtgattacaa | gtcaatgcca | ttcacacaa  | gtgtggttaa | tgagacgcta  | 1080 |
| cgagtggcta  | acatctcggg | cggtgttttc | agacgtgcaa | tgacggatgt | tgagatcaaa  | 1140 |
| ggttataaaa  | ttccaaaagg | gtggaaagta | ttctcatcgt | ttagagcggg | tcatttagac  | 1200 |
| ccaaaccact  | tcaaagatgc | tcgcactttc | aacccttgga | gatggcagag | caactcggtg  | 1260 |
| acgacaggcc  | cttctaattg | gttcacaccg | tttggtggag | ggccaaggct | atgtcccggg  | 1320 |
| tacgagctgg  | ctagggttgc | actctctgtt | ttccttcacc | gcctagtgc  | aggcttcagt  | 1380 |
| tgggttctctg | cagagcaaga | caagctgggt | ttctttccaa | ctacaagaac | gcagaaacgg  | 1440 |



```
tacccgatct tcgtgaagcg ccgtgatttt gctacttgaa gaagaagaga cccatctgat 1500
tttatttata gaacaacagt atttttcagg attaatctt tcttcttttt ttgcctcctt 1560
gtgggtctag tgtttgacaa taaaagttat cattactcta taaagcctta gcttctgtgt 1620
acataaaaaa aaaaaaactt ttgtttacc
```

(2) INFORMATION FOR SEQ ID NO:1984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..492

(D) OTHER INFORMATION: / Ceres Seq. ID 1571488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:

```
Ser Ile Asn Thr Leu Ser Pro Ser Ser Ser Leu Leu Leu Ser Ser Ser
1 5 10 15
Ser Ser Ser Ser Met Ala Phe Thr Ala Phe Leu Leu Leu Leu Ser Ser
20 25 30
Ile Ala Ala Gly Phe Leu Leu Leu Leu Arg Arg Thr Arg Tyr Arg Arg
35 40 45
Met Gly Leu Pro Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr
50 55 60
Phe Gln Leu Ile Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile
65 70 75 80
Asp Glu Arg Val Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe
85 90 95
Gly Glu Pro Thr Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val
100 105 110
Leu Gln Asn Glu Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile
115 120 125
Cys Asn Leu Leu Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu
130 135 140
His Lys Arg Met His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile
145 150 155 160
Ile Lys Asp His Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn
165 170 175
Leu Asp Ser Trp Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys
180 185 190
Ile Thr Phe Glu Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly
195 200 205
Glu Trp Ser Glu Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly
210 215 220
Phe Phe Ser Leu Pro Leu Pro Leu Phe Ser Thr Thr Tyr Arg Lys Ala
225 230 235 240
Ile Gln Ala Arg Arg Lys Val Ala Glu Ala Leu Thr Val Val Val Met
245 250 255
Lys Arg Arg Glu Glu Glu Glu Gly Ala Glu Arg Lys Lys Asp Met
260 265 270
Leu Ala Ala Leu Leu Ala Ala Asp Asp Gly Phe Ser Asp Glu Glu Ile
275 280 285
Val Asp Phe Leu Val Ala Leu Leu Val Ala Gly Tyr Glu Thr Thr Ser
290 295 300
Thr Ile Met Thr Leu Ala Val Lys Phe Leu Thr Glu Thr Pro Leu Ala
305 310 315 320
Leu Ala Gln Leu Lys Glu Glu His Glu Lys Ile Arg Ala Met Lys Ser
325 330 335
Asp Ser Tyr Ser Leu Glu Trp Ser Asp Tyr Lys Ser Met Pro Phe Thr
340 345 350
Gln Cys Val Val Asn Glu Thr Leu Arg Val Ala Asn Ile Ile Gly Gly
```

|                                                                 |                                 |     |
|-----------------------------------------------------------------|---------------------------------|-----|
| 355                                                             | 360                             | 365 |
| Val Phe Arg Arg Ala Met Thr Asp                                 | Val Glu Ile Lys Gly Tyr Lys Ile |     |
| 370                                                             | 375                             | 380 |
| Pro Lys Gly Trp Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp |                                 |     |
| 385                                                             | 390                             | 395 |
| Pro Asn His Phe Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln |                                 | 400 |
|                                                                 | 405                             | 410 |
| Ser Asn Ser Val Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly |                                 | 415 |
|                                                                 | 420                             | 425 |
|                                                                 |                                 | 430 |
| Gly Gly Pro Arg Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu |                                 |     |
| 435                                                             | 440                             | 445 |
| Ser Val Phe Leu His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala |                                 |     |
| 450                                                             | 455                             | 460 |
| Glu Gln Asp Lys Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg |                                 |     |
| 465                                                             | 470                             | 475 |
|                                                                 |                                 | 480 |
| Tyr Pro Ile Phe Val Lys Arg Arg Asp Phe Ala Thr                 |                                 |     |
|                                                                 | 485                             | 490 |

(2) INFORMATION FOR SEQ ID NO:1985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1571489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Ala Phe Thr Ala Phe Leu Leu Leu Ser Ser Ile Ala Ala Gly     |             |
| 1                                                               | 5 10 15     |
| Phe Leu Leu Leu Leu Arg Arg Thr Arg Tyr Arg Arg Met Gly Leu Pro |             |
|                                                                 | 20 25 30    |
| Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr Phe Gln Leu Ile |             |
|                                                                 | 35 40 45    |
| Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile Asp Glu Arg Val |             |
| 50                                                              | 55 60       |
| Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe Gly Glu Pro Thr |             |
| 65                                                              | 70 75 80    |
| Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val Leu Gln Asn Glu |             |
|                                                                 | 85 90 95    |
| Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile Cys Asn Leu Leu |             |
|                                                                 | 100 105 110 |
| Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu His Lys Arg Met |             |
|                                                                 | 115 120 125 |
| His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile Ile Lys Asp His |             |
| 130                                                             | 135 140     |
| Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn Leu Asp Ser Trp |             |
| 145                                                             | 150 155 160 |
| Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys Ile Thr Phe Glu |             |
|                                                                 | 165 170 175 |
| Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly Glu Trp Ser Glu |             |
|                                                                 | 180 185 190 |
| Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly Phe Phe Ser Leu |             |
| 195                                                             | 200 205     |
| Pro Leu Pro Leu Phe Ser Thr Tyr Arg Lys Ala Ile Gln Ala Arg     |             |
| 210                                                             | 215 220     |
| Arg Lys Val Ala Glu Ala Leu Thr Val Val Val Met Lys Arg Arg Glu |             |
| 225                                                             | 230 235 240 |
| Glu Glu Glu Glu Gly Ala Glu Arg Lys Lys Asp Met Leu Ala Ala Leu |             |
|                                                                 | 245 250 255 |

Leu Ala Ala Asp Asp Gly Phe Ser Asp Glu Glu Ile Val Asp Phe Leu  
260 265 270  
Val Ala Leu Val Ala Gly Tyr Glu Thr Thr Ser Thr Ile Met Thr  
275 280 285  
Leu Ala Val Lys Phe Leu Thr Glu Thr Pro Leu Ala Leu Ala Gln Leu  
290 295 300  
Lys Glu Glu His Glu Lys Ile Arg Ala Met Lys Ser Asp Ser Tyr Ser  
305 310 315 320  
Leu Glu Trp Ser Asp Tyr Lys Ser Met Pro Phe Thr Gln Cys Val Val  
325 330 335  
Asn Glu Thr Leu Arg Val Ala Asn Ile Ile Gly Gly Val Phe Arg Arg  
340 345 350  
Ala Met Thr Asp Val Glu Ile Lys Gly Tyr Lys Ile Pro Lys Gly Trp  
355 360 365  
Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp Pro Asn His Phe  
370 375 380  
Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln Ser Asn Ser Val  
385 390 395 400  
Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly Gly Gly Pro Arg  
405 410 415  
Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu Ser Val Phe Leu  
420 425 430  
His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala Glu Gln Asp Lys  
435 440 445  
Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg Tyr Pro Ile Phe  
450 455 460  
Val Lys Arg Arg Asp Phe Ala Thr  
465 470

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1571490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

Met Gly Leu Pro Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr  
1 5 10 15  
Phe Gln Leu Ile Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile  
20 25 30  
Asp Glu Arg Val Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe  
35 40 45  
Gly Glu Pro Thr Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val  
50 55 60  
Leu Gln Asn Glu Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile  
65 70 75 80  
Cys Asn Leu Leu Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu  
85 90 95  
His Lys Arg Met His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile  
100 105 110  
Ile Lys Asp His Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn  
115 120 125  
Leu Asp Ser Trp Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys  
130 135 140  
Ile Thr Phe Glu Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly  
145 150 155 160  
Glu Trp Ser Glu Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly

165 170 175  
Phe Phe Ser Leu Pro Leu Pro Leu Phe Ser Thr Thr Tyr Arg Lys Ala  
180 185 190  
Ile Gln Ala Arg Arg Lys Val Ala Glu Ala Leu Thr Val Val Met  
195 200 205  
Lys Arg Arg Glu Glu Glu Glu Glu Gly Ala Glu Arg Lys Lys Asp Met  
210 215 220  
Leu Ala Ala Leu Leu Ala Ala Asp Asp Gly Phe Ser Asp Glu Glu Ile  
225 230 235 240  
Val Asp Phe Leu Val Ala Leu Leu Val Ala Gly Tyr Glu Thr Thr Ser  
245 250 255  
Thr Ile Met Thr Leu Ala Val Lys Phe Leu Thr Glu Thr Pro Leu Ala  
260 265 270  
Leu Ala Gln Leu Lys Glu Glu His Glu Lys Ile Arg Ala Met Lys Ser  
275 280 285  
Asp Ser Tyr Ser Leu Glu Trp Ser Asp Tyr Lys Ser Met Pro Phe Thr  
290 295 300  
Gln Cys Val Val Asn Glu Thr Leu Arg Val Ala Asn Ile Ile Gly Gly  
305 310 315 320  
Val Phe Arg Arg Ala Met Thr Asp Val Glu Ile Lys Gly Tyr Lys Ile  
325 330 335  
Pro Lys Gly Trp Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp  
340 345 350  
Pro Asn His Phe Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln  
355 360 365  
Ser Asn Ser Val Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly  
370 375 380  
Gly Gly Pro Arg Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu  
385 390 395 400  
Ser Val Phe Leu His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala  
405 410 415  
Glu Gln Asp Lys Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg  
420 425 430  
Tyr Pro Ile Phe Val Lys Arg Arg Asp Phe Ala Thr  
435 440

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| amcatccwaa  | tcgaaaaatt | ttaaccagca  | tatacaaaaa  | acttccgata  | ccccttagcg  | 60  |
| tttctttctc  | cggcgatatt | cttctttctt  | ggctcacatt  | gcatcgtctc  | tcaactcgatc | 120 |
| cttcgtttctt | tcagggacaa | tcattttcgga | aacatgccag  | gtcagaagat  | tgaaaacgggt | 180 |
| catgaggaca  | ttgtccatga | tgtgcagatg  | gattactatg  | gaaagcgaat  | tgcaactgca  | 240 |
| tcatctgact  | gcaccatcaa | gataaccggg  | gtcagcaaca  | acgggtggatc | gcagcaacta  | 300 |
| gccacattaa  | cgggccaccg | tggtcctgtc  | tgggaagtgc  | cgtgggcaca  | cccaaagtat  | 360 |
| ggatcaatcc  | ttgtctcatg | ctcctatgat  | gggtcaagtca | tactctggaa  | agaaggcaac  | 420 |
| cagaaccaat  | ggacccaaga | tcatgttttc  | acagaccaca  | aatcttcagt  | caactccatt  | 480 |
| gcatgggctc  | ctcatgatat | cggactatcc  | ttggcctgcg  | ggatcatctga | tggcaacatt  | 540 |
| tcggttttca  | cagcccggtg | tgacgggtgg  | tgggacacat  | caaggattga  | ccaagcacat  | 600 |
| cgggttgag   | tcacttcagt | ctcatgggcc  | ccagccacag  | cgcttggtgc  | tcttgtgagc  | 660 |
| tctggtcttc  | tcgatccggg | ttacaagcta  | gcttctggtg  | gatgtgataa  | taccgtgaaa  | 720 |
| gtgtggaagc  | tcgctaacgg | gtcatggaag  | atggattgct  | ttccagctct  | tcaaaagcac  | 780 |
| actgattggg  | tcogtgatgt | ggcttgggca  | ccaaacttgg  | gtctcccaa   | gtccaccata  | 840 |

(2) INFORMATION FOR SEQ ID NO:1988:

(A) LENGTH: 302 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1571500

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Gln | Lys | Ile | Glu | Thr | Gly | His | Glu | Asp | Ile | Val | His | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gln | Met | Asp | Tyr | Tyr | Gly | Lys | Arg | Ile | Ala | Thr | Ala | Ser | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Thr | Ile | Lys | Ile | Thr | Gly | Val | Ser | Asn | Asn | Gly | Gly | Ser | Gln | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Ala | Thr | Leu | Thr | Gly | His | Arg | Gly | Pro | Val | Trp | Glu | Val | Ala | Trp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | His | Pro | Lys | Tyr | Gly | Ser | Ile | Leu | Ala | Ser | Cys | Ser | Tyr | Asp | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Val | Ile | Leu | Trp | Lys | Glu | Gly | Asn | Gln | Asn | Gln | Trp | Thr | Gln | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| His | Val | Phe | Thr | Asp | His | Lys | Ser | Ser | Val | Asn | Ser | Ile | Ala | Trp | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Pro | His | Asp | Ile | Gly | Leu | Ser | Leu | Ala | Cys | Gly | Ser | Ser | Asp | Gly | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ile | Ser | Val | Phe | Thr | Ala | Arg | Ala | Asp | Gly | Gly | Trp | Asp | Thr | Ser | Arg |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Asp | Gln | Ala | His | Pro | Val | Gly | Val | Thr | Ser | Val | Ser | Trp | Ala | Pro |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Thr | Ala | Pro | Gly | Ala | Leu | Val | Ser | Ser | Gly | Leu | Leu | Asp | Pro | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Tyr | Lys | Leu | Ala | Ser | Gly | Gly | Cys | Asp | Asn | Thr | Val | Lys | Val | Trp | Lys |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Leu | Ala | Asn | Gly | Ser | Trp | Lys | Met | Asp | Cys | Phe | Pro | Ala | Leu | Gln | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |     |
| His | Thr | Asp | Trp | Val | Arg | Asp | Val | Ala | Trp | Ala | Pro | Asn | Leu | Gly | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Pro | Lys | Ser | Thr | Ile | Ala | Ser | Gly | Ser | Gln | Asp | Gly | Lys | Val | Ile | Ile |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Trp | Thr | Val | Gly | Lys | Glu | Gly | Glu | Gln | Trp | Glu | Gly | Lys | Val | Leu | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Asp | Phe | Met | Thr | Pro | Val | Trp | Arg | Val | Ser | Ser | Ser | Leu | Thr | Gly | Asn |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |
| Leu | Leu | Ala | Val | Ser | Asp | Gly | Asn | Asn | Asn | Val | Thr | Val | Trp | Lys | Glu |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ala | Val | Asp | Gly | Glu | Trp | Glu | Gln | Val | Thr | Ala | Val | Glu | Pro |     |     |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..284  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571501  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

Met Asp Tyr Tyr Gly Lys Arg Ile Ala Thr Ala Ser Ser Asp Cys Thr  
1                   5                   10                   15  
Ile Lys Ile Thr Gly Val Ser Asn Asn Gly Gly Ser Gln Gln Leu Ala  
20                   25                   30  
Thr Leu Thr Gly His Arg Gly Pro Val Trp Glu Val Ala Trp Ala His  
35                   40                   45  
Pro Lys Tyr Gly Ser Ile Leu Ala Ser Cys Ser Tyr Asp Gly Gln Val  
50                   55                   60  
Ile Leu Trp Lys Glu Gly Asn Gln Asn Gln Trp Thr Gln Asp His Val  
65                   70                   75                   80  
Phe Thr Asp His Lys Ser Ser Val Asn Ser Ile Ala Trp Ala Pro His  
85                   90                   95  
Asp Ile Gly Leu Ser Leu Ala Cys Gly Ser Ser Asp Gly Asn Ile Ser  
100                   105                   110  
Val Phe Thr Ala Arg Ala Asp Gly Gly Trp Asp Thr Ser Arg Ile Asp  
115                   120                   125  
Gln Ala His Pro Val Gly Val Thr Ser Val Ser Trp Ala Pro Ala Thr  
130                   135                   140  
Ala Pro Gly Ala Leu Val Ser Ser Gly Leu Leu Asp Pro Val Tyr Lys  
145                   150                   155                   160  
Leu Ala Ser Gly Gly Cys Asp Asn Thr Val Lys Val Trp Lys Leu Ala  
165                   170                   175  
Asn Gly Ser Trp Lys Met Asp Cys Phe Pro Ala Leu Gln Lys His Thr  
180                   185                   190  
Asp Trp Val Arg Asp Val Ala Trp Ala Pro Asn Leu Gly Leu Pro Lys  
195                   200                   205  
Ser Thr Ile Ala Ser Gly Ser Gln Asp Gly Lys Val Ile Ile Trp Thr  
210                   215                   220  
Val Gly Lys Glu Gly Glu Gln Trp Glu Gly Lys Val Leu Lys Asp Phe  
225                   230                   235                   240  
Met Thr Pro Val Trp Arg Val Ser Ser Ser Leu Thr Gly Asn Leu Leu  
245                   250                   255  
Ala Val Ser Asp Gly Asn Asn Asn Val Thr Val Trp Lys Glu Ala Val  
260                   265                   270  
Asp Gly Glu Trp Glu Gln Val Thr Ala Val Glu Pro  
275                   280

(2) INFORMATION FOR SEQ ID NO:1990:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1194 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1194  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571502  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacaacaatg ggccttctt cgctgagcgg tctcacgttc aagctacatc ctctggtgat   | 60  |
| gcttaacata tccgatcact tcaactagggt taaaactcag cttaatcctc ccgccgcttc | 120 |
| ttgcgccacc gggaatggct ccaacaacgc cgacgcgatg ttactgcaaa accctagggt  | 180 |
| ttatggctgc gtcacggtc tccagagagg tcgtacggtt gagatcttca acagtttcga   | 240 |
| gctgatattc gatcctgctc ttgatactct cgacagatcc ttctctgaga agaagcaaga  | 300 |

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actctataag aaggtgttcc ctgacttcta cgtattggga tgggtattcta cgggaagtga 360
cgctaccgaa tctgatatgc atatccacaa agctctgatg gacattaatg aatctcctgt 420
gtatgttctt ttaaactcctg ctatcaatca tgcacagaag gatcttcctg tgactatcta 480
cgaaagcgaa tttcatgtca ttgatggaat tcctcagtcg attttcgtgc ataccagcta 540
cacaattgag acagttgaag ctgaaagaat atctgttgat catgtTgcac atcttaagcc 600
atctgatgga ggctcagctg cgactcagtt ggctgctcat cttactggaa tacatagtgc 660
catcaagatg cttaatagca gaatcagagt gctataccag catattgtcg ctatgcagaa 720
aggtgataaa ccttgtgaga actcagttct gagacaagta tctagtctgc tcagaagttt 780
gcctgccgca gaatcagaga agttcaatga aaatttcttg atggagtaca acgacaaatt 840
gctgatgtct tacctagcaa tgatcacgaa ttgtaccagc aacatgaacg aggtgggtga 900
caaattcaac actgcatacg acaaacacag ccgaagaggt ggtaggactg cgttcatgta 960
aagattagtt tcaatgtaaa aaaacctttt ctttcttttg gtggtctggt ccctaagtga 1020
aaatttagaa ctcttttaag gcatttcact tttcggaacc aaacaaacag ctaggaagct 1080
tttcttctgt ttaagctttg tctagacaga agctaagttt aggcctaact aaattttgcg 1140
acaagactgt aaaaacaaaa cagcttttac cttctctcaa tttttcattt attc

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(2) INFORMATION FOR SEQ ID NO:1991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:

```

Thr Thr Met Ala Pro Ser Ser Ser Ser Gly Leu Thr Phe Lys Leu His
1 5 10 15
Pro Leu Val Met Leu Asn Ile Ser Asp His Phe Thr Arg Val Lys Thr
20 25 30
Gln Leu Asn Pro Pro Ala Ala Ser Cys Ala Thr Gly Asn Gly Ser Asn
35 40 45
Asn Ala Asp Ala Met Leu Leu Gln Asn Pro Arg Val Tyr Gly Cys Val
50 55 60
Ile Gly Leu Gln Arg Gly Arg Thr Val Glu Ile Phe Asn Ser Phe Glu
65 70 75 80
Leu Ile Phe Asp Pro Ala Leu Asp Thr Leu Asp Arg Ser Phe Leu Glu
85 90 95
Lys Lys Gln Glu Leu Tyr Lys Lys Val Phe Pro Asp Phe Tyr Val Leu
100 105 110
Gly Trp Tyr Ser Thr Gly Ser Asp Ala Thr Glu Ser Asp Met His Ile
115 120 125
His Lys Ala Leu Met Asp Ile Asn Glu Ser Pro Val Tyr Val Leu Leu
130 135 140
Asn Pro Ala Ile Asn His Ala Gln Lys Asp Leu Pro Val Thr Ile Tyr
145 150 155 160
Glu Ser Glu Phe His Val Ile Asp Gly Ile Pro Gln Ser Ile Phe Val
165 170 175
His Thr Ser Tyr Thr Ile Glu Thr Val Glu Ala Glu Arg Ile Ser Val
180 185 190
Asp His Val Ala His Leu Lys Pro Ser Asp Gly Gly Ser Ala Ala Thr
195 200 205
Gln Leu Ala Ala His Leu Thr Gly Ile His Ser Ala Ile Lys Met Leu
210 215 220
Asn Ser Arg Ile Arg Val Leu Tyr Gln His Ile Val Ala Met Gln Lys
225 230 235 240
Gly Asp Lys Pro Cys Glu Asn Ser Val Leu Arg Gln Val Ser Ser Leu
245 250 255
Leu Arg Ser Leu Pro Ala Ala Glu Ser Glu Lys Phe Asn Glu Asn Phe
260 265 270

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Leu Met Glu Tyr Asn Asp Lys Leu Leu Met Ser Tyr Leu Ala Met Ile  
275 280 285  
Thr Asn Cys Thr Ser Asn Met Asn Glu Val Val Asp Lys Phe Asn Thr  
290 295 300  
Ala Tyr Asp Lys His Ser Arg Arg Gly Gly Arg Thr Ala Phe Met  
305 310 315

(2) INFORMATION FOR SEQ ID NO:1992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1571504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:

Met Ala Pro Ser Ser Ser Ser Gly Leu Thr Phe Lys Leu His Pro Leu  
1 5 10 15  
Val Met Leu Asn Ile Ser Asp His Phe Thr Arg Val Lys Thr Gln Leu  
20 25 30  
Asn Pro Pro Ala Ala Ser Cys Ala Thr Gly Asn Gly Ser Asn Asn Ala  
35 40 45  
Asp Ala Met Leu Leu Gln Asn Pro Arg Val Tyr Gly Cys Val Ile Gly  
50 55 60  
Leu Gln Arg Gly Arg Thr Val Glu Ile Phe Asn Ser Phe Glu Leu Ile  
65 70 75 80  
Phe Asp Pro Ala Leu Asp Thr Leu Asp Arg Ser Phe Leu Glu Lys Lys  
85 90 95  
Gln Glu Leu Tyr Lys Lys Val Phe Pro Asp Phe Tyr Val Leu Gly Trp  
100 105 110  
Tyr Ser Thr Gly Ser Asp Ala Thr Glu Ser Asp Met His Ile His Lys  
115 120 125  
Ala Leu Met Asp Ile Asn Glu Ser Pro Val Tyr Val Leu Leu Asn Pro  
130 135 140  
Ala Ile Asn His Ala Gln Lys Asp Leu Pro Val Thr Ile Tyr Glu Ser  
145 150 155 160  
Glu Phe His Val Ile Asp Gly Ile Pro Gln Ser Ile Phe Val His Thr  
165 170 175  
Ser Tyr Thr Ile Glu Thr Val Glu Ala Glu Arg Ile Ser Val Asp His  
180 185 190  
Val Ala His Leu Lys Pro Ser Asp Gly Gly Ser Ala Ala Thr Gln Leu  
195 200 205  
Ala Ala His Leu Thr Gly Ile His Ser Ala Ile Lys Met Leu Asn Ser  
210 215 220  
Arg Ile Arg Val Leu Tyr Gln His Ile Val Ala Met Gln Lys Gly Asp  
225 230 235 240  
Lys Pro Cys Glu Asn Ser Val Leu Arg Gln Val Ser Ser Leu Leu Arg  
245 250 255  
Ser Leu Pro Ala Ala Glu Ser Glu Lys Phe Asn Glu Asn Phe Leu Met  
260 265 270  
Glu Tyr Asn Asp Lys Leu Leu Met Ser Tyr Leu Ala Met Ile Thr Asn  
275 280 285  
Cys Thr Ser Asn Met Asn Glu Val Val Asp Lys Phe Asn Thr Ala Tyr  
290 295 300  
Asp Lys His Ser Arg Arg Gly Gly Arg Thr Ala Phe Met  
305 310 315

(2) INFORMATION FOR SEQ ID NO:1993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids



- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..300  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571505  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:

Met Leu Asn Ile Ser Asp His Phe Thr Arg Val Lys Thr Gln Leu Asn  
1                  5                  10                  15  
Pro Pro Ala Ala Ser Cys Ala Thr Gly Asn Gly Ser Asn Asn Ala Asp  
                  20                  25                  30  
Ala Met Leu Leu Gln Asn Pro Arg Val Tyr Gly Cys Val Ile Gly Leu  
                  35                  40                  45  
Gln Arg Gly Arg Thr Val Glu Ile Phe Asn Ser Phe Glu Leu Ile Phe  
50                  55                  60  
Asp Pro Ala Leu Asp Thr Leu Asp Arg Ser Phe Leu Glu Lys Lys Gln  
65                  70                  75                  80  
Glu Leu Tyr Lys Lys Val Phe Pro Asp Phe Tyr Val Leu Gly Trp Tyr  
                  85                  90                  95  
Ser Thr Gly Ser Asp Ala Thr Glu Ser Asp Met His Ile His Lys Ala  
                  100                  105                  110  
Leu Met Asp Ile Asn Glu Ser Pro Val Tyr Val Leu Leu Asn Pro Ala  
                  115                  120                  125  
Ile Asn His Ala Gln Lys Asp Leu Pro Val Thr Ile Tyr Glu Ser Glu  
130                  135                  140  
Phe His Val Ile Asp Gly Ile Pro Gln Ser Ile Phe Val His Thr Ser  
145                  150                  155                  160  
Tyr Thr Ile Glu Thr Val Glu Ala Glu Arg Ile Ser Val Asp His Val  
                  165                  170                  175  
Ala His Leu Lys Pro Ser Asp Gly Gly Ser Ala Ala Thr Gln Leu Ala  
                  180                  185                  190  
Ala His Leu Thr Gly Ile His Ser Ala Ile Lys Met Leu Asn Ser Arg  
                  195                  200                  205  
Ile Arg Val Leu Tyr Gln His Ile Val Ala Met Gln Lys Gly Asp Lys  
210                  215                  220  
Pro Cys Glu Asn Ser Val Leu Arg Gln Val Ser Ser Leu Leu Arg Ser  
225                  230                  235                  240  
Leu Pro Ala Ala Glu Ser Glu Lys Phe Asn Glu Asn Phe Leu Met Glu  
                  245                  250                  255  
Tyr Asn Asp Lys Leu Leu Met Ser Tyr Leu Ala Met Ile Thr Asn Cys  
                  260                  265                  270  
Thr Ser Asn Met Asn Glu Val Val Asp Lys Phe Asn Thr Ala Tyr Asp  
                  275                  280                  285  
Lys His Ser Arg Arg Gly Gly Arg Thr Ala Phe Met  
290                  295                  300

(2) INFORMATION FOR SEQ ID NO:1994:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1965 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1965  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571522  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

aaaacacaaa catatcttct atcaaacc accagctcta ttctctacct catttctcat  
cataacaaag agagagaaaa aaactatgga attgacactg aattcctcga gttctcttat

60  
120

```
caaacgtaaa gatgccaaga gttctagaaa ccaagaaagt tcctccaaca acatgacctt 180
tgccaagatg aagccgccaa catatcaatt ccaagcaaag aactcgggta aggaaatgaa 240
gttcactcac gagaagacct tcacgccaga aggtgaaacc cttgagaaat gggagaagct 300
ccaagttctc tcataccacc actccaagaa cgacgctagc gttccgggtg tcgtcatggt 360
accgctcgac acagtaacaa tgtcagggca tttgaacaaa ccacgagcca tgaacgctag 420
tttgatggcc ctgaaaggag ctggtgtgga aggtgtgatg gtggatgctt ggtggggatt 480
ggtggagaaa gatggacctt tgaattataa ctgggaaggc tatgccgagc ttatacagat 540
ggttcaaaaag cacgggtctc aactccagggt cgttatgtca ttccatcaat gtggaggaaa 600
cgtaggagac ttttgcagta tccccttgcc tccatgggtg cttgaagaga tcagcaagaa 660
ccctgatctt gtctacacag acaaatctgg gagaaggaaac cctgaatata tctccttggg 720
atgtgattct gtgcctgtcc taagaggaag aacacctatc caggtctact cagatttcat 780
gaggagcttc cgtgaacgat ttgaaggcta cataggagga gttattgcgg aaattcaagt 840
aggaatggga ccttgtggag aattgagata cccatcatac cctgagagca acgggacctg 900
gagattcccc ggaattggag agttccagtg ctacgacaag tatatgaaat cgtcacttca 960
agcatatgct gagtcaatcg ggaaaactaa ctggggaaca agtggacctc atgatgccgg 1020
cgagtacaag aacctcccag aagatactga atttttcagg agagacggaa catggaatag 1080
cgagtatgga aagtttttca tggaatggta ctccgggaag ctgctagaac atggagacca 1140
actcctatct tcagcgaaag gtatctttca aggaagcgga gcaaagctat caggaaaggt 1200
agctggaatt cactggcact acaacaccag gtcacacgca gctgagctaa ccgctggata 1260
ctacaacaca agaaaccatg acgggtatct gccaatagct aagatgttca acaaacatgg 1320
agttgtgctc aacttcacct gcatggagat gaaagacggg gagcaacctg agcacgcgaa 1380
ttgtcacca gaaggtctgg tcaagcaagt acagaacgcg acaaggcagg ccggaaccga 1440
actagcaggg gagaacgcgc tagaacgata tgactcaagc gcattcggac aagtggtagc 1500
aacaatatagg tcagattctg gaaatgggtt aaccgcattt acttacctaa gaatgaacaa 1560
gcggttatatt gaggggtcaaa attggcagca gttagtggag tttgttaaga acatgaagga 1620
aggtggtcat gggaggagac tctcaaaaga agacacaact ggaagtgacc tttatgttgg 1680
atttgtcaaa ggcaagatcg ctgagaatgt ggaggaggct gctttagtgt aatttccac 1740
Rataggtaca tacatatagt gtggtgttta ttgtattcct gtctgataaa taactagaga 1800
gatcaaacca gtaagagtgt taaagctata gatttgcaca attctgggtc agagtcagag 1860
caaagagaag caaaatcaag atgatgtaca cttagatgtt tcctatgagt tttccttgta 1920
catcatcttc atactcttaa tctcaaatac tatgcatttt tctcc
```

(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1571523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

```
Lys His Lys His Ile Phe Tyr Gln Thr Pro Thr Ala Leu Phe Ser Thr
1 5 10 15
Ser Phe Leu Ile Ile Thr Lys Arg Glu Lys Lys Thr Met Glu Leu Thr
20 25 30
Leu Asn Ser Ser Ser Ser Leu Ile Lys Arg Lys Asp Ala Lys Ser Ser
35 40 45
Arg Asn Gln Glu Ser Ser Ser Asn Asn Met Thr Phe Ala Lys Met Lys
50 55 60
Pro Pro Thr Tyr Gln Phe Gln Ala Lys Asn Ser Val Lys Glu Met Lys
65 70 75 80
Phe Thr His Glu Lys Thr Phe Thr Pro Glu Gly Glu Thr Leu Glu Lys
85 90 95
Trp Glu Lys Leu His Val Leu Ser Tyr Pro His Ser Lys Asn Asp Ala
100 105 110
Ser Val Pro Val Phe Val Met Leu Pro Leu Asp Thr Val Thr Met Ser
115 120 125
Gly His Leu Asn Lys Pro Arg Ala Met Asn Ala Ser Leu Met Ala Leu
130 135 140
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Ala | Gly | Val | Glu | Gly | Val | Met | Val | Asp | Ala | Trp | Trp | Gly | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Glu | Lys | Asp | Gly | Pro | Met | Asn | Tyr | Asn | Trp | Glu | Gly | Tyr | Ala | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |
| Leu | Ile | Gln | Met | Val | Gln | Lys | His | Gly | Leu | Lys | Leu | Gln | Val | Val | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Phe | His | Gln | Cys | Gly | Gly | Asn | Val | Gly | Asp | Ser | Cys | Ser | Ile | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Pro | Pro | Trp | Val | Leu | Glu | Glu | Ile | Ser | Lys | Asn | Pro | Asp | Leu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Thr | Asp | Lys | Ser | Gly | Arg | Arg | Asn | Pro | Glu | Tyr | Ile | Ser | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Asp | Ser | Val | Pro | Val | Leu | Arg | Gly | Arg | Thr | Pro | Ile | Gln | Val | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Asp | Phe | Met | Arg | Ser | Phe | Arg | Glu | Arg | Phe | Glu | Gly | Tyr | Ile | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Val | Ile | Ala | Glu | Ile | Gln | Val | Gly | Met | Gly | Pro | Cys | Gly | Glu | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Tyr | Pro | Ser | Tyr | Pro | Glu | Ser | Asn | Gly | Thr | Trp | Arg | Phe | Pro | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Gly | Glu | Phe | Gln | Cys | Tyr | Asp | Lys | Tyr | Met | Lys | Ser | Ser | Leu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Tyr | Ala | Glu | Ser | Ile | Gly | Lys | Thr | Asn | Trp | Gly | Thr | Ser | Gly | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | Asp | Ala | Gly | Glu | Tyr | Lys | Asn | Leu | Pro | Glu | Asp | Thr | Glu | Phe | Phe |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg | Arg | Asp | Gly | Thr | Trp | Asn | Ser | Glu | Tyr | Gly | Lys | Phe | Phe | Met | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Trp | Tyr | Ser | Gly | Lys | Leu | Leu | Glu | His | Gly | Asp | Gln | Leu | Leu | Ser | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Lys | Gly | Ile | Phe | Gln | Gly | Ser | Gly | Ala | Lys | Leu | Ser | Gly | Lys | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Gly | Ile | His | Trp | His | Tyr | Asn | Thr | Arg | Ser | His | Ala | Ala | Glu | Leu |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Thr | Ala | Gly | Tyr | Tyr | Asn | Thr | Arg | Asn | His | Asp | Gly | Tyr | Leu | Pro | Ile |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Lys | Met | Phe | Asn | Lys | His | Gly | Val | Val | Leu | Asn | Phe | Thr | Cys | Met |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Met | Lys | Asp | Gly | Glu | Gln | Pro | Glu | His | Ala | Asn | Cys | Ser | Pro | Glu |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Leu | Val | Lys | Gln | Val | Gln | Asn | Ala | Thr | Arg | Gln | Ala | Gly | Thr | Glu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Ala | Gly | Glu | Asn | Ala | Leu | Glu | Arg | Tyr | Asp | Ser | Ser | Ala | Phe | Gly |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Gln | Val | Val | Ala | Thr | Asn | Arg | Ser | Asp | Ser | Gly | Asn | Gly | Leu | Thr | Ala |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Phe | Thr | Tyr | Leu | Arg | Met | Asn | Lys | Arg | Leu | Phe | Glu | Gly | Gln | Asn | Trp |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Gln | Gln | Leu | Val | Glu | Phe | Val | Lys | Asn | Met | Lys | Glu | Gly | Gly | His | Gly |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Arg | Arg | Leu | Ser | Lys | Glu | Asp | Thr | Thr | Gly | Ser | Asp | Leu | Tyr | Val | Gly |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Phe | Val | Lys | Gly | Lys | Ile | Ala | Glu | Asn | Val | Glu | Glu | Ala | Ala | Leu | Val |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |

- (2) INFORMATION FOR SEQ ID NO:1996:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 548 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..548  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571524  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Thr | Leu | Asn | Ser | Ser | Ser | Ser | Leu | Ile | Lys | Arg | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Lys | Ser | Ser | Arg | Asn | Gln | Glu | Ser | Ser | Ser | Asn | Asn | Met | Thr | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Lys | Met | Lys | Pro | Pro | Thr | Tyr | Gln | Phe | Gln | Ala | Lys | Asn | Ser | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Met | Lys | Phe | Thr | His | Glu | Lys | Thr | Phe | Thr | Pro | Glu | Gly | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Leu | Glu | Lys | Trp | Glu | Lys | Leu | His | Val | Leu | Ser | Tyr | Pro | His | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Asn | Asp | Ala | Ser | Val | Pro | Val | Phe | Val | Met | Leu | Pro | Leu | Asp | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Thr | Met | Ser | Gly | His | Leu | Asn | Lys | Pro | Arg | Ala | Met | Asn | Ala | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Met | Ala | Leu | Lys | Gly | Ala | Gly | Val | Glu | Gly | Val | Met | Val | Asp | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Trp | Gly | Leu | Val | Glu | Lys | Asp | Gly | Pro | Met | Asn | Tyr | Asn | Trp | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Tyr | Ala | Glu | Leu | Ile | Gln | Met | Val | Gln | Lys | His | Gly | Leu | Lys | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Val | Val | Met | Ser | Phe | His | Gln | Cys | Gly | Gly | Asn | Val | Gly | Asp | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Ser | Ile | Pro | Leu | Pro | Pro | Trp | Val | Leu | Glu | Glu | Ile | Ser | Lys | Asn |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Asp | Leu | Val | Tyr | Thr | Asp | Lys | Ser | Gly | Arg | Arg | Asn | Pro | Glu | Tyr |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Ser | Leu | Gly | Cys | Asp | Ser | Val | Pro | Val | Leu | Arg | Gly | Arg | Thr | Pro |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ile | Gln | Val | Tyr | Ser | Asp | Phe | Met | Arg | Ser | Phe | Arg | Glu | Arg | Phe | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Tyr | Ile | Gly | Gly | Val | Ile | Ala | Glu | Ile | Gln | Val | Gly | Met | Gly | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys | Gly | Glu | Leu | Arg | Tyr | Pro | Ser | Tyr | Pro | Glu | Ser | Asn | Gly | Thr | Trp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | Phe | Pro | Gly | Ile | Gly | Glu | Phe | Gln | Cys | Tyr | Asp | Lys | Tyr | Met | Lys |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Ser | Leu | Gln | Ala | Tyr | Ala | Glu | Ser | Ile | Gly | Lys | Thr | Asn | Trp | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ser | Gly | Pro | His | Asp | Ala | Gly | Glu | Tyr | Lys | Asn | Leu | Pro | Glu | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Thr | Glu | Phe | Phe | Arg | Arg | Asp | Gly | Thr | Trp | Asn | Ser | Glu | Tyr | Gly | Lys |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Phe | Met | Glu | Trp | Tyr | Ser | Gly | Lys | Leu | Leu | Glu | His | Gly | Asp | Gln |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Leu | Ser | Ser | Ala | Lys | Gly | Ile | Phe | Gln | Gly | Ser | Gly | Ala | Lys | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Gly | Lys | Val | Ala | Gly | Ile | His | Trp | His | Tyr | Asn | Thr | Arg | Ser | His |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Ala | Glu | Leu | Thr | Ala | Gly | Tyr | Tyr | Asn | Thr | Arg | Asn | His | Asp | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Tyr | Leu | Pro | Ile | Ala | Lys | Met | Phe | Asn | Lys | His | Gly | Val | Val | Leu | Asn |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Phe | Thr | Cys | Met | Glu | Met | Lys | Asp | Gly | Glu | Gln | Pro | Glu | His | Ala | Asn |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     |     | 430 |     |

Cys Ser Pro Glu Gly Leu Val Lys Gln Val Gln Asn Ala Thr Arg Gln  
435 440 445  
Ala Gly Thr Glu Leu Ala Gly Glu Asn Ala Leu Glu Arg Tyr Asp Ser  
450 455 460  
Ser Ala Phe Gly Gln Val Val Ala Thr Asn Arg Ser Asp Ser Gly Asn  
465 470 475 480  
Gly Leu Thr Ala Phe Thr Tyr Leu Arg Met Asn Lys Arg Leu Phe Glu  
485 490 495  
Gly Gln Asn Trp Gln Gln Leu Val Glu Phe Val Lys Asn Met Lys Glu  
500 505 510  
Gly Gly His Gly Arg Arg Leu Ser Lys Glu Asp Thr Thr Gly Ser Asp  
515 520 525  
Leu Tyr Val Gly Phe Val Lys Gly Lys Ile Ala Glu Asn Val Glu Glu  
530 535 540  
Ala Ala Leu Val  
545

(2) INFORMATION FOR SEQ ID NO:1997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1571525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

Met Thr Phe Ala Lys Met Lys Pro Pro Thr Tyr Gln Phe Gln Ala Lys  
1 5 10 15  
Asn Ser Val Lys Glu Met Lys Phe Thr His Glu Lys Thr Phe Thr Pro  
20 25 30  
Glu Gly Glu Thr Leu Glu Lys Trp Glu Lys Leu His Val Leu Ser Tyr  
35 40 45  
Pro His Ser Lys Asn Asp Ala Ser Val Pro Val Phe Val Met Leu Pro  
50 55 60  
Leu Asp Thr Val Thr Met Ser Gly His Leu Asn Lys Pro Arg Ala Met  
65 70 75 80  
Asn Ala Ser Leu Met Ala Leu Lys Gly Ala Gly Val Glu Gly Val Met  
85 90 95  
Val Asp Ala Trp Trp Gly Leu Val Glu Lys Asp Gly Pro Met Asn Tyr  
100 105 110  
Asn Trp Glu Gly Tyr Ala Glu Leu Ile Gln Met Val Gln Lys His Gly  
115 120 125  
Leu Lys Leu Gln Val Val Met Ser Phe His Gln Cys Gly Gly Asn Val  
130 135 140  
Gly Asp Ser Cys Ser Ile Pro Leu Pro Pro Trp Val Leu Glu Glu Ile  
145 150 155 160  
Ser Lys Asn Pro Asp Leu Val Tyr Thr Asp Lys Ser Gly Arg Arg Asn  
165 170 175  
Pro Glu Tyr Ile Ser Leu Gly Cys Asp Ser Val Pro Val Leu Arg Gly  
180 185 190  
Arg Thr Pro Ile Gln Val Tyr Ser Asp Phe Met Arg Ser Phe Arg Glu  
195 200 205  
Arg Phe Glu Gly Tyr Ile Gly Gly Val Ile Ala Glu Ile Gln Val Gly  
210 215 220  
Met Gly Pro Cys Gly Glu Leu Arg Tyr Pro Ser Tyr Pro Glu Ser Asn  
225 230 235 240  
Gly Thr Trp Arg Phe Pro Gly Ile Gly Glu Phe Gln Cys Tyr Asp Lys  
245 250 255  
Tyr Met Lys Ser Ser Leu Gln Ala Tyr Ala Glu Ser Ile Gly Lys Thr

260 265 270  
Asn Trp Gly Thr Ser Gly Pro His Asp Ala Gly Glu Tyr Lys Asn Leu  
275 280 285  
Pro Glu Asp Thr Glu Phe Phe Arg Arg Asp Gly Thr Trp Asn Ser Glu  
290 295 300  
Tyr Gly Lys Phe Phe Met Glu Trp Tyr Ser Gly Lys Leu Leu Glu His  
305 310 315 320  
Gly Asp Gln Leu Leu Ser Ser Ala Lys Gly Ile Phe Gln Gly Ser Gly  
325 330 335  
Ala Lys Leu Ser Gly Lys Val Ala Gly Ile His Trp His Tyr Asn Thr  
340 345 350  
Arg Ser His Ala Ala Glu Leu Thr Ala Gly Tyr Tyr Asn Thr Arg Asn  
355 360 365  
His Asp Gly Tyr Leu Pro Ile Ala Lys Met Phe Asn Lys His Gly Val  
370 375 380  
Val Leu Asn Phe Thr Cys Met Glu Met Lys Asp Gly Glu Gln Pro Glu  
385 390 395 400  
His Ala Asn Cys Ser Pro Glu Gly Leu Val Lys Gln Val Gln Asn Ala  
405 410 415  
Thr Arg Gln Ala Gly Thr Glu Leu Ala Gly Glu Asn Ala Leu Glu Arg  
420 425 430  
Tyr Asp Ser Ser Ala Phe Gly Gln Val Val Ala Thr Asn Arg Ser Asp  
435 440 445  
Ser Gly Asn Gly Leu Thr Ala Phe Thr Tyr Leu Arg Met Asn Lys Arg  
450 455 460  
Leu Phe Glu Gly Gln Asn Trp Gln Gln Leu Val Glu Phe Val Lys Asn  
465 470 475 480  
Met Lys Glu Gly Gly His Gly Arg Arg Leu Ser Lys Glu Asp Thr Thr  
485 490 495  
Gly Ser Asp Leu Tyr Val Gly Phe Val Lys Gly Lys Ile Ala Glu Asn  
500 505 510  
Val Glu Glu Ala Ala Leu Val  
515

(2) INFORMATION FOR SEQ ID NO:1998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gacacgatcc atcctaagaa acttcaattt tggggtttct cttcgttttc ttctttcttct  | 60  |
| ttctttcttcta gatcgagagg gacatgggtc ttaccagccg ccgttgacga ctacgacgac | 120 |
| cattctcttc ctcttcatct tctctccttc tgcttttctc tatttcctat tctctccaaa   | 180 |
| ttcaccattt ccttcaccca ctacagatc tccctttctt attagctatg ttcttttcta    | 240 |
| acacgccatc ttctagcgcc gccgctgccg gatcgataga ttcttccgcc gcccgagaaa   | 300 |
| attccaagag acccaagtat tcgaaattta ctacgacgga gcttctgtct tgcaaaccaa   | 360 |
| ttcttacgcc tgggtgggtg atttcaacgt ttttgatcat tagtggtatc ttcattcccc   | 420 |
| ttggtgttat ttctctcttt gcttctcagg atgttggtga gatcgttgat cggtatgata   | 480 |
| gtgcatgcat acctctatct gatagggcta acaagggtgc atacattcaa ggaactggaa   | 540 |
| ataaatcttg tacccggaag ctaattgtgc ctaagcgtat gaagcagcct atctacgtat   | 600 |
| attaccagct tgagaacttc taccagaatc accgcaggtg tgtgaaaagc cgaagtgatt   | 660 |
| cgcaattgag aagtgtgaaa gatgagaatc aaatagacgc atgcaagcct gaggatgatt   | 720 |
| ttggtgggca gccaatgtg ccatgtggtc taattgcttg gagtctcttt aatgacacat    | 780 |
| acgttctatc aagaaataac cagggtttta cggtaaacia gaaaggaatt gcatggaaga   | 840 |
| gcgacaagga acacaagttt gggaaaaatg tgtttcccaa gaactttcag aagggaatc    | 900 |
| tcactggtgg tgccagtcta gatccaaata aaccattgag tgatcaagag gatctgatcg   | 960 |

(2) INFORMATION FOR SEQ ID NO:1999:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1571530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

| Parameter                           | Value | Unit                                                 |
|-------------------------------------|-------|------------------------------------------------------|
| Temperature                         | 25    | °C                                                   |
| Pressure                            | 101.3 | kPa                                                  |
| Humidity                            | 50    | %                                                    |
| Light intensity                     | 100   | μmol photons m <sup>-2</sup> s <sup>-1</sup>         |
| CO <sub>2</sub> concentration       | 400   | ppm                                                  |
| Water potential                     | -0.1  | MPa                                                  |
| Soil moisture                       | 0.15  | g g <sup>-1</sup>                                    |
| Root length                         | 10    | cm                                                   |
| Leaf area                           | 15    | cm <sup>2</sup>                                      |
| Chlorophyll content                 | 25    | mg g <sup>-1</sup>                                   |
| Stomatal conductance                | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                | 10    | g C mol <sup>-1</sup> H <sub>2</sub> O               |
| Stomatal conductance to water vapor | 0.1   | mol m <sup>-2</sup> s <sup>-1</sup>                  |
| Transpiration rate                  | 1.0   | mmol m <sup>-2</sup> s <sup>-1</sup>                 |
| Photosynthetic rate                 | 10    | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Respiration rate                    | 2     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Gross primary productivity          | 8     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Net primary productivity            | 6     | μmol CO <sub>2</sub> m <sup>-2</sup> s <sup>-1</sup> |
| Carbon use efficiency               | 0.6   | g C g <sup>-1</sup> H <sub>2</sub> O                 |
| Water use efficiency                |       |                                                      |

(2) INFORMATION FOR SEQ ID NO:2000:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1571531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

|            |            |            |            |            |     |            |            |            |            |           |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----|
| Met<br>1   | Lys        | Gln        | Pro        | Ile<br>5   | Tyr | Val        | Tyr        | Tyr        | Gln<br>10  | Leu       | Glu        | Asn        | Phe        | Tyr<br>15  | Gln |
| Asn        | His        | Arg        | Arg<br>20  | Tyr        | Val | Lys        | Ser        | Arg<br>25  | Ser        | Asp       | Ser        | Gln        | Leu<br>30  | Arg        | Ser |
| Val        | Lys        | Asp<br>35  | Glu        | Asn        | Gln | Ile        | Asp<br>40  | Ala        | Cys        | Lys       | Pro        | Glu<br>45  | Asp        | Asp        | Phe |
| Gly<br>50  | Gly        | Gln        | Pro        | Ile        | Val | Pro<br>55  | Cys        | Gly        | Leu        | Ile       | Ala<br>60  | Trp        | Ser        | Leu        | Phe |
| Asn<br>65  | Asp        | Thr        | Tyr        | Val<br>70  | Leu | Ser        | Arg        | Asn        | Asn        | Gln<br>75 | Gly        | Leu        | Thr        | Val<br>80  | Asn |
| Lys        | Lys        | Gly        | Ile        | Ala<br>85  | Trp | Lys        | Ser        | Asp        | Lys<br>90  | Glu       | His        | Lys        | Phe        | Gly<br>95  | Lys |
| Asn        | Val        | Phe        | Pro<br>100 | Lys        | Asn | Phe        | Gln        | Lys<br>105 | Gly        | Asn       | Leu        | Thr        | Gly<br>110 | Gly        | Ala |
| Ser        | Leu        | Asp<br>115 | Pro        | Asn        | Lys | Pro        | Leu<br>120 | Ser        | Asp        | Gln       | Glu        | Asp<br>125 | Leu        | Ile        | Val |
| Trp<br>130 | Met        | Arg        | Thr        | Ala        | Ala | Leu<br>135 | Pro        | Thr        | Phe        | Arg       | Lys<br>140 | Leu        | Tyr        | Gly        | Lys |
| Ile<br>145 | Glu        | Ser        | Asp        | Leu<br>150 | Glu | Lys        | Gly        | Glu        | Asn<br>155 | Ile       | Gln        | Val        | Thr        | Leu<br>160 | Gln |
| Asn        | Asn        | Tyr        | Asn<br>165 | Thr        | Tyr | Ser        | Phe        | Ser        | Gly<br>170 | Lys       | Lys        | Lys        | Leu        | Val<br>175 | Leu |
| Ser        | Thr        | Thr        | Ser<br>180 | Trp        | Leu | Gly        | Gly        | Lys<br>185 | Asn        | Asp       | Phe        | Leu        | Gly<br>190 | Ile        | Ala |
| Tyr        | Leu        | Thr<br>195 | Val        | Gly        | Gly | Ile        | Cys<br>200 | Phe        | Val        | Leu       | Ala        | Leu<br>205 | Ala        | Phe        | Thr |
| Val        | Met<br>210 | Tyr        | Leu        | Val        | Lys | Pro<br>215 | Arg        | Arg        | Leu        | Gly       | Asp<br>220 | Pro        | Thr        | Tyr        | Leu |
| Ser<br>225 | Trp        | Asn        | Arg        | Ile<br>230 | Pro | Gly        | Gly        | Arg        |            |           |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1458 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1458

(D) OTHER INFORMATION: / Ceres Seq. ID 1571543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaatttgc | aaatcgga   | atttacacag | agaagcgcca | tgacctaaaa | atctcaaaac | 60  |
| ttccccaaca | aaaatggcgc | ttttactcaa | cccatttctt | tttacctacc | ttgtacatta | 120 |
| ccccttttct | caaattctac | tttcccactg | aaataacccc | atggcggaga | atcagaactg | 180 |



|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| tgcgaggatg | acgagagcgg | cggcgaaaacg | aaaagcgctcg | tccatggcgt  | tagacgaaaa  | 240  |
| cccagttagt | aagaagagag | ttgttctcgg  | agagcttccg  | aatatgtcca  | atgtcgttgc  | 300  |
| tgtacccaat | caagaaagag | agacccttaa  | ggctaaaaca  | agtgttaata  | cctcgaagag  | 360  |
| gcagatgaag | aaggctttga | tgattcctga  | agctagcgta  | ctaatacgat  | cgagatctgt  | 420  |
| tgatcctcag | atgtgtgagc | cttttgctag  | tgatatattgt | gottatctcc  | gtgaaatgga  | 480  |
| ggggaagccg | aaacatagac | cactacctga  | ttatattgaa  | aagggttcaga | gtgatttaac  | 540  |
| tccacacatg | agagcgggtt | tggtggattg  | gttagtggag  | gttgctgagg  | agtacaagct  | 600  |
| tgtttcggat | acgctttatc | tcactatctc  | ctatgttgat  | agattcttgt  | ctgtgaagcc  | 660  |
| tattaacagg | cagaagcttc | agcttggtgg  | agtttctgca  | atgcttattg  | cgtcgaaata  | 720  |
| tgaagagata | ggctctccta | aagttgaaga  | tttttgttac  | attacggata  | atacatttac  | 780  |
| taaacaagaa | gtggtgtcga | tggaggcgga  | tatacttctt  | gctctgcagt  | ttgaattagg  | 840  |
| aagcccaacc | atcaaaacat | tcctaagacg  | gtttacacgg  | gttgacacaag | aagatttcaa  | 900  |
| agactcaca  | ttgcagatag | agttcctttg  | ttgctatcta  | tcagaattga  | gtatgttaga  | 960  |
| ttacacctgt | gtgaagtatt | tgccatctct  | tttgtctgct  | tcagctgtat  | ttcttgcccg  | 1020 |
| gttcatcatc | cgtccaaaac | aacatccttg  | gaatcaaata  | ctagaagaat  | acacaaagta  | 1080 |
| caaagcagct | gatctacaag | tgtgcgtggg  | tatcatacat  | gacttgtatc  | taagcagaag  | 1140 |
| aggaaacact | ctagaagctg | ttagaaataa  | gtacaagcaa  | cacaagtaca  | agtgcgttgc  | 1200 |
| gaccatgcct | gtttcaccgg | agctacctct  | tgctttcttt  | gaagatatta  | ccatttagagg | 1260 |
| aatggcgtaa | aagaagcttg | aagcttatgt  | attggaagtg  | ttagttacct  | gaattttggg  | 1320 |
| ttgtatatat | ctgttagaat | ggcagattag  | tattgagtat  | tatctctttt  | agcgtatgtt  | 1380 |
| caatgatttt | ttGctwacac | tagttaAgaa  | actttttttt  | ttTgctTgac  | catttttttca | 1440 |
| atggtttatt | agattttt   |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1571544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Asn | Gln | Asn | Cys | Ala | Arg | Met | Thr | Arg | Ala | Ala | Ala | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Lys | Ala | Ser | Ser | Met | Ala | Leu | Asp | Glu | Asn | Pro | Val | Ser | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Val | Leu | Gly | Glu | Leu | Pro | Asn | Met | Ser | Asn | Val | Val | Ala | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Asn | Gln | Glu | Arg | Glu | Thr | Leu | Lys | Ala | Lys | Thr | Ser | Val | Asn | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Lys | Arg | Gln | Met | Lys | Lys | Ala | Leu | Met | Ile | Pro | Glu | Ala | Ser | Val |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Leu | Ile | Glu | Ser | Arg | Ser | Val | Asp | Pro | Gln | Met | Cys | Glu | Pro | Phe | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Asp | Ile | Cys | Ala | Tyr | Leu | Arg | Glu | Met | Glu | Gly | Lys | Pro | Lys | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Pro | Leu | Pro | Asp | Tyr | Ile | Glu | Lys | Val | Gln | Ser | Asp | Leu | Thr | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Met | Arg | Ala | Val | Leu | Val | Asp | Trp | Leu | Val | Glu | Val | Ala | Glu | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Tyr | Lys | Leu | Val | Ser | Asp | Thr | Leu | Tyr | Leu | Thr | Ile | Ser | Tyr | Val | Asp |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     | 160 |     |
| Arg | Phe | Leu | Ser | Val | Lys | Pro | Ile | Asn | Arg | Gln | Lys | Leu | Gln | Leu | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Val | Ser | Ala | Met | Leu | Ile | Ala | Ser | Lys | Tyr | Glu | Glu | Ile | Gly | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Lys | Val | Glu | Asp | Phe | Cys | Tyr | Ile | Thr | Asp | Asn | Thr | Phe | Thr | Lys |
|     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Gln | Glu | Val | Val | Ser | Met | Glu | Ala | Asp | Ile | Leu | Leu | Ala | Leu | Gln | Phe |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Arg | Ala | Ala | Lys | Arg | Lys | Ala | Ser | Ser | Met | Ala | Leu | Asp |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Asn | Pro | Val | Ser | Lys | Lys | Arg | Val | Val | Leu | Gly | Glu | Leu | Pro | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ser | Asn | Val | Val | Ala | Val | Pro | Asn | Gln | Glu | Arg | Glu | Thr | Leu | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Lys | Thr | Ser | Val | Asn | Thr | Ser | Lys | Arg | Gln | Met | Lys | Lys | Ala | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Met | Ile | Pro | Glu | Ala | Ser | Val | Leu | Ile | Glu | Ser | Arg | Ser | Val | Asp | Pro |
| 65  |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Gln | Met | Cys | Glu | Pro | Phe | Ala | Ser | Asp | Ile | Cys | Ala | Tyr | Leu | Arg | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Glu | Gly | Lys | Pro | Lys | His | Arg | Pro | Leu | Pro | Asp | Tyr | Ile | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Gln | Ser | Asp | Leu | Thr | Pro | His | Met | Arg | Ala | Val | Leu | Val | Asp | Trp |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Leu | Val | Glu | Val | Ala | Glu | Glu | Tyr | Lys | Leu | Val | Ser | Asp | Thr | Leu | Tyr |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Thr | Ile | Ser | Tyr | Val | Asp | Arg | Phe | Leu | Ser | Val | Lys | Pro | Ile | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Gln | Lys | Leu | Gln | Leu | Val | Gly | Val | Ser | Ala | Met | Leu | Ile | Ala | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Tyr | Glu | Glu | Ile | Gly | Pro | Pro | Lys | Val | Glu | Asp | Phe | Cys | Tyr | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Asp | Asn | Thr | Phe | Thr | Lys | Gln | Glu | Val | Val | Ser | Met | Glu | Ala | Asp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Leu | Leu | Ala | Leu | Gln | Phe | Glu | Leu | Gly | Ser | Pro | Thr | Ile | Lys | Thr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2004:

(A) LENGTH: 348 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1571546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Asp | Glu | Asn | Pro | Val | Ser | Lys | Lys | Arg | Val | Val | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Pro | Asn | Met | Ser | Asn | Val | Val | Ala | Val | Pro | Asn | Gln | Glu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Leu | Lys | Ala | Lys | Thr | Ser | Val | Asn | Thr | Ser | Lys | Arg | Gln | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Lys | Ala | Leu | Met | Ile | Pro | Glu | Ala | Ser | Val | Leu | Ile | Glu | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Val | Asp | Pro | Gln | Met | Cys | Glu | Pro | Phe | Ala | Ser | Asp | Ile | Cys | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Leu | Arg | Glu | Met | Glu | Gly | Lys | Pro | Lys | His | Arg | Pro | Leu | Pro | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Ile | Glu | Lys | Val | Gln | Ser | Asp | Leu | Thr | Pro | His | Met | Arg | Ala | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Val | Asp | Trp | Leu | Val | Glu | Val | Ala | Glu | Glu | Tyr | Lys | Leu | Val | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Thr | Leu | Tyr | Leu | Thr | Ile | Ser | Tyr | Val | Asp | Arg | Phe | Leu | Ser | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Pro | Ile | Asn | Arg | Gln | Lys | Leu | Gln | Leu | Val | Gly | Val | Ser | Ala | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Ile | Ala | Ser | Lys | Tyr | Glu | Glu | Ile | Gly | Pro | Pro | Lys | Val | Glu | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Cys | Tyr | Ile | Thr | Asp | Asn | Thr | Phe | Thr | Lys | Gln | Glu | Val | Val | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Glu | Ala | Asp | Ile | Leu | Leu | Ala | Leu | Gln | Phe | Glu | Leu | Gly | Ser | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ile | Lys | Thr | Phe | Leu | Arg | Arg | Phe | Thr | Arg | Val | Ala | Gln | Glu | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Lys | Asp | Ser | Gln | Leu | Gln | Ile | Glu | Phe | Leu | Cys | Cys | Tyr | Leu | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Leu | Ser | Met | Leu | Asp | Tyr | Thr | Cys | Val | Lys | Tyr | Leu | Pro | Ser | Leu |

245 250 255  
Leu Ser Ala Ser Ala Val Phe Leu Ala Arg Phe Ile Ile Arg Pro Lys  
260 265 270  
Gln His Pro Trp Asn Gln Met Leu Glu Glu Tyr Thr Lys Tyr Lys Ala  
275 280 285  
Ala Asp Leu Gln Val Cys Val Gly Ile Ile His Asp Leu Tyr Leu Ser  
290 295 300  
Arg Arg Gly Asn Thr Leu Glu Ala Val Arg Asn Lys Tyr Lys Gln His  
305 310 315 320  
Lys Tyr Lys Cys Val Ala Thr Met Pro Val Ser Pro Glu Leu Pro Leu  
325 330 335  
Ala Phe Phe Glu Asp Ile Thr Ile Arg Gly Met Ala  
340 345

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

acaaaagcat cataagaaga agaagaaact acaatagtta atcaatcaaa gagaagtaag 60  
agaaatggca gattctaact gtggatgtgg ctctctctgc aaatgtgggtg actctttcgg 120  
tgtgataatt ggaaagcttg ttcttttcag caagaatttg ctttcaaagt atgaagattg 180  
ggaggcaggt acaaaagctt tgctcgacaa ggaaaatata atcggcatgg gatcgattgg 240  
atcagtcctat agagcatctt tcgaaggagg agtttccatt gcagtgaaga agcttgagac 300  
cttaggaaga atcagaaacc aagaagagtt tgagcaagaa attggacggc ttggaggttt 360  
gcaacatccg aatctgtctt ctttccaagg ttactacttt tcctcaacaa tgcagttgat 420  
tctctctgag tttgtcccta atggtagcct ctacgataat ctacacctaa gaattttccc 480  
gggaaccagc tcaagctatg ggaatactga tttgaattgg cacagaagat ttcagattgc 540  
tttaggaact gcaaaagcgc tctctttcct tcacaatgac tgtaaaccgg cgattcttca 600  
tctcaatggt aagtccacca acattcttct agacgaaagg tacgaggcaa agctatcgga 660  
ttatgggtta gaaaagtttc ttccggttat ggacagcttt ggtttgacta agaagttcca 720  
caacgcggtt gggtagattg ctccagagtt agctcagcag agtttgagag cgagtgaaga 780  
atgcgatgtg tatagttacg gtgtggttct tcttgagctg gttacaggta gaaaaccggt 840  
ggagtctcca tcggaaaacc aagtcttgat cttgagagac tatgtgaggg atttggttga 900  
gactgggtca gcttctgatt gttttgacag TYTaagACgt tgagagagtt tgaagagaat 960  
gagctgattc aagtcattga gttaggactc ctttgtacgt ccgagaatcc actgaagaga 1020  
ccgagcatgg ctgaggttgt gcaggttctt gaatcaatca gaaatggatt tggatcatga 1080  
tgaagctttt tccctttttt tgagcaaaga ttgcatagga aatgtgcaga taagtttatt 1140  
cttttgggat tttccagttt tagattttacg tttgttcaat gaaattgtta ctctggtttm 1200  
cac

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

Met Ala Asp Ser Asn Cys Gly Cys Gly Ser Ser Cys Lys Cys Gly Asp  
1 5 10 15  
Ser Phe Gly Val Ile Ile Gly Lys Leu Val Leu Phe Ser Lys Asn Leu

00000000-00000000

20 25 30  
Pro Ser Lys Tyr Glu Asp Trp Glu Ala Gly Thr Lys Ala Leu Leu Asp  
35 40 45  
Lys Glu Asn Ile Ile Gly Met Gly Ser Ile Gly Ser Val Tyr Arg Ala  
50 55 60  
Ser Phe Glu Gly Gly Val Ser Ile Ala Val Lys Lys Leu Glu Thr Leu  
65 70 75 80  
Gly Arg Ile Arg Asn Gln Glu Glu Phe Glu Gln Glu Ile Gly Arg Leu  
85 90 95  
Gly Gly Leu Gln His Pro Asn Leu Ser Ser Phe Gln Gly Tyr Tyr Phe  
100 105 110  
Ser Ser Thr Met Gln Leu Ile Leu Ser Glu Phe Val Pro Asn Gly Ser  
115 120 125  
Leu Tyr Asp Asn Leu His Leu Arg Ile Phe Pro Gly Thr Ser Ser Ser  
130 135 140  
Tyr Gly Asn Thr Asp Leu Asn Trp His Arg Arg Phe Gln Ile Ala Leu  
145 150 155 160  
Gly Thr Ala Lys Ala Leu Ser Phe Leu His Asn Asp Cys Lys Pro Ala  
165 170 175  
Ile Leu His Leu Asn Val Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg  
180 185 190  
Tyr Glu Ala Lys Leu Ser Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val  
195 200 205  
Met Asp Ser Phe Gly Leu Thr Lys Lys Phe His Asn Ala Val Gly Tyr  
210 215 220  
Ile Ala Pro Glu Leu Ala Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys  
225 230 235 240  
Asp Val Tyr Ser Tyr Gly Val Val Leu Leu Glu Leu Val Thr Gly Arg  
245 250 255  
Lys Pro Val Glu Ser Pro Ser Glu Asn Gln Val Leu Ile Leu Arg Asp  
260 265 270  
Tyr Val Arg Asp Leu Leu Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp  
275 280 285  
Ser Xaa Arg Arg  
290

(2) INFORMATION FOR SEQ ID NO:2007:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1571549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Met Gly Ser Ile Gly Ser Val Tyr Arg Ala Ser Phe Glu Gly Gly Val  
1 5 10 15  
Ser Ile Ala Val Lys Lys Leu Glu Thr Leu Gly Arg Ile Arg Asn Gln  
20 25 30  
Glu Glu Phe Glu Gln Glu Ile Gly Arg Leu Gly Gly Leu Gln His Pro  
35 40 45  
Asn Leu Ser Ser Phe Gln Gly Tyr Tyr Phe Ser Ser Thr Met Gln Leu  
50 55 60  
Ile Leu Ser Glu Phe Val Pro Asn Gly Ser Leu Tyr Asp Asn Leu His  
65 70 75 80  
Leu Arg Ile Phe Pro Gly Thr Ser Ser Ser Tyr Gly Asn Thr Asp Leu  
85 90 95  
Asn Trp His Arg Arg Phe Gln Ile Ala Leu Gly Thr Ala Lys Ala Leu  
100 105 110

Ser Phe Leu His Asn Asp Cys Lys Pro Ala Ile Leu His Leu Asn Val  
115 120 125  
Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg Tyr Glu Ala Lys Leu Ser  
130 135 140  
Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val Met Asp Ser Phe Gly Leu  
145 150 155 160  
Thr Lys Lys Phe His Asn Ala Val Gly Tyr Ile Ala Pro Glu Leu Ala  
165 170 175  
Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys Asp Val Tyr Ser Tyr Gly  
180 185 190  
Val Val Leu Leu Glu Leu Val Thr Gly Arg Lys Pro Val Glu Ser Pro  
195 200 205  
Ser Glu Asn Gln Val Leu Ile Leu Arg Asp Tyr Val Arg Asp Leu Leu  
210 215 220  
Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp Ser Xaa Arg Arg  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Met Gln Leu Ile Leu Ser Glu Phe Val Pro Asn Gly Ser Leu Tyr Asp  
1 5 10 15  
Asn Leu His Leu Arg Ile Phe Pro Gly Thr Ser Ser Ser Tyr Gly Asn  
20 25 30  
Thr Asp Leu Asn Trp His Arg Arg Phe Gln Ile Ala Leu Gly Thr Ala  
35 40 45  
Lys Ala Leu Ser Phe Leu His Asn Asp Cys Lys Pro Ala Ile Leu His  
50 55 60  
Leu Asn Val Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg Tyr Glu Ala  
65 70 75 80  
Lys Leu Ser Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val Met Asp Ser  
85 90 95  
Phe Gly Leu Thr Lys Lys Phe His Asn Ala Val Gly Tyr Ile Ala Pro  
100 105 110  
Glu Leu Ala Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys Asp Val Tyr  
115 120 125  
Ser Tyr Gly Val Val Leu Leu Glu Leu Val Thr Gly Arg Lys Pro Val  
130 135 140  
Glu Ser Pro Ser Glu Asn Gln Val Leu Ile Leu Arg Asp Tyr Val Arg  
145 150 155 160  
Asp Leu Leu Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp Ser Xaa Arg  
165 170 175  
Arg

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

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(B) LOCATION: 1..1154

(D) OTHER INFORMATION: / Ceres Seq. ID 1571559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

|              |              |             |            |            |            |      |
|--------------|--------------|-------------|------------|------------|------------|------|
| agccccccttcc | ccaatatatttg | atcaattttct | aaagaaaacc | ccttcctcta | ctagtcctcc | 60   |
| tcctatatata  | acaaaatctt   | aagaaatctc  | tctacttggt | tcctctgtta | tcataatctc | 120  |
| ttctctctat   | atctctcttc   | ttctctcttt  | accctgtttt | tttttttcat | tccacagagc | 180  |
| ccagggttgat  | tgattttggt   | attcagagat  | atggggagag | gaaggattga | gattaagaag | 240  |
| attgagaata   | tcaacagtcg   | tcaagtcact  | ttctctaaga | gacgaaacgg | tttgatcaag | 300  |
| aaggctaaag   | agcttttcgat  | tctctgtgac  | gccgagggtg | ctcttatcat | cttctccagc | 360  |
| accggcaaga   | tttacgattt   | ctccagcgtc  | tgtatggagc | aaattccttc | tagatatgga | 420  |
| tacactactg   | cgtccactga   | gcataaacia  | caaagagaac | accaacttct | aatttggtgt | 480  |
| tcacatggaa   | atgaagctgt   | gttgcgaaat  | gatgattcta | tgaagggtga | acttgaaaga | 540  |
| ttacagcttg   | caattgagag   | acttaagggt  | aaggagcttg | aaggatatga | tttcccggat | 600  |
| cttattttctt  | ttgaaaacca   | gttgaaacgag | agcttgcata | gtgtcaagga | tcaaaagaca | 660  |
| caaatcctgc   | tcaaccagat   | tgagagatcc  | aggatacagg | agaaaaaagc | attggaagaa | 720  |
| aaccaaactct  | tgcgcaaaaca  | ggttgagatg  | ttggggagag | gttcaggacc | aaaagtgttg | 780  |
| aatgaaaggc   | ctcaagattc   | tagcccagaa  | gccgatcccg | agagctcttc | atcagaagag | 840  |
| gatgagaatg   | acaacgagga   | gcaccattcc  | gacacttcct | tgcagttggg | gttgctcgtc | 900  |
| acgggggtatt  | gcacaaagag   | aaagaagccg  | aagatcgaa  | tggtctgcga | taactctggg | 960  |
| agtcaagtgg   | cttctgattg   | atggaatcga  | ttatttttct | aattctggtt | gtttaggggt | 1020 |
| ctctatgtgt   | cttcttggtt   | ctggctgttc  | ttttgcttta | tttcatctca | agtagagttt | 1080 |
| tcctaatggt   | taggtggaac   | atttttccat  | aatcaagaag | ggatttgatc | aatcaataac | 1140 |
| attagatttt   | cYtt         |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1571560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Gly | Arg | Ile | Glu | Ile | Lys | Lys | Ile | Glu | Asn | Ile | Asn | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gln | Val | Thr | Phe | Ser | Lys | Arg | Arg | Asn | Gly | Leu | Ile | Lys | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Leu | Ser | Ile | Leu | Cys | Asp | Ala | Glu | Val | Ala | Leu | Ile | Ile | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ser | Thr | Gly | Lys | Ile | Tyr | Asp | Phe | Ser | Ser | Val | Cys | Met | Glu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Ser | Arg | Tyr | Gly | Tyr | Thr | Thr | Ala | Ser | Thr | Glu | His | Lys | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Arg | Glu | His | Gln | Leu | Leu | Ile | Cys | Ala | Ser | His | Gly | Asn | Glu | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Leu | Arg | Asn | Asp | Asp | Ser | Met | Lys | Val | Glu | Leu | Glu | Arg | Leu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Ile | Glu | Arg | Leu | Lys | Gly | Lys | Glu | Leu | Glu | Gly | Met | Ser | Phe |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Asp | Leu | Ile | Ser | Phe | Glu | Asn | Gln | Leu | Asn | Glu | Ser | Leu | His | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Lys | Asp | Gln | Lys | Thr | Gln | Ile | Leu | Leu | Asn | Gln | Ile | Glu | Arg | Ser |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | Ile | Gln | Glu | Lys | Lys | Ala | Leu | Glu | Glu | Asn | Gln | Ile | Leu | Arg | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gln | Val | Glu | Met | Leu | Gly | Arg | Gly | Ser | Gly | Pro | Lys | Val | Leu | Asn | Glu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Arg | Pro | Gln | Asp | Ser | Ser | Pro | Glu | Ala | Asp | Pro | Glu | Ser | Ser | Ser | Ser |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Asp | Glu | Asn | Asp | Asn | Glu | Glu | His | His | Ser | Asp | Thr | Ser | Leu |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Leu | Gly | Leu | Ser | Ser | Thr | Gly | Tyr | Cys | Thr | Lys | Arg | Lys | Lys | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Ile | Glu | Leu | Val | Cys | Asp | Asn | Ser | Gly | Ser | Gln | Val | Ala | Ser | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1571561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gln | Ile | Leu | Ser | Arg | Tyr | Gly | Tyr | Thr | Thr | Ala | Ser | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Lys | Gln | Gln | Arg | Glu | His | Gln | Leu | Leu | Ile | Cys | Ala | Ser | His | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Glu | Ala | Val | Leu | Arg | Asn | Asp | Asp | Ser | Met | Lys | Val | Glu | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Gln | Leu | Ala | Ile | Glu | Arg | Leu | Lys | Gly | Lys | Glu | Leu | Glu | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Ser | Phe | Pro | Asp | Leu | Ile | Ser | Phe | Glu | Asn | Gln | Leu | Asn | Glu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | His | Ser | Val | Lys | Asp | Gln | Lys | Thr | Gln | Ile | Leu | Leu | Asn | Gln | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Arg | Ser | Arg | Ile | Gln | Glu | Lys | Lys | Ala | Leu | Glu | Glu | Asn | Gln | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Arg | Lys | Gln | Val | Glu | Met | Leu | Gly | Arg | Gly | Ser | Gly | Pro | Lys | Val |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Asn | Glu | Arg | Pro | Gln | Asp | Ser | Ser | Pro | Glu | Ala | Asp | Pro | Glu | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ser | Ser | Ser | Glu | Glu | Asp | Glu | Asn | Asp | Asn | Glu | Glu | His | His | Ser | Asp |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Ser | Leu | Gln | Leu | Gly | Leu | Ser | Ser | Thr | Gly | Tyr | Cys | Thr | Lys | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Lys | Pro | Lys | Ile | Glu | Leu | Val | Cys | Asp | Asn | Ser | Gly | Ser | Gln | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ser | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1571562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Glu | Leu | Glu | Arg | Leu | Gln | Leu | Ala | Ile | Glu | Arg | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Lys | Glu | Leu | Glu | Gly | Met | Ser | Phe | Pro | Asp | Leu | Ile | Ser | Phe | Glu |



Met Ala Val Ser Cys Asn His Ser Ala Ile Leu Phe Ser Pro Ser Ser

1 5 10 15  
Thr Ala Gly Ser Ser Val Thr Ser Ser Ser Leu Ile Gly Phe  
20 25 30  
Pro Arg Phe Gln Thr Leu Arg Phe Lys Ser Arg Ser Val Tyr Ser Lys  
35 40 45  
Ser Arg Ala Ser Ser Pro Val Ser Ala Leu Pro Ser Arg Ser Leu Glu  
50 55 60  
Ala Leu Ile Phe Asp Cys Asp Gly Val Ile Leu Glu Ser Glu Asn Leu  
65 70 75 80  
His Arg Gln Ala Tyr Asn Asp Ala Phe Ser His Phe Asp Val Arg Cys  
85 90 95  
Pro Pro Ser Ser Ala Ser Leu Asp Trp Ser Leu Glu Phe Tyr Asp  
100 105 110  
Lys Phe Gln Asn Leu Val Gly Gly Gly Lys Pro Lys Met Arg Trp Tyr  
115 120 125  
Phe Lys Glu Asn Gly Trp Pro Thr Ser Thr Ile Phe Asp Ser Pro Pro  
130 135 140  
Gln Asn Asp Asp Asp Arg Ala Lys Leu Ile Asp Thr Leu Gln Asp Trp  
145 150 155 160  
Lys Thr Asp Arg Tyr Lys Glu Ile Ile Lys Ser Gly Ser Val Glu Pro  
165 170 175  
Arg Pro Gly Val Ile Arg Leu Met Asp Glu Ala Lys Ala Ala Gly Lys  
180 185 190  
Lys Leu Ala Val Cys Ser Ala Ala Thr Lys Ser Ser Val Ile Leu Cys  
195 200 205  
Leu Glu Asn Leu Leu Asp Ile Glu Arg Phe Gln Gly Leu Asp Cys Phe  
210 215 220  
Leu Ala Gly Asp Asp Val Lys Glu Lys Lys Pro Asp Pro Ser Ile Tyr  
225 230 235 240  
Ile Thr Ala Ala Glu Lys Leu Gly Val Ser Val Lys Asp Cys Leu Val  
245 250 255  
Val Gly Asp Ser Val Ile Gly Leu Gln Ala Ala Thr Lys Ala Gly Met  
260 265 270  
Ser Cys Val Ile Thr Tyr Thr Ser Ser Thr Ser Asp Gln Asp Phe Asn  
275 280 285  
Asp Ala Ile Ala Val Tyr Pro Asp Leu Ser Asn Val Lys Leu Thr Asp  
290 295 300  
Leu Glu Thr Leu Leu Gln Thr Ile Val Thr Ala Ala  
305 310 315

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

Met Arg Trp Tyr Phe Lys Glu Asn Gly Trp Pro Thr Ser Thr Ile Phe  
1 5 10 15  
Asp Ser Pro Pro Gln Asn Asp Asp Asp Arg Ala Lys Leu Ile Asp Thr  
20 25 30  
Leu Gln Asp Trp Lys Thr Asp Arg Tyr Lys Glu Ile Ile Lys Ser Gly  
35 40 45  
Ser Val Glu Pro Arg Pro Gly Val Ile Arg Leu Met Asp Glu Ala Lys  
50 55 60  
Ala Ala Gly Lys Lys Leu Ala Val Cys Ser Ala Ala Thr Lys Ser Ser  
65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Leu | Cys | Leu | Glu | Asn | Leu | Leu | Asp | Ile | Glu | Arg | Phe | Gln | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | Cys | Phe | Leu | Ala | Gly | Asp | Asp | Val | Lys | Glu | Lys | Lys | Pro | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ser | Ile | Tyr | Ile | Thr | Ala | Ala | Glu | Lys | Leu | Gly | Val | Ser | Val | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Cys | Leu | Val | Val | Gly | Asp | Ser | Val | Ile | Gly | Leu | Gln | Ala | Ala | Thr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ala | Gly | Met | Ser | Cys | Val | Ile | Thr | Tyr | Thr | Ser | Ser | Thr | Ser | Asp |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Asp | Phe | Asn | Asp | Ala | Ile | Ala | Val | Tyr | Pro | Asp | Leu | Ser | Asn | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Leu | Thr | Asp | Leu | Glu | Thr | Leu | Leu | Gln | Thr | Ile | Val | Thr | Ala | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

|             |            |             |             |            |              |      |
|-------------|------------|-------------|-------------|------------|--------------|------|
| aaatataaaa  | aatggatgga | tcaacgKgct  | gogatcatcc  | ttaccctcat | cgtaacctac   | 60   |
| attatatggt  | ttgtttcttt | acgtcggttcg | tataaaggtc  | cacgtgtctg | gcccttagtg   | 120  |
| ggcagtcctc  | cagcactcat | aacaaatgct  | caocgcattgc | acgacttcat | cgccgataac   | 180  |
| ctccgcatgt  | gcggcggtac | gtaccaaacg  | tgcattattcc | cgatcccgtt | cttggctaag   | 240  |
| aaacaaggtc  | acgtgactgt | cacgtgtgac  | ccaaagaatc  | tggagcatat | cttgaagacc   | 300  |
| cggttcgata  | attaccccaa | gggtcctagc  | tggcaatcag  | tcttcacga  | tctgttagga   | 360  |
| gatgggatct  | ttaattcaga | tgggtgacaca | tggcggtttc  | aacgtaagac | cgctgcattg   | 420  |
| gagttcacta  | cacgtaccct | tgcccaagcc  | atggctcggt  | gggttgatcg | agccatcaag   | 480  |
| aaccgtctcg  | tgccgattct | tgaatcagct  | aggagtcgag  | ccgagccgat | tgatcttcaa   | 540  |
| gatgttcttt  | tacggctcac | tttcgataac  | atttgcggtc  | taacatttgg | taaagatcca   | 600  |
| cggacactct  | cgccggagtt | tccctgagaac | ggattcgcg   | tggcttttga | tggagccacc   | 660  |
| gaagccactc  | ttcaacggtt | tatcatgcct  | gagtttattt  | ggaagatcag | aaaatggctt   | 720  |
| cggctcgggt  | tggaagatga | tatgagccga  | agcatcagcc  | acgtggataa | ttacttatca   | 780  |
| gagatcataa  | atacacgtaa | gctcgaattg  | ctaggctcagc | aacaagatgg | atcccgccat   | 840  |
| gatgatctat  | tgtcacggtt | catgaagaaa  | aaagaatcct  | actcggataa | atatcttaaa   | 900  |
| tacgtggcgt  | taaatttcat | cctagctgga  | cgtaaacacgt | catcggttgc | tatgagttgg   | 960  |
| ttcttctggt  | tggttagtct | taacccacga  | gtcgaagaaa  | aaatcataaa | cgagatctgc   | 1020 |
| accattctga  | tcaagacacg | tgacaccaat  | gtgtcgaagt  | ggaccgacga | gccgttgact   | 1080 |
| ttcgatgaaa  | ttgaccagtt | ggtctactta  | aaagcggcat  | tgtccgaaac | attgaggcta   | 1140 |
| tatccatcgg  | taccagaaga | ttcaaaaattt | gttgttgcca  | acgatgtttt | acctgacggg   | 1200 |
| acatttggtc  | catcgggatc | aaacggttaca | tattcgatat  | attcggttgg | gcgtatgaaa   | 1260 |
| ttcatttggg  | gtgaagattg | tctcgagttt  | aaaccggaaa  | gatggttaga | ggaaagccgg   | 1320 |
| gacgaaaaat  | gtaaccaata | caaattcgta  | gcgttcaatg  | ccggtccaog | gatttgtcta   | 1380 |
| ggcaaagact  | tggcttattt | gcagatgaaa  | tcaattactg  | cttcgatttt | gctccggcat   | 1440 |
| cggcttacgg  | tggctccggg | acatcgagtg  | gagcagaaga  | tgctattgac | gttggttcattg | 1500 |
| aagtttggtc  | ttaaaatgga | tgtgcataaa  | agggatttga  | cgttgccggt | ggagaaagtg   | 1560 |
| gttaatgaga  | tgaggaaaaa | gtgagattat  | tgggactaat  | gatggtaact | atgatgaagt   | 1620 |
| taaattgggtc | accggttttg | cataagcatt  | aatgtggacg  | atggtaattt | agaaattgtg   | 1680 |
| ttgttgtaag  | caaaaataat | ttaaaacata  | cttt        |            |              |      |

(2) INFORMATION FOR SEQ ID NO:2017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid

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|             |                         |                             |                 |  |     |
|-------------|-------------------------|-----------------------------|-----------------|--|-----|
|             | 420                     |                             | 425             |  | 430 |
| Glu Arg Trp | Leu Glu Glu Ser Arg     | Asp Glu Lys Cys             | Asn Gln Tyr Lys |  |     |
|             | 435                     | 440                         | 445             |  |     |
| Phe Val Ala | Phe Asn Ala Gly Pro Arg | Ile Cys Leu Gly Lys Asp Leu |                 |  |     |
|             | 450                     | 455                         | 460             |  |     |
| Ala Tyr Leu | Gln Met Lys Ser Ile Thr | Ala Ser Ile Leu Leu Arg His |                 |  |     |
|             | 465                     | 470                         | 475             |  | 480 |
| Arg Leu Thr | Val Ala Pro Gly His Arg | Val Glu Gln Lys Met Ser Leu |                 |  |     |
|             | 485                     | 490                         | 495             |  |     |
| Thr Leu Phe | Met Lys Phe Gly Leu Lys | Met Asp Val His Lys Arg Asp |                 |  |     |
|             | 500                     | 505                         | 510             |  |     |
| Leu Thr Leu | Pro Val Glu Lys Val Val | Asn Glu Met Arg Lys Lys     |                 |  |     |
|             | 515                     | 520                         | 525             |  |     |

(2) INFORMATION FOR SEQ ID NO:2018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1571572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

|                 |                                                 |     |     |
|-----------------|-------------------------------------------------|-----|-----|
| Met Asp Gln Xaa | Ala Ala Ile Ile Leu Thr Leu Ile Val Thr Tyr Ile |     |     |
| 1               | 5                                               | 10  | 15  |
| Ile Trp Phe Val | Ser Leu Arg Arg Ser Tyr Lys Gly Pro Arg Val Trp |     |     |
|                 | 20                                              | 25  | 30  |
| Pro Leu Val Gly | Ser Leu Pro Ala Leu Ile Thr Asn Ala His Arg Met |     |     |
|                 | 35                                              | 40  | 45  |
| His Asp Phe Ile | Ala Asp Asn Leu Arg Met Cys Gly Gly Thr Tyr Gln |     |     |
|                 | 50                                              | 55  | 60  |
| Thr Cys Ile Phe | Pro Ile Pro Phe Leu Ala Lys Lys Gln Gly His Val |     |     |
|                 | 65                                              | 70  | 75  |
| Thr Val Thr Cys | Asp Pro Lys Asn Leu Glu His Ile Leu Lys Thr Arg |     |     |
|                 | 85                                              | 90  | 95  |
| Phe Asp Asn Tyr | Pro Lys Gly Pro Ser Trp Gln Ser Val Phe His Asp |     |     |
|                 | 100                                             | 105 | 110 |
| Leu Leu Gly Asp | Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Arg Phe |     |     |
|                 | 115                                             | 120 | 125 |
| Gln Arg Lys Thr | Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg Gln |     |     |
|                 | 130                                             | 135 | 140 |
| Ala Met Ala Arg | Trp Val Asp Arg Ala Ile Lys Asn Arg Leu Val Pro |     |     |
|                 | 145                                             | 150 | 155 |
| Ile Leu Glu Ser | Ala Arg Ser Arg Ala Glu Pro Ile Asp Leu Gln Asp |     |     |
|                 | 165                                             | 170 | 175 |
| Val Leu Leu Arg | Leu Thr Phe Asp Asn Ile Cys Gly Leu Thr Phe Gly |     |     |
|                 | 180                                             | 185 | 190 |
| Lys Asp Pro Arg | Thr Leu Ser Pro Glu Phe Pro Glu Asn Gly Phe Ala |     |     |
|                 | 195                                             | 200 | 205 |
| Val Ala Phe Asp | Gly Ala Thr Glu Ala Thr Leu Gln Arg Phe Ile Met |     |     |
|                 | 210                                             | 215 | 220 |
| Pro Glu Phe Ile | Trp Lys Ile Arg Lys Trp Leu Arg Leu Gly Leu Glu |     |     |
|                 | 225                                             | 230 | 235 |
| Asp Asp Met Ser | Arg Ser Ile Ser His Val Asp Asn Tyr Leu Ser Glu |     |     |
|                 | 245                                             | 250 | 255 |
| Ile Ile Asn Thr | Arg Lys Leu Glu Leu Leu Gly Gln Gln Gln Asp Gly |     |     |
|                 | 260                                             | 265 | 270 |
| Ser Arg His Asp | Asp Leu Leu Ser Arg Phe Met Lys Lys Lys Glu Ser |     |     |
|                 | 275                                             | 280 | 285 |

Tyr Ser Asp Lys Tyr Leu Lys Tyr Val Ala Leu Asn Phe Ile Leu Ala  
290 295 300  
Gly Arg Asn Thr Ser Ser Val Ala Met Ser Trp Phe Phe Trp Leu Val  
305 310 315 320  
Ser Leu Asn Pro Arg Val Glu Glu Lys Ile Ile Asn Glu Ile Cys Thr  
325 330 335  
Ile Leu Ile Lys Thr Arg Asp Thr Asn Val Ser Lys Trp Thr Asp Glu  
340 345 350  
Pro Leu Thr Phe Asp Glu Ile Asp Gln Leu Val Tyr Leu Lys Ala Ala  
355 360 365  
Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp Ser Lys  
370 375 380  
Phe Val Val Ala Asn Asp Val Leu Pro Asp Gly Thr Phe Val Pro Ser  
385 390 395 400  
Gly Ser Asn Val Thr Tyr Ser Ile Tyr Ser Val Gly Arg Met Lys Phe  
405 410 415  
Ile Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp Leu Glu  
420 425 430  
Glu Ser Arg Asp Glu Lys Cys Asn Gln Tyr Lys Phe Val Ala Phe Asn  
435 440 445  
Ala Gly Pro Arg Ile Cys Leu Gly Lys Asp Leu Ala Tyr Leu Gln Met  
450 455 460  
Lys Ser Ile Thr Ala Ser Ile Leu Leu Arg His Arg Leu Thr Val Ala  
465 470 475 480  
Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met Lys  
485 490 495  
Phe Gly Leu Lys Met Asp Val His Lys Arg Asp Leu Thr Leu Pro Val  
500 505 510  
Glu Lys Val Val Asn Glu Met Arg Lys Lys  
515 520

(2) INFORMATION FOR SEQ ID NO:2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

Met His Asp Phe Ile Ala Asp Asn Leu Arg Met Cys Gly Gly Thr Tyr  
1 5 10 15  
Gln Thr Cys Ile Phe Pro Ile Pro Phe Leu Ala Lys Lys Gln Gly His  
20 25 30  
Val Thr Val Thr Cys Asp Pro Lys Gly Pro Ser Trp Gln Ser Val Phe His  
35 40 45  
Arg Phe Asp Asn Tyr Pro Lys Gly Pro Ser Trp Gln Ser Val Phe His  
50 55 60  
Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Arg  
65 70 75 80  
Phe Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Leu Arg  
85 90 95  
Gln Ala Met Ala Arg Trp Val Asp Arg Ala Ile Lys Asn Arg Leu Val  
100 105 110  
Pro Ile Leu Glu Ser Ala Arg Ser Arg Ala Glu Pro Ile Asp Leu Gln  
115 120 125  
Asp Val Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Thr Phe  
130 135 140  
Gly Lys Asp Pro Arg Thr Leu Ser Pro Glu Phe Pro Glu Asn Gly Phe

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 145                                                             | 150 | 155 | 160 |
| Ala Val Ala Phe Asp Gly Ala Thr Glu Ala Thr Leu Gln Arg Phe Ile |     |     |     |
|                                                                 | 165 | 170 | 175 |
| Met Pro Glu Phe Ile Trp Lys Ile Arg Lys Trp Leu Arg Leu Gly Leu |     |     |     |
|                                                                 | 180 | 185 | 190 |
| Glu Asp Asp Met Ser Arg Ser Ile Ser His Val Asp Asn Tyr Leu Ser |     |     |     |
|                                                                 | 195 | 200 | 205 |
| Glu Ile Ile Asn Thr Arg Lys Leu Glu Leu Leu Gly Gln Gln Gln Asp |     |     |     |
|                                                                 | 210 | 215 | 220 |
| Gly Ser Arg His Asp Asp Leu Leu Ser Arg Phe Met Lys Lys Lys Glu |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Ser Tyr Ser Asp Lys Tyr Leu Lys Tyr Val Ala Leu Asn Phe Ile Leu |     |     |     |
|                                                                 | 245 | 250 | 255 |
| Ala Gly Arg Asn Thr Ser Ser Val Ala Met Ser Trp Phe Phe Trp Leu |     |     |     |
|                                                                 | 260 | 265 | 270 |
| Val Ser Leu Asn Pro Arg Val Glu Glu Lys Ile Ile Asn Glu Ile Cys |     |     |     |
|                                                                 | 275 | 280 | 285 |
| Thr Ile Leu Ile Lys Thr Arg Asp Thr Asn Val Ser Lys Trp Thr Asp |     |     |     |
| 290                                                             | 295 | 300 |     |
| Glu Pro Leu Thr Phe Asp Glu Ile Asp Gln Leu Val Tyr Leu Lys Ala |     |     |     |
| 305                                                             | 310 | 315 | 320 |
| Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp Ser |     |     |     |
|                                                                 | 325 | 330 | 335 |
| Lys Phe Val Val Ala Asn Asp Val Leu Pro Asp Gly Thr Phe Val Pro |     |     |     |
|                                                                 | 340 | 345 | 350 |
| Ser Gly Ser Asn Val Thr Tyr Ser Ile Tyr Ser Val Gly Arg Met Lys |     |     |     |
|                                                                 | 355 | 360 | 365 |
| Phe Ile Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp Leu |     |     |     |
| 370                                                             | 375 | 380 |     |
| Glu Glu Ser Arg Asp Glu Lys Cys Asn Gln Tyr Lys Phe Val Ala Phe |     |     |     |
| 385                                                             | 390 | 395 | 400 |
| Asn Ala Gly Pro Arg Ile Cys Leu Gly Lys Asp Leu Ala Tyr Leu Gln |     |     |     |
|                                                                 | 405 | 410 | 415 |
| Met Lys Ser Ile Thr Ala Ser Ile Leu Leu Arg His Arg Leu Thr Val |     |     |     |
|                                                                 | 420 | 425 | 430 |
| Ala Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met |     |     |     |
|                                                                 | 435 | 440 | 445 |
| Lys Phe Gly Leu Lys Met Asp Val His Lys Arg Asp Leu Thr Leu Pro |     |     |     |
| 450                                                             | 455 | 460 |     |
| Val Glu Lys Val Val Asn Glu Met Arg Lys Lys                     |     |     |     |
| 465                                                             | 470 | 475 |     |

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaWgaagtt cctcattcaa aaaagatttc tcagccatca aaattctctt tctcttcac  | 60  |
| caacaaaaaa aaagcatacc tctttttctt coatatagat aagttaatta agaaaacgaa | 120 |
| ttatcaggtt ttgtttcggc tgatctgagg aagttcatct atggatacgg ctcaagtggc | 180 |
| acaggagatt gtagtgaagc ccttgaaga aatagtaaca aacacatgcc caaagccaca  | 240 |
| accgcaaccg cttcaaaccg agcagccacc gtcggtGggt ggagagagga aggcaagacc | 300 |
| agaaaaggat caagctgtaa actgtccgag atgtaactca accaacacaa agttttgtta | 360 |
| ctacaacaat tatagtttga cgcagccaag atacttctgc aaaggttgta gaaggattg  | 420 |
| gaccgaaGgc ggttcgctta ggaacattcc tgttggcggg ggctcaagaa agaacaagag | 480 |

```
atctcactct ttttctttctg atattagtaa caatcactcg gattctacac aaccagctac 540
aaagaagcat ctctctgata atcaccacca cctcatgagc atgtctcaac aaggtttgac 600
cgggtcaaaa cctaaattcc ttgagacgac ccaacaagat ctcaatttag gtttttcacc 660
acaatgggatg attaggacca acttcactga cctcatccac aacattggca acaacaccaa 720
caagagcaac aacaataaca atccattgat tgtttcttca tgttctacca tggctacttc 780
ttctctggat ctcataagaa acaatagtaa caatgggaat tcttcaaatt ctcccttcac 840
gggattttcca gttcataatg aagatccagc atcaggaggg ttttcaatgc aagatcatta 900
caagccttgc aacacaaaca ccacactgct aggggttttca ttagatcatc atcataataa 960
tggatttcat ggaggggttcc aaggaggaga agaaggtgga gaaggtggtg atgatgtgaa 1020
tgggaaggcac ttgtttcctt ttgaggattt gaaattgcc a gtttcttctt catcagcaac 1080
aattaatgtc gacattaatg aacatcagaa gcgaggaagc ggtagtgatg cagctgctac 1140
gtctggtggg tattggactg ggatgttgag tggaggatca tgggtgcta taatttctcg 1200
gtttggttga tgaagatagt actattagt gttaattatt gctatttatt taattaatca 1260
atatgttctt aatttc
```

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

```
Met Asp Thr Ala Gln Trp Pro Gln Glu Ile Val Val Lys Pro Leu Glu
1 5 10 15
Glu Ile Val Thr Asn Thr Cys Pro Lys Pro Gln Pro Gln Pro Leu Gln
20 25 30
Thr Gln Gln Pro Pro Ser Val Gly Gly Glu Arg Lys Ala Arg Pro Glu
35 40 45
Lys Asp Gln Ala Val Asn Cys Pro Arg Cys Asn Ser Thr Asn Thr Lys
50 55 60
Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys
65 70 75 80
Lys Gly Cys Arg Arg Tyr Trp Thr Glu Gly Gly Ser Leu Arg Asn Ile
85 90 95
Pro Val Gly Gly Ser Arg Lys Asn Lys Arg Ser His Ser Phe Ser
100 105 110
Ser Asp Ile Ser Asn Asn His Ser Asp Ser Thr Gln Pro Ala Thr Lys
115 120 125
Lys His Leu Ser Asp His His His His Leu Met Ser Met Ser Gln Gln
130 135 140
Gly Leu Thr Gly Gln Asn Pro Lys Phe Leu Glu Thr Thr Gln Gln Asp
145 150 155 160
Leu Asn Leu Gly Phe Ser Pro His Gly Met Ile Arg Thr Asn Phe Thr
165 170 175
Asp Leu Ile His Asn Ile Gly Asn Asn Thr Asn Lys Ser Asn Asn Asn
180 185 190
Asn Asn Pro Leu Ile Val Ser Ser Cys Ser Thr Met Ala Thr Ser Ser
195 200 205
Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn Gly Asn Ser Ser Asn Ser
210 215 220
Ser Phe Met Gly Phe Pro Val His Asn Glu Asp Pro Ala Ser Gly Gly
225 230 235 240
Phe Ser Met Gln Asp His Tyr Lys Pro Cys Asn Thr Asn Thr Thr Leu
245 250 255
Leu Gly Phe Ser Leu Asp His His His Asn Asn Gly Phe His Gly Gly
260 265 270
Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly Gly Asp Asp Val Asn Gly
```

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275 280 285  
Arg His Leu Phe Pro Phe Glu Asp Leu Lys Leu Pro Val Ser Ser Ser  
290 295 300  
Ser Ala Thr Ile Asn Val Asp Ile Asn Glu His Gln Lys Arg Gly Ser  
305 310 315 320  
Gly Ser Asp Ala Ala Ala Thr Ser Gly Gly Tyr Trp Thr Gly Met Leu  
325 330 335  
Ser Gly Gly Ser Trp Cys  
340

(2) INFORMATION FOR SEQ ID NO:2022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

Met Ser Met Ser Gln Gly Leu Thr Gly Gln Asn Pro Lys Phe Leu  
1 5 10 15  
Glu Thr Thr Gln Gln Asp Leu Asn Leu Gly Phe Ser Pro His Gly Met  
20 25 30  
Ile Arg Thr Asn Phe Thr Asp Leu Ile His Asn Ile Gly Asn Asn Thr  
35 40 45  
Asn Lys Ser Asn Asn Asn Asn Asn Pro Leu Ile Val Ser Ser Cys Ser  
50 55 60  
Thr Met Ala Thr Ser Ser Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn  
65 70 75 80  
Gly Asn Ser Ser Asn Ser Ser Phe Met Gly Phe Pro Val His Asn Glu  
85 90 95  
Asp Pro Ala Ser Gly Gly Phe Ser Met Gln Asp His Tyr Lys Pro Cys  
100 105 110  
Asn Thr Asn Thr Thr Leu Leu Gly Phe Ser Leu Asp His His His Asn  
115 120 125  
Asn Gly Phe His Gly Gly Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly  
130 135 140  
Gly Asp Asp Val Asn Gly Arg His Leu Phe Pro Phe Glu Asp Leu Lys  
145 150 155 160  
Leu Pro Val Ser Ser Ser Ser Ala Thr Ile Asn Val Asp Ile Asn Glu  
165 170 175  
His Gln Lys Arg Gly Ser Gly Ser Asp Ala Ala Ala Thr Ser Gly Gly  
180 185 190  
Tyr Trp Thr Gly Met Leu Ser Gly Ser Trp Cys  
195 200

(2) INFORMATION FOR SEQ ID NO:2023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1571585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Met Ser Gln Gln Gly Leu Thr Gly Gln Asn Pro Lys Phe Leu Glu Thr  
1 5 10 15

Thr Gln Gln Asp Leu Asn Leu Gly Phe Ser Pro His Gly Met Ile Arg  
20 25 30  
Thr Asn Phe Thr Asp Leu Ile His Asn Ile Gly Asn Asn Thr Asn Lys  
35 40 45  
Ser Asn Asn Asn Asn Asn Pro Leu Ile Val Ser Ser Cys Ser Thr Met  
50 55 60  
Ala Thr Ser Ser Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn Gly Asn  
65 70 75 80  
Ser Ser Asn Ser Ser Phe Met Gly Phe Pro Val His Asn Glu Asp Pro  
85 90 95  
Ala Ser Gly Gly Phe Ser Met Gln Asp His Tyr Lys Pro Cys Asn Thr  
100 105 110  
Asn Thr Thr Leu Leu Gly Phe Ser Leu Asp His His His Asn Asn Gly  
115 120 125  
Phe His Gly Gly Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly Gly Asp  
130 135 140  
Asp Val Asn Gly Arg His Leu Phe Pro Phe Glu Asp Leu Lys Leu Pro  
145 150 155 160  
Val Ser Ser Ser Ser Ala Thr Ile Asn Val Asp Ile Asn Glu His Gln  
165 170 175  
Lys Arg Gly Ser Gly Ser Asp Ala Ala Thr Ser Gly Gly Tyr Trp  
180 185 190  
Thr Gly Met Leu Ser Gly Gly Ser Trp Cys  
195 200

(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1709
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| attttggtgca | tcttcttcaa  | gctgcgcgc   | tttctcactc | ttttttatct | ctcaaatttg  | 60   |
| accttctccg  | ttgttctttc  | gcacgcgtca  | ggagcagaag | cttcaatctt | tgataatgtc  | 120  |
| gaggaacaag  | ggtttggtg   | agcaagatct  | taaaaaattg | gatgtaactg | tgctacatcc  | 180  |
| tctgtctcct  | gaggtcattt  | ctcgccaggc  | cactattaat | ataggaacca | ttggtcatgt  | 240  |
| cgctcatgga  | aagtccactg  | ttgttaaagc  | tatttctggt | gtccagactg | tccgttttaa  | 300  |
| aaatgaattg  | gagcgttaaca | ttaccattaa  | gcttggtat  | gcaaacgcca | agattttaca  | 360  |
| atgtgaggat  | gagaaatgcc  | ctagaccaat  | gtgctacaag | gcctacggaa | gtggaaagga  | 420  |
| agacactccc  | aattgtgatg  | tccccggatt  | tgaaaactcc | aagatgaaac | tattgaggca  | 480  |
| tgtctcattc  | gttgattgcc  | cgggtcacga  | tattctcatg | gcMacaatgc | ttaatggagc  | 540  |
| agccatcatg  | gatggtgcac  | tacttttaat  | cgctgcaaat | gaaacttgtc | cacaaccaca  | 600  |
| aacgtctgaa  | catcttgctg  | cogttgagat  | tatgcaactt | aagcatatca | tcattccttca | 660  |
| gaacaagatt  | gatcttattc  | aagagaatgt  | tgccattaat | cagcacgagg | caattcagaa  | 720  |
| atttataatg  | aacactgttg  | ctgatgctgc  | tccgatcgtc | cctgtctcag | cacaactgaa  | 780  |
| atacaacatt  | gatgtggtgt  | gcgagtacat  | tgtcaagaag | atcccaatcc | ctgagaggaa  | 840  |
| ttttgtgtca  | cccccaaata  | tgatagtgat  | tccgtctttt | gatgtcaaca | aacctgggta  | 900  |
| tgaggttgat  | gagatcaaag  | gtggagttgc  | aggtggaagt | atcctacggg | gtgttttgag  | 960  |
| agtcaaccaa  | ttaatcgaaa  | tccgacctgg  | tatcgttacc | aaagacgagc | gtggcaactc  | 1020 |
| aaaatgcact  | ccaatttact  | ctcgcatcat  | ttcactctac | gcggaacaga | acgagcttca  | 1080 |
| gtttgctggt  | cctgaagggtc | taataggagt  | tggaacaaca | atggacccaa | ctctcactcg  | 1140 |
| tgcagatcga  | ttagttgggtc | aagtccttgg  | tgaaatcggt | tcacttcctg | atgtatttgt  | 1200 |
| tgaaactcga  | gtgaacttct  | ttcttctaag  | acgtttgttg | ggagtggaga | caaagggatc  | 1260 |
| agagaaacaa  | gggaaagtgt  | caaagctaac  | gaaaggagag | attctgatgc | tcaacattgg  | 1320 |
| ttcgatgtcc  | actggagcca  | aagttgtagg  | agttaaagtc | gatctggcta | aactgcaact  | 1380 |
| gactgcgcct  | gtttgtacca  | gcaaaggaga  | gaaagtggct | ctaagcagac | gtgtggaaaa  | 1440 |
| gcattggcgt  | ttgattgggt  | gggggtcagat | tcaagctgga | accaccatcg | aagttcctcc  | 1500 |

```
ttcacctttc taagctatgt gttatTTTTg tctTTTTgt ttgtgtttct gaaaaaaga 1560
ttgttaaacc cctcaaaaag ataataaaac tctTTTTctc gttgggggat tttggagagt 1620
tcgtctttgc ggattaaaca tcttcaaaca gtacctgatt tggtattggt actagtttgc 1680
tctttgttat tgttactagt ttgctcttt
```

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Arg | Asn | Lys | Gly | Leu | Ala | Glu | Gln | Asp | Leu | Lys | Lys | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Thr | Val | Leu | His | Pro | Leu | Ser | Pro | Glu | Val | Ile | Ser | Arg | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ile | Asn | Ile | Gly | Thr | Ile | Gly | His | Val | Ala | His | Gly | Lys | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Lys | Ala | Ile | Ser | Gly | Val | Gln | Thr | Val | Arg | Phe | Lys | Asn | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Arg | Asn | Ile | Thr | Ile | Lys | Leu | Gly | Tyr | Ala | Asn | Ala | Lys | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Lys | Cys | Glu | Asp | Glu | Lys | Cys | Pro | Arg | Pro | Met | Cys | Tyr | Lys | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Gly | Ser | Gly | Lys | Glu | Asp | Thr | Pro | Asn | Cys | Asp | Val | Pro | Gly | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asn | Ser | Lys | Met | Lys | Leu | Leu | Arg | His | Val | Ser | Phe | Val | Asp | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gly | His | Asp | Ile | Leu | Met | Xaa | Thr | Met | Leu | Asn | Gly | Ala | Ala | Ile |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Asp | Gly | Ala | Leu | Leu | Leu | Ile | Ala | Ala | Asn | Glu | Thr | Cys | Pro | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Gln | Thr | Ser | Glu | His | Leu | Ala | Ala | Val | Glu | Ile | Met | Gln | Leu | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Ile | Ile | Ile | Leu | Gln | Asn | Lys | Ile | Asp | Leu | Ile | Gln | Glu | Asn | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Asn | Gln | His | Glu | Ala | Ile | Gln | Lys | Phe | Ile | Met | Asn | Thr | Val |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Asp | Ala | Ala | Pro | Ile | Val | Pro | Val | Ser | Ala | Gln | Leu | Lys | Tyr | Asn |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Ile | Asp | Val | Val | Cys | Glu | Tyr | Ile | Val | Lys | Lys | Ile | Pro | Ile | Pro | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Asn | Phe | Val | Ser | Pro | Pro | Asn | Met | Ile | Val | Ile | Arg | Ser | Phe | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Asn | Lys | Pro | Gly | Tyr | Glu | Val | Asp | Glu | Ile | Lys | Gly | Gly | Val | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Gly | Ser | Ile | Leu | Arg | Gly | Val | Leu | Arg | Val | Asn | Gln | Leu | Ile | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Arg | Pro | Gly | Ile | Val | Thr | Lys | Asp | Glu | Arg | Gly | Asn | Ser | Lys | Cys |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Thr | Pro | Ile | Tyr | Ser | Arg | Ile | Ile | Ser | Leu | Tyr | Ala | Glu | Gln | Asn | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Leu | Gln | Phe | Ala | Val | Pro | Glu | Gly | Leu | Ile | Gly | Val | Gly | Thr | Thr | Met |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Pro | Thr | Leu | Thr | Arg | Ala | Asp | Arg | Leu | Val | Gly | Gln | Val | Leu | Gly |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Glu | Ile | Gly | Ser | Leu | Pro | Asp | Val | Phe | Val | Glu | Leu | Glu | Val | Asn | Phe |

355 360 365  
Phe Leu Leu Arg Arg Leu Leu Gly Val Arg Thr Lys Gly Ser Glu Lys  
370 375 380  
Gln Gly Lys Val Ser Lys Leu Thr Lys Gly Glu Ile Leu Met Leu Asn  
385 390 395 400  
Ile Gly Ser Met Ser Thr Gly Ala Lys Val Val Gly Val Lys Val Asp  
405 410 415  
Leu Ala Lys Leu Gln Leu Thr Ala Pro Val Cys Thr Ser Lys Gly Glu  
420 425 430  
Lys Val Ala Leu Ser Arg Arg Val Glu Lys His Trp Arg Leu Ile Gly  
435 440 445  
Trp Gly Gln Ile Gln Ala Gly Thr Thr Ile Glu Val Pro Pro Ser Pro  
450 455 460  
Phe  
465

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1571588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

Met Cys Tyr Lys Ala Tyr Gly Ser Gly Lys Glu Asp Thr Pro Asn Cys  
1 5 10 15  
Asp Val Pro Gly Phe Glu Asn Ser Lys Met Lys Leu Leu Arg His Val  
20 25 30  
Ser Phe Val Asp Cys Pro Gly His Asp Ile Leu Met Xaa Thr Met Leu  
35 40 45  
Asn Gly Ala Ala Ile Met Asp Gly Ala Leu Leu Leu Ile Ala Ala Asn  
50 55 60  
Glu Thr Cys Pro Gln Pro Gln Thr Ser Glu His Leu Ala Ala Val Glu  
65 70 75 80  
Ile Met Gln Leu Lys His Ile Ile Ile Leu Gln Asn Lys Ile Asp Leu  
85 90 95  
Ile Gln Glu Asn Val Ala Ile Asn Gln His Glu Ala Ile Gln Lys Phe  
100 105 110  
Ile Met Asn Thr Val Ala Asp Ala Ala Pro Ile Val Pro Val Ser Ala  
115 120 125  
Gln Leu Lys Tyr Asn Ile Asp Val Val Cys Glu Tyr Ile Val Lys Lys  
130 135 140  
Ile Pro Ile Pro Glu Arg Asn Phe Val Ser Pro Pro Asn Met Ile Val  
145 150 155 160  
Ile Arg Ser Phe Asp Val Asn Lys Pro Gly Tyr Glu Val Asp Glu Ile  
165 170 175  
Lys Gly Gly Val Ala Gly Gly Ser Ile Leu Arg Gly Val Leu Arg Val  
180 185 190  
Asn Gln Leu Ile Glu Ile Arg Pro Gly Ile Val Thr Lys Asp Glu Arg  
195 200 205  
Gly Asn Ser Lys Cys Thr Pro Ile Tyr Ser Arg Ile Ile Ser Leu Tyr  
210 215 220  
Ala Glu Gln Asn Glu Leu Gln Phe Ala Val Pro Glu Gly Leu Ile Gly  
225 230 235 240  
Val Gly Thr Thr Met Asp Pro Thr Leu Thr Arg Ala Asp Arg Leu Val  
245 250 255  
Gly Gln Val Leu Gly Glu Ile Gly Ser Leu Pro Asp Val Phe Val Glu  
260 265 270

Leu Glu Val Asn Phe Phe Leu Leu Arg Arg Leu Leu Gly Val Arg Thr  
275 280 285  
Lys Gly Ser Glu Lys Gln Gly Lys Val Ser Lys Leu Thr Lys Gly Glu  
290 295 300  
Ile Leu Met Leu Asn Ile Gly Ser Met Ser Thr Gly Ala Lys Val Val  
305 310 315 320  
Gly Val Lys Val Asp Leu Ala Lys Leu Gln Leu Thr Ala Pro Val Cys  
325 330 335  
Thr Ser Lys Gly Glu Lys Val Ala Leu Ser Arg Arg Val Glu Lys His  
340 345 350  
Trp Arg Leu Ile Gly Trp Gly Gln Ile Gln Ala Gly Thr Thr Ile Glu  
355 360 365  
Val Pro Pro Ser Pro Phe  
370

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1571589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Met Lys Leu Leu Arg His Val Ser Phe Val Asp Cys Pro Gly His Asp  
1 5 10 15  
Ile Leu Met Xaa Thr Met Leu Asn Gly Ala Ala Ile Met Asp Gly Ala  
20 25 30  
Leu Leu Leu Ile Ala Ala Asn Glu Thr Cys Pro Gln Pro Gln Thr Ser  
35 40 45  
Glu His Leu Ala Ala Val Glu Ile Met Gln Leu Lys His Ile Ile Ile  
50 55 60  
Leu Gln Asn Lys Ile Asp Leu Ile Gln Glu Asn Val Ala Ile Asn Gln  
65 70 75 80  
His Glu Ala Ile Gln Lys Phe Ile Met Asn Thr Val Ala Asp Ala Ala  
85 90 95  
Pro Ile Val Pro Val Ser Ala Gln Leu Lys Tyr Asn Ile Asp Val Val  
100 105 110  
Cys Glu Tyr Ile Val Lys Lys Ile Pro Ile Pro Glu Arg Asn Phe Val  
115 120 125  
Ser Pro Pro Asn Met Ile Val Ile Arg Ser Phe Asp Val Asn Lys Pro  
130 135 140  
Gly Tyr Glu Val Asp Glu Ile Lys Gly Gly Val Ala Gly Gly Ser Ile  
145 150 155 160  
Leu Arg Gly Val Leu Arg Val Asn Gln Leu Ile Glu Ile Arg Pro Gly  
165 170 175  
Ile Val Thr Lys Asp Glu Arg Gly Asn Ser Lys Cys Thr Pro Ile Tyr  
180 185 190  
Ser Arg Ile Ile Ser Leu Tyr Ala Glu Gln Asn Glu Leu Gln Phe Ala  
195 200 205  
Val Pro Glu Gly Leu Ile Gly Val Gly Thr Thr Met Asp Pro Thr Leu  
210 215 220  
Thr Arg Ala Asp Arg Leu Val Gly Gln Val Leu Gly Glu Ile Gly Ser  
225 230 235 240  
Leu Pro Asp Val Phe Val Glu Leu Glu Val Asn Phe Phe Leu Leu Arg  
245 250 255  
Arg Leu Leu Gly Val Arg Thr Lys Gly Ser Glu Lys Gln Gly Lys Val  
260 265 270  
Ser Lys Leu Thr Lys Gly Glu Ile Leu Met Leu Asn Ile Gly Ser Met

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275 280 285  
Ser Thr Gly Ala Lys Val Val Gly Val Lys Val Asp Leu Ala Lys Leu  
290 295 300  
Gln Leu Thr Ala Pro Val Cys Thr Ser Lys Gly Glu Lys Val Ala Leu  
305 310 315 320  
Ser Arg Arg Val Glu Lys His Trp Arg Leu Ile Gly Trp Gly Gln Ile  
325 330 335  
Gln Ala Gly Thr Thr Ile Glu Val Pro Ser Pro Phe  
340 345

(2) INFORMATION FOR SEQ ID NO:2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

atctttacaa aaccgattac ttttgctgga atctgacgtc agcatacctg ctaccacttc 60  
cagagttcaa tcgattcttcg cctcgcttgAa acgttttCcc tcttcgatta tcaacagtgt 120  
ctccactcgt atcatcaccg cctccaacta attttgccat ctctctcgtt gttccaattt 180  
gattctacta gtgagctccg atttaattta ggggttttgaa agatgtcagc tttgaaaaat 240  
tacggcttga tctccattga ttctgccctc cattttcctc gatcaaatac attgcagagc 300  
tataagagga atgcaaaatg ggtctctcca atagcagctg ttgtacctaa cttccatctt 360  
cctatgcgca gtctcgagga taaaaacagg acaaacacag acgacataag gtcctctaga 420  
gtgatcacag ccattaagac accgtattta cctgatggaa gattcgacct ccaagcatac 480  
gatgacttag tcaacacgca gatagaaaac ggtgctgaag gtgtgattgt tgggtgtaca 540  
actggtgaag gccaatgcat gagctgggat gagcacataa tgcttatcgg ccatactgta 600  
aattgttttg ggggaaggat caaagtcatt ggaaacactg gaagtaactc gactagggaa 660  
gctattcatg ccactgagca aggattcgcc atgggaatgc acggggcact gcacattaac 720  
ccttactatg gaaaaacatc cattgaaggc atgaatgcgc attttcaaac cgttcttcat 780  
atgggaccga ctattatata caacgtgccca ggtcgaaagt gtcaggatat acctccccag 840  
gttatcttta aactctctca gaaccctaata atggctgggg ttaaggaatg cgttggtaat 900  
aaccgagttg aagagtatac tgagaaggga attgtcgttt ggagtggaaa tgatgatcag 960  
tgccatgatt ctatagtgga tcacggtgac actggagtga tatcggttac tagcaattta 1020  
gttcggggtt tgatgaggaa gttgatgttt gaaggtagaa actcagcgtt gaacgcaaag 1080  
cttcttcctt taatggattg gctattccaa gaaccgaatc ccattgggtg aaacactgct 1140  
ttggctcagt taggagttgc gaggccggtt tttcggttac cttatgtgcc attgcctctg 1200  
tccaaaagga ttgagttcgt taaactggtg aaggaaatcg gaagggagca tttttagtag 1260  
gacagagatg ttcaggtact tgatgatgat gacttcatct taatcggtcg atattagagt 1320  
ctcttccttg aagattggtt gtgtttatata tttcttcggt cagttgttag ttatttagct 1380  
gatgagaaac tcacagatgg atcaagactt ctacttggtt taatgttttg tctgttactt 1440  
ttggtgatga atctaattgc ttttgctg

(2) INFORMATION FOR SEQ ID NO:2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:

Met Ser Ala Leu Lys Asn Tyr Gly Leu Ile Ser Ile Asp Ser Ala Leu  
1 5 10 15  
His Phe Pro Arg Ser Asn Gln Leu Gln Ser Tyr Lys Arg Asn Ala Lys

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20 25 30  
Trp Val Ser Pro Ile Ala Ala Val Val Pro Asn Phe His Leu Pro Met  
35 40 45  
Arg Ser Leu Glu Asp Lys Asn Arg Thr Asn Thr Asp Asp Ile Arg Ser  
50 55 60  
Leu Arg Val Ile Thr Ala Ile Lys Thr Pro Tyr Leu Pro Asp Gly Arg  
65 70 75 80  
Phe Asp Leu Gln Ala Tyr Asp Asp Leu Val Asn Thr Gln Ile Glu Asn  
85 90 95  
Gly Ala Glu Gly Val Ile Val Gly Gly Thr Thr Gly Glu Gly Gln Leu  
100 105 110  
Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn Cys  
115 120 125  
Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr  
130 135 140  
Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met His  
145 150 155 160  
Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu Gly  
165 170 175  
Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile Ile  
180 185 190  
Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val Ile  
195 200 205  
Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys Val  
210 215 220  
Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val Trp  
225 230 235 240  
Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly Ala  
245 250 255  
Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met Arg  
260 265 270  
Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu Leu  
275 280 285  
Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val Asn  
290 295 300  
Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu Pro  
305 310 315 320  
Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu Val  
325 330 335  
Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln Val  
340 345 350  
Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr  
355 360

(2) INFORMATION FOR SEQ ID NO:2030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1571614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

Met Arg Ser Leu Glu Asp Lys Asn Arg Thr Asn Thr Asp Asp Ile Arg  
1 5 10 15  
Ser Leu Arg Val Ile Thr Ala Ile Lys Thr Pro Tyr Leu Pro Asp Gly  
20 25 30  
Arg Phe Asp Leu Gln Ala Tyr Asp Asp Leu Val Asn Thr Gln Ile Glu  
35 40 45

```

Asn Gly Ala Glu Gly Val Ile Val Gly Gly Thr Thr Gly Glu Gly Gln
 50 55 60
Leu Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn
 65 70 75 80
Cys Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser
 85 90 95
Thr Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met
 100 105 110
His Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu
 115 120 125
Gly Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile
 130 135 140
Ile Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val
145 150 155 160
Ile Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys
 165 170 175
Val Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val
 180 185 190
Trp Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly
 195 200 205
Ala Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met
 210 215 220
Arg Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu
225 230 235 240
Leu Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val
 245 250 255
Asn Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu
 260 265 270
Pro Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu
 275 280 285
Val Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln
 290 295 300
Val Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr
305 310 315

```

(2) INFORMATION FOR SEQ ID NO:2031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1571615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

```

Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn Cys
 1 5 10 15
Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr
 20 25 30
Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met His
 35 40 45
Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu Gly
 50 55 60
Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile Ile
 65 70 75 80
Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val Ile
 85 90 95
Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys Val
 100 105 110
Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val Trp

```

2025 RELEASE UNDER E.O. 14176



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly Ala |     |     |
| 130                                                             | 135 | 140 |
| Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met Arg |     |     |
| 145                                                             | 150 | 155 |
| Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu Leu |     |     |
| 165                                                             | 170 | 175 |
| Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val Asn |     |     |
| 180                                                             | 185 | 190 |
| Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu Pro |     |     |
| 195                                                             | 200 | 205 |
| Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu Val |     |     |
| 210                                                             | 215 | 220 |
| Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln Val |     |     |
| 225                                                             | 230 | 235 |
| Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr                 |     |     |
| 245                                                             | 250 |     |

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1786
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| acattcactg | tctttaactc | tcactactct | ctctctctct | ctcctctggt  | ctaattctct | 60   |
| aggaacagag | taaaagactt | tggctcagct | tctgcctctc | cAaatggcgg  | ttcttccgac | 120  |
| atggctttta | gcaatgatgt | gtttactctt | cttcgctcga | gctatggaga  | acactacaca | 180  |
| cgacaacatc | tcttctctcc | ctagatccga | cgaaaccgaa | tgaaccaac   | acgcagTgaN | 240  |
| cgaatccaga | tgaagtagcg | gacgAagttc | tcgccttgac | agaaatgagt  | gtgagaaacc | 300  |
| ataccgagag | gaggaaacta | ggttacttta | cttgcggaac | aggaaaccct  | atcgacgatt | 360  |
| gttggcgatg | tgaccccaat | tggcacaaga | accgtaaacc | cctagcggat  | tgcggtatcg | 420  |
| gatttggaag | aaacgcgatc | ggtggctcgt | atggacgatt | ctacgtagtc  | actgacccaa | 480  |
| gagacgacaa | tcgggttaac | cctagaccgg | ggactttacg | WhAcidYKccg | tgatccaaga | 540  |
| cogaccacta | tggatcggtt | tcaaaccgtg | catggtgatt | cagctaaaac  | aagagcttat | 600  |
| cgttaacagt | ttcaaaaacg | tcgatggacg | tggcgcaaac | gttcacattg  | ctaacggtgg | 660  |
| ttgcatcacg | attcagtttg | tgacgaatgt | gatcggtcac | ggattgcata  | ttcatgactg | 720  |
| taaaccaact | ggtaacgcta | tggtgagaag | ctcagagacg | cattttgggt  | ggaggacaat | 780  |
| ggcagatggt | gacgcgattt | cgatcttttg | atcgagtcac | gtatggattg  | atcataactc | 840  |
| gttgtcccat | tgcgctgatg | ggcttggtga | cgcagtcacg | ggctcaaccg  | cgattaccat | 900  |
| ctctaacaac | cacttaactc | accataacga | ggttatggtg | ctaggacata  | gtgactcgta | 960  |
| catgagggac | aaagctatgc | aagtgaacct | tgcttacaat | cattttggag  | tcggacttat | 1020 |
| tcaaagaatg | ccgaggtgtc | gacacgggta | cttccatggt | gttaacaacg  | actacactca | 1080 |
| ctgggaaatg | tacgcaatag | gtggtagcgc | aaaccgcaca | atcaacagtc  | aaggaaaccg | 1140 |
| ctatgccgcc | ccaaaaaacc | cctttgctaa | agaggtgacg | aagagagtgg  | acacaccggc | 1200 |
| tagtcattgg | aaaggatgga | attggagatc | ggaaggagat | ttgcttcaga  | acggtgctta | 1260 |
| cttcacttct | tcaggagccg | ccgcgtctgg | cagCtaacga | cgtgcctcca  | gcctttccgc | 1320 |
| gaaatcttcg | tcattggctg | gacacattac | ttccgacgct | ggagctctac  | cttgctgcag | 1380 |
| aggacgtcaa | tgttcctcat | agttactacc | ccaccaccaa | aattcaaaac  | catcttccat | 1440 |
| tatattcaga | caaaaagtga | aatttacaca | catttgtcat | ttaaaaagcc  | aattatcttt | 1500 |
| tttttttgtc | ttttcgggtg | gtgtggttgt | gtcgattttt | ctcaacctcg  | ggtttgcttg | 1560 |
| cttcaaccgc | aagttaacac | aagaaaagg  | aaaagaacca | acctttcatg  | aaaaaagaga | 1620 |
| aatccccgaa | gtgttggttg | ttgtttgggt | ctatctgatc | aactcagatt  | gttcttcgtc | 1680 |
| tgccctgtc  | ttctatccag | agaaacaaga | atattatctc | ttgttttctt  | ttcttcttgt | 1740 |
| aatttttgag | gtttataaat | taatataggg | tctataaatg | atttgc      |            |      |

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..276
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571617
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

Met Val Ile Gln Leu Lys Gln Glu Leu Ile Val Asn Ser Phe Lys Thr  
1 5 10 15  
Ile Asp Gly Arg Gly Ala Asn Val His Ile Ala Asn Gly Gly Cys Ile  
20 25 30  
Thr Ile Gln Phe Val Thr Asn Val Ile Val His Gly Leu His Ile His  
35 40 45  
Asp Cys Lys Pro Thr Gly Asn Ala Met Val Arg Ser Ser Glu Thr His  
50 55 60  
Phe Gly Trp Arg Thr Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly  
65 70 75 80  
Ser Ser His Val Trp Ile Asp His Asn Ser Leu Ser His Cys Ala Asp  
85 90 95  
Gly Leu Val Asp Ala Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn  
100 105 110  
Asn His Leu Thr His His Asn Glu Val Met Leu Leu Gly His Ser Asp  
115 120 125  
Ser Tyr Met Arg Asp Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His  
130 135 140  
Phe Gly Val Gly Leu Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr  
145 150 155 160  
Phe His Val Val Asn Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile  
165 170 175  
Gly Gly Ser Ala Asn Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala  
180 185 190  
Ala Pro Lys Asn Pro Phe Ala Lys Glu Val Thr Lys Arg Val Asp Thr  
195 200 205  
Pro Ala Ser His Trp Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu  
210 215 220  
Leu Gln Asn Gly Ala Tyr Phe Thr Ser Ser Gly Ala Ala Ala Ser Gly  
225 230 235 240  
Ser Tyr Ala Arg Ala Ser Ser Leu Ser Ala Lys Ser Ser Ser Leu Val  
245 250 255  
Gly His Ile Thr Ser Asp Ala Gly Ala Leu Pro Cys Arg Arg Gly Arg  
260 265 270  
Gln Cys Ser Ser  
275

(2) INFORMATION FOR SEQ ID NO:2034:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 220 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..220
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571618
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:

Met Val Arg Ser Ser Glu Thr His Phe Gly Trp Arg Thr Met Ala Asp  
1 5 10 15  
Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp Ile Asp His

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Gly | Asp | Ala | Ile | Ser | Ile | Phe | Gly | Ser | Ser | His | Val | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asp | His | Asn | Ser | Leu | Ser | His | Cys | Ala | Asp | Gly | Leu | Val | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Met | Gly | Ser | Thr | Ala | Ile | Thr | Ile | Ser | Asn | Asn | His | Leu | Thr | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Asn | Glu | Val | Met | Leu | Leu | Gly | His | Ser | Asp | Ser | Tyr | Met | Arg | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Met | Gln | Val | Thr | Ile | Ala | Tyr | Asn | His | Phe | Gly | Val | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Gln | Arg | Met | Pro | Arg | Cys | Arg | His | Gly | Tyr | Phe | His | Val | Val | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Asp | Tyr | Thr | His | Trp | Glu | Met | Tyr | Ala | Ile | Gly | Gly | Ser | Ala | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Ile | Asn | Ser | Gln | Gly | Asn | Arg | Tyr | Ala | Ala | Pro | Lys | Asn | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ala | Lys | Glu | Val | Thr | Lys | Arg | Val | Asp | Thr | Pro | Ala | Ser | His | Trp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Gly | Trp | Asn | Trp | Arg | Ser | Glu | Gly | Asp | Leu | Leu | Gln | Asn | Gly | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Tyr | Phe | Thr | Ser | Ser | Gly | Ala | Ala | Ala | Ser | Gly | Ser | Tyr | Ala | Arg | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ser | Leu | Ser | Ala | Lys | Ser | Ser | Ser | Leu | Val | Gly | His | Ile | Thr | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Ser | Ser | Val | Asp | Ile | Pro | Pro | Lys | Gly | Gly | Phe | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Cys | Lys | Arg | Asn | Asp | Met | Leu | Thr | Gln | Lys | Gly | Leu | Lys | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Phe | Leu | Lys | Thr | Gly | Thr | Thr | Ile | Val | Gly | Leu | Ile | Phe | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gly | Val | Ile | Leu | Gly | Ala | Asp | Thr | Arg | Ala | Thr | Glu | Gly | Pro | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Asp | Lys | Asn | Cys | Glu | Lys | Ile | His | Tyr | Met | Ala | Pro | Asn | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Cys | Cys | Gly | Ala | Gly | Thr | Ala | Ala | Asp | Thr | Glu | Ala | Val | Thr | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Val | Ser | Ser | Gln | Leu | Arg | Leu | His | Arg | Tyr | Gln | Thr | Gly | Arg | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Val | Val | Thr | Ala | Leu | Thr | Leu | Leu | Lys | Lys | Xaa | Leu | Phe | Ser |

```
(2) INFORMATION FOR SEQ ID NO:2038:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..251
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571630
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Gln | Lys | Gly | Leu | Lys | Ala | Pro | Ser | Phe | Leu | Lys | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Thr | Ile | Val | Gly | Leu | Ile | Phe | Lys | Asp | Gly | Val | Ile | Leu | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Thr | Arg | Ala | Thr | Glu | Gly | Pro | Ile | Val | Ala | Asp | Lys | Asn | Cys | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | His | Tyr | Met | Ala | Pro | Asn | Ile | Tyr | Cys | Cys | Gly | Ala | Gly | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Asp | Thr | Glu | Ala | Val | Thr | Asp | Met | Val | Ser | Ser | Gln | Leu | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | His | Arg | Tyr | Gln | Thr | Gly | Arg | Asp | Ser | Arg | Val | Val | Thr | Ala | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Leu | Leu | Lys | Lys | Xaa | Leu | Phe | Ser | Tyr | Gln | Gly | His | Val | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Val | Leu | Gly | Gly | Val | Asp | Ile | Thr | Gly | Pro | His | Leu | His | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Tyr | Pro | His | Gly | Ser | Thr | Asp | Thr | Leu | Pro | Phe | Ala | Thr | Met | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gly | Ser | Leu | Ala | Ala | Met | Ser | Val | Phe | Glu | Ala | Lys | Tyr | Lys | Glu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Leu | Thr | Arg | Asp | Glu | Gly | Ile | Lys | Leu | Val | Ala | Glu | Ala | Ile | Cys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Gly | Ile | Phe | Asn | Asp | Leu | Gly | Ser | Gly | Ser | Asn | Val | Asp | Ile | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ile | Thr | Lys | Gly | His | Lys | Glu | Tyr | Leu | Arg | Asn | Tyr | Met | Glu | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Pro | Arg | Thr | Tyr | Val | Ser | Ser | Lys | Gly | Tyr | Ser | Phe | Thr | Lys | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

Thr Glu Val Leu Leu Thr Lys Ile Thr Pro Leu Leu Glu Arg Val Glu  
225 230 235 240  
Ile Val Glu Val Ala Gly Glu Ala Met Glu Glu  
245 250

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..199
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

Met Ala Pro Asn Ile Tyr Cys Cys Gly Ala Gly Thr Ala Ala Asp Thr  
1 5 10 15  
Glu Ala Val Thr Asp Met Val Ser Ser Gln Leu Arg Leu His Arg Tyr  
20 25 30  
Gln Thr Gly Arg Asp Ser Arg Val Thr Ala Leu Thr Leu Leu Lys  
35 40 45  
Lys Xaa Leu Phe Ser Tyr Gln Gly His Val Ser Ala Ala Leu Val Leu  
50 55 60  
Gly Gly Val Asp Ile Thr Gly Pro His Leu His Thr Ile Tyr Pro His  
65 70 75 80  
Gly Ser Thr Asp Thr Leu Pro Phe Ala Thr Met Gly Ser Gly Ser Leu  
85 90 95  
Ala Ala Met Ser Val Phe Glu Ala Lys Tyr Lys Glu Gly Leu Thr Arg  
100 105 110  
Asp Glu Gly Ile Lys Leu Val Ala Glu Ala Ile Cys Ser Gly Ile Phe  
115 120 125  
Asn Asp Leu Gly Ser Gly Ser Asn Val Asp Ile Cys Val Ile Thr Lys  
130 135 140  
Gly His Lys Glu Tyr Leu Arg Asn Tyr Met Glu Pro Asn Pro Arg Thr  
145 150 155 160  
Tyr Val Ser Ser Lys Gly Tyr Ser Phe Thr Lys Lys Thr Glu Val Leu  
165 170 175  
Leu Thr Lys Ile Thr Pro Leu Leu Glu Arg Val Glu Ile Val Glu Val  
180 185 190  
Ala Gly Glu Ala Met Glu Glu  
195

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

aaaaacttca aattaaaagc ttcgtgtctt cataaaaccc taatctcgcg acttcgtctc 60  
tatccccaaa aaccctttcc tctcttctt cttgtgtgag aacgagaaaa aaagatgact 120  
aagaacagta accacgacga gaatgagttc atcagctttg aaccaaata gaacacgaag 180  
atacgtcttg aagatgctga tgaagacgaa gttgctgaag ggtctggtgt tgccggcgag 240  
gaaactcccc aagatgagtc catgttcgac gccggagaga gcgcgacac cgctgaagta 300  
actgatgata ccaccagtgc cgattactac ttcgattctt actctcactt tggaatccat 360  
gaagagatgt tgaaggatgt tgtgagaaca aagacttatc agaatgttat ttatcagaac 420

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| aagtttctta | tcaaggacaa | aattgttctt | gatgttgagg  | ctggaaccgg | aattttgtct | 480  |
| ctgttctgtg | ccaaggcagg | agctgtcat  | gtctacgtg   | ttgagtgttc | tcaaatggct | 540  |
| gacatggcaa | aggagattgt | taaagcta   | ggattttctg  | atgttattac | ggtattgaaa | 600  |
| gggaagattg | aggagataga | gcttcccact | cctaaagtgg  | atgtgattat | atcggaatgg | 660  |
| atgggttact | ttttgttgtt | tgaaaatatg | ttggacagt   | tcttgtatgc | tcgtgataaa | 720  |
| tggcttggtg | aaggtggagt | tgtgctacca | gacaaagcct  | ctctgcatct | tacagccata | 780  |
| gaggattcag | agtacaaaga | agacaaaatc | gaattttgga  | acagtgtgta | tggttttgac | 840  |
| atgtcatgta | ttaagaaaaa | agctatgatg | gaaccacttg  | ttgacacagt | cgacaaaaac | 900  |
| caaatcgta  | ccgatagtag | gcttctaaag | acgatggata  | tctcaaagat | gtcctctggt | 960  |
| gatgcttctt | tcacagctcc | ctttaagctt | gttgacacaac | gcaatgacta | catccacgcc | 1020 |
| cttgtagcct | actttgatgt | atcgtttacc | atgtgccaca  | agctgctggg | cttctcaaca | 1080 |
| ggaccgaaat | cccgagctac | acactggaaa | caaacagttc  | tgtatctaga | agatgtgtta | 1140 |
| accatagtgt | agggtgagac | aatcactgga | actatgtccg  | tttctcctaa | caagaagaat | 1200 |
| cctcgagaca | ttgacataaa | gctaagctat | tctttgaatg  | gccagcattg | caagatctca | 1260 |
| aggacccaac | actacaaaat | gcgttaaagt | tctctcataa  | gaagcagaac | ttcagaagat | 1320 |
| acaattctca | tattgtgatt | tagtttttat | atttSccttt  | tctccagatt | acaactttcc | 1380 |
| atttgcttca | cattgcaaca | tttgcttcat | ctcaagttaa  | attaatgatt | ttgctcc    |      |

(2) INFORMATION FOR SEQ ID NO:2041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..390

(D) OTHER INFORMATION: / Ceres Seq. ID 1571643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Asn | Ser | Asn | His | Asp | Glu | Asn | Glu | Phe | Ile | Ser | Phe | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Asn | Gln | Asn | Thr | Lys | Ile | Arg | Phe | Glu | Asp | Ala | Asp | Glu | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ala | Glu | Gly | Ser | Gly | Val | Ala | Gly | Glu | Glu | Thr | Pro | Gln | Asp | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Met | Phe | Asp | Ala | Gly | Glu | Ser | Ala | Asp | Thr | Ala | Glu | Val | Thr | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Thr | Thr | Ser | Ala | Asp | Tyr | Tyr | Phe | Asp | Ser | Tyr | Ser | His | Phe | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | His | Glu | Glu | Met | Leu | Lys | Asp | Val | Val | Arg | Thr | Lys | Thr | Tyr | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Val | Ile | Tyr | Gln | Asn | Lys | Phe | Leu | Ile | Lys | Asp | Lys | Ile | Val | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Val | Gly | Ala | Gly | Thr | Gly | Ile | Leu | Ser | Leu | Phe | Cys | Ala | Lys | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Ala | His | Val | Tyr | Ala | Val | Glu | Cys | Ser | Gln | Met | Ala | Asp | Met |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Lys | Glu | Ile | Val | Lys | Ala | Asn | Gly | Phe | Ser | Asp | Val | Ile | Thr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Lys | Gly | Lys | Ile | Glu | Glu | Ile | Glu | Leu | Pro | Thr | Pro | Lys | Val | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ile | Ile | Ser | Glu | Trp | Met | Gly | Tyr | Phe | Leu | Leu | Phe | Glu | Asn | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Asp | Ser | Val | Leu | Tyr | Ala | Arg | Asp | Lys | Trp | Leu | Val | Glu | Gly | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Val | Leu | Pro | Asp | Lys | Ala | Ser | Leu | His | Leu | Thr | Ala | Ile | Glu | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Glu | Tyr | Lys | Glu | Asp | Lys | Ile | Glu | Phe | Trp | Asn | Ser | Val | Tyr | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Phe | Asp | Met | Ser | Cys | Ile | Lys | Lys | Lys | Ala | Met | Met | Glu | Pro | Leu | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

Asp Thr Val Asp Gln Asn Gln Ile Val Thr Asp Ser Arg Leu Leu Lys  
260 265 270  
Thr Met Asp Ile Ser Lys Met Ser Ser Gly Asp Ala Ser Phe Thr Ala  
275 280 285  
Pro Phe Lys Leu Val Ala Gln Arg Asn Asp Tyr Ile His Ala Leu Val  
290 295 300  
Ala Tyr Phe Asp Val Ser Phe Thr Met Cys His Lys Leu Leu Gly Phe  
305 310 315 320  
Ser Thr Gly Pro Lys Ser Arg Ala Thr His Trp Lys Gln Thr Val Leu  
325 330 335  
Tyr Leu Glu Asp Val Leu Thr Ile Cys Glu Gly Glu Thr Ile Thr Gly  
340 345 350  
Thr Met Ser Val Ser Pro Asn Lys Lys Asn Pro Arg Asp Ile Asp Ile  
355 360 365  
Lys Leu Ser Tyr Ser Leu Asn Gly Gln His Cys Lys Ile Ser Arg Thr  
370 375 380  
Gln His Tyr Lys Met Arg  
385 390

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1571644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

Met Phe Asp Ala Gly Glu Ser Ala Asp Thr Ala Glu Val Thr Asp Asp  
1 5 10 15  
Thr Thr Ser Ala Asp Tyr Tyr Phe Asp Ser Tyr Ser His Phe Gly Ile  
20 25 30  
His Glu Glu Met Leu Lys Asp Val Val Arg Thr Lys Thr Tyr Gln Asn  
35 40 45  
Val Ile Tyr Gln Asn Lys Phe Leu Ile Lys Asp Lys Ile Val Leu Asp  
50 55 60  
Val Gly Ala Gly Thr Gly Ile Leu Ser Leu Phe Cys Ala Lys Ala Gly  
65 70 75 80  
Ala Ala His Val Tyr Ala Val Glu Cys Ser Gln Met Ala Asp Met Ala  
85 90 95  
Lys Glu Ile Val Lys Ala Asn Gly Phe Ser Asp Val Ile Thr Val Leu  
100 105 110  
Lys Gly Lys Ile Glu Glu Ile Glu Leu Pro Thr Pro Lys Val Asp Val  
115 120 125  
Ile Ile Ser Glu Trp Met Gly Tyr Phe Leu Leu Phe Glu Asn Met Leu  
130 135 140  
Asp Ser Val Leu Tyr Ala Arg Asp Lys Trp Leu Val Glu Gly Gly Val  
145 150 155 160  
Val Leu Pro Asp Lys Ala Ser Leu His Leu Thr Ala Ile Glu Asp Ser  
165 170 175  
Glu Tyr Lys Glu Asp Lys Ile Glu Phe Trp Asn Ser Val Tyr Gly Phe  
180 185 190  
Asp Met Ser Cys Ile Lys Lys Lys Ala Met Met Glu Pro Leu Val Asp  
195 200 205  
Thr Val Asp Gln Asn Gln Ile Val Thr Asp Ser Arg Leu Leu Lys Thr  
210 215 220  
Met Asp Ile Ser Lys Met Ser Ser Gly Asp Ala Ser Phe Thr Ala Pro  
225 230 235 240  
Phe Lys Leu Val Ala Gln Arg Asn Asp Tyr Ile His Ala Leu Val Ala



245 250 255  
Tyr Phe Asp Val Ser Phe Thr Met Cys His Lys Leu Leu Gly Phe Ser  
260 265 270  
Thr Gly Pro Lys Ser Arg Ala Thr His Trp Lys Gln Thr Val Leu Tyr  
275 280 285  
Leu Glu Asp Val Leu Thr Ile Cys Glu Gly Glu Thr Ile Thr Gly Thr  
290 295 300  
Met Ser Val Ser Pro Asn Lys Lys Asn Pro Arg Asp Ile Asp Ile Lys  
305 310 315 320  
Leu Ser Tyr Ser Leu Asn Gly Gln His Cys Lys Ile Ser Arg Thr Gln  
325 330 335  
His Tyr Lys Met Arg  
340

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1571645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

Met Leu Lys Asp Val Val Arg Thr Lys Thr Tyr Gln Asn Val Ile Tyr  
1 5 10 15  
Gln Asn Lys Phe Leu Ile Lys Asp Lys Ile Val Leu Asp Val Gly Ala  
20 25 30  
Gly Thr Gly Ile Leu Ser Leu Phe Cys Ala Lys Ala Gly Ala Ala His  
35 40 45  
Val Tyr Ala Val Glu Cys Ser Gln Met Ala Asp Met Ala Lys Glu Ile  
50 55 60  
Val Lys Ala Asn Gly Phe Ser Asp Val Ile Thr Val Leu Lys Gly Lys  
65 70 75 80  
Ile Glu Glu Ile Glu Leu Pro Thr Pro Lys Val Asp Val Ile Ile Ser  
85 90 95  
Glu Trp Met Gly Tyr Phe Leu Leu Phe Glu Asn Met Leu Asp Ser Val  
100 105 110  
Leu Tyr Ala Arg Asp Lys Trp Leu Val Glu Gly Gly Val Val Leu Pro  
115 120 125  
Asp Lys Ala Ser Leu His Leu Thr Ala Ile Glu Asp Ser Glu Tyr Lys  
130 135 140  
Glu Asp Lys Ile Glu Phe Trp Asn Ser Val Tyr Gly Phe Asp Met Ser  
145 150 155 160  
Cys Ile Lys Lys Lys Ala Met Met Glu Pro Leu Val Asp Thr Val Asp  
165 170 175  
Gln Asn Gln Ile Val Thr Asp Ser Arg Leu Leu Lys Thr Met Asp Ile  
180 185 190  
Ser Lys Met Ser Ser Gly Asp Ala Ser Phe Thr Ala Pro Phe Lys Leu  
195 200 205  
Val Ala Gln Arg Asn Asp Tyr Ile His Ala Leu Val Ala Tyr Phe Asp  
210 215 220  
Val Ser Phe Thr Met Cys His Lys Leu Leu Gly Phe Ser Thr Gly Pro  
225 230 235 240  
Lys Ser Arg Ala Thr His Trp Lys Gln Thr Val Leu Tyr Leu Glu Asp  
245 250 255  
Val Leu Thr Ile Cys Glu Gly Glu Thr Ile Thr Gly Thr Met Ser Val  
260 265 270  
Ser Pro Asn Lys Lys Asn Pro Arg Asp Ile Asp Ile Lys Leu Ser Tyr  
275 280 285

Ser Leu Asn Gly Gln His Cys Lys Ile Ser Arg Thr Gln His Tyr Lys  
290 295 300  
Met Arg  
305

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| agtcgtctag  | ggtttgttt  | tcgtttcttc | tccgattgtt  | cagaggaatt | gcgaattaag | 60  |
| ataaagatga  | ggccagtgtt | cgtcggcaat | ttcgagtatg  | aaactcgcca | gtcggatctg | 120 |
| gaacggttgt  | tcgacaagta | tgggagagtc | gaccgagtgg  | acatgaaatc | tggatatgct | 180 |
| tttgtgtact  | ttgaggatga | acgtgatgct | gaagacgcta  | ttcgcaaact | cgacaatttt | 240 |
| ccttttggtat | atgagaaacg | caggttatca | gttgaatggg  | caaagggtga | acgtggcagg | 300 |
| cctcgtggtg  | acgcgaaagc | ccottcaaat | ctgaagccta  | caaagacact | gtttgtcatt | 360 |
| aactttgacc  | ccattagaac | aaaagagcac | gacattgaaa  | aacactttga | gccctatggt | 420 |
| aaggtcacca  | acgtgcgtat | cagacgcaac | ttctcatttg  | ttcagtttga | aacacaagag | 480 |
| gatgctacaa  | aagcccttga | agctactcaa | agaagcaaaa  | tattggatag | ggttgtttcc | 540 |
| gtggagtatg  | cgttgaaaga | tgacgatgaa | agagatgatc  | gaaatgggtg | tcgtagccCg | 600 |
| agaaggtctc  | ttagtcCtgt | gtatcgtagG | cgtcattgta  | tgatgtactg | tcgttatttt | 660 |
| aaagaaaatt  | tggcaccttt | tgtataaaca | gaattttctta | tacctcgcat | tttgtgttta | 720 |

cgt

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Arg Leu Gly Phe Val Phe Arg Phe Phe Ser Asp Cys Ser Glu Glu |  |
| 1 5 10 15                                                       |  |
| Leu Arg Ile Lys Ile Lys Met Arg Pro Val Phe Val Gly Asn Phe Glu |  |
| 20 25 30                                                        |  |
| Tyr Glu Thr Arg Gln Ser Asp Leu Glu Arg Leu Phe Asp Lys Tyr Gly |  |
| 35 40 45                                                        |  |
| Arg Val Asp Arg Val Asp Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe |  |
| 50 55 60                                                        |  |
| Glu Asp Glu Arg Asp Ala Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe |  |
| 65 70 75 80                                                     |  |
| Pro Phe Gly Tyr Glu Lys Arg Arg Leu Ser Val Glu Trp Ala Lys Gly |  |
| 85 90 95                                                        |  |
| Glu Arg Gly Arg Pro Arg Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys |  |
| 100 105 110                                                     |  |
| Pro Thr Lys Thr Leu Phe Val Ile Asn Phe Asp Pro Ile Arg Thr Lys |  |
| 115 120 125                                                     |  |
| Glu His Asp Ile Glu Lys His Phe Glu Pro Tyr Gly Lys Val Thr Asn |  |
| 130 135 140                                                     |  |
| Val Arg Ile Arg Arg Asn Phe Ser Phe Val Gln Phe Glu Thr Gln Glu |  |
| 145 150 155 160                                                 |  |

(2) INFORMATION FOR SEQ ID NO:2046:

(A) LENGTH: 206 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..206  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571671

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Pro | Val | Phe | Val | Gly | Asn | Phe | Glu | Tyr | Glu | Thr | Arg | Gln | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Glu | Arg | Leu | Phe | Asp | Lys | Tyr | Gly | Arg | Val | Asp | Arg | Val | Asp |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Met | Lys | Ser | Gly | Tyr | Ala | Phe | Val | Tyr | Phe | Glu | Asp | Glu | Arg | Asp | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Ala | Ile | Arg | Lys | Leu | Asp | Asn | Phe | Pro | Phe | Gly | Tyr | Glu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Leu | Ser | Val | Glu | Trp | Ala | Lys | Gly | Glu | Arg | Gly | Arg | Pro | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Asp | Ala | Lys | Ala | Pro | Ser | Asn | Leu | Lys | Pro | Thr | Lys | Thr | Leu | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ile | Asn | Phe | Asp | Pro | Ile | Arg | Thr | Lys | Glu | His | Asp | Ile | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Phe | Glu | Pro | Tyr | Gly | Lys | Val | Thr | Asn | Val | Arg | Ile | Arg | Arg | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ser | Phe | Val | Gln | Phe | Glu | Thr | Gln | Glu | Asp | Ala | Thr | Lys | Ala | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Thr | Gln | Arg | Ser | Lys | Ile | Leu | Asp | Arg | Val | Val | Ser | Val | Glu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Ala | Leu | Lys | Asp | Asp | Asp | Glu | Arg | Asp | Asp | Arg | Asn | Gly | Gly | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Pro | Arg | Arg | Ser | Leu | Ser | Pro | Val | Tyr | Arg | Arg | Arg | His | Val | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Tyr | Cys | Arg | Tyr | Phe | Lys | Glu | Asn | Leu | Ala | Pro | Phe | Val |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..174
(D) OTHER INFORMATION: / Ceres Seq. ID 1571672
```

Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala

1 5 10 15
Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys
20 25 30
Arg Arg Leu Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg
35 40 45
Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe
50 55 60
Val Ile Asn Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys
65 70 75 80
His Phe Glu Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn
85 90 95
Phe Ser Phe Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu
100 105 110
Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu
115 120 125
Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp Asp Arg Asn Gly Gly Arg
130 135 140
Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met
145 150 155 160
Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val
165 170

(2) INFORMATION FOR SEQ ID NO:2048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

actcatttta	ctgttaagca	aacacaagat	aagaagaaac	aaacaatggc	gatttctttc	60
atttagatat	tttctcgat	tcttagcttc	tggatttttg	tgaaaggatt	tgaaatggcg	120
gtgtcgcttt	tatcgaaatt	acggtgtata	acagtagatg	ttactggtag	acttatagct	180
tacaaaggag	agcttgggtga	ttactattgt	atggctgcta	aagccattgg	tttgccttgt	240
cctgattata	aacgagttca	tgaaggtttt	aaactagctt	atacagatat	ggcacaaaag	300
tatccttggt	tcggtttcca	tgccaaaatg	ccaaacattg	tttgggtgga	aacttgtgtg	360
agagattcat	ttgtcaaggc	aggatatgag	tatgatgagg	agacatttga	gaagatattt	420
aggagaatct	attcgacgtt	tggttctgct	gcaccttact	ctgbgtttca	agattctcaa	480
ccgtttttta	gatgggcacg	caggaaaggt	cttatagtcg	gacttgtag	caatgcggaa	540
taccgatatc	aagaagttat	tttaccttCc	ttcggtttga	gcaaggcaga	gtgggatatt	600
ggtgtattct	ctggaattga	agggatagag	aaaccagatc	cgaggatttt	tacGctcgcg	660
ctagagagag	ccgggaataa	tattgcgcct	gaagagggtt	tgcatatttg	agacagcatg	720
cgcaaagatt	atgttccagc	aaagagtatt	gggatgcatg	ctttgttggt	tgatagggtt	780
aagacggaag	ctgctaaaga	ctggatagaa	gctggagcca	ttgtgcttcc	agatttggtt	840
gctgttcaac	aacttttgga	gtctgataag	ttgaaatggt	agaaaacaga	cctctcttaa	900
gtatgaaatc	taatgtattg	tagtattgca	catttgagta	aaataagttt	caacggcttc	960
tttggtt						

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

Met Ala Val Ser Leu Leu Ser Lys Leu Arg Cys Ile Thr Val Asp Val
1 5 10 15
Thr Gly Thr Leu Ile Ala Tyr Lys Gly Glu Leu Gly Asp Tyr Tyr Cys
20 25 30
Met Ala Ala Lys Ala Ile Gly Leu Pro Cys Pro Asp Tyr Lys Arg Val
35 40 45
His Glu Gly Phe Lys Leu Ala Tyr Thr Asp Met Ala Gln Lys Tyr Pro
50 55 60
Cys Phe Gly Phe His Ala Lys Met Pro Asn Ile Val Trp Trp Lys Thr
65 70 75 80
Cys Val Arg Asp Ser Phe Val Lys Ala Gly Tyr Glu Tyr Asp Glu Glu
85 90 95
Thr Phe Glu Lys Ile Phe Arg Arg Ile Tyr Ser Thr Phe Gly Ser Ala
100 105 110
Ala Pro Tyr Ser Xaa Phe Gln Asp Ser Gln Pro Phe Leu Arg Trp Ala
115 120 125
Arg Arg Lys Gly Leu Ile Val Gly Leu Val Ser Asn Ala Glu Tyr Arg
130 135 140
Tyr Gln Glu Val Ile Leu Pro Ser Phe Gly Leu Ser Lys Ala Glu Trp
145 150 155 160
Asp Phe Gly Val Phe Ser Gly Ile Glu Gly Ile Glu Lys Pro Asp Pro
165 170 175
Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala Gly Asn Asn Ile Ala Pro
180 185 190
Glu Glu Val Leu His Ile Gly Asp Ser Met Arg Lys Asp Tyr Val Pro
195 200 205
Ala Lys Ser Ile Gly Met His Ala Leu Leu Val Asp Arg Phe Lys Thr
210 215 220
Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly Ala Ile Val Leu Pro Asp
225 230 235 240
Leu Val Ala Val Gln Gln Leu Leu Glu Ser Asp Lys Leu Lys Cys
245 250 255

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1571679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

Met Ala Ala Lys Ala Ile Gly Leu Pro Cys Pro Asp Tyr Lys Arg Val
1 5 10 15
His Glu Gly Phe Lys Leu Ala Tyr Thr Asp Met Ala Gln Lys Tyr Pro
20 25 30
Cys Phe Gly Phe His Ala Lys Met Pro Asn Ile Val Trp Trp Lys Thr
35 40 45
Cys Val Arg Asp Ser Phe Val Lys Ala Gly Tyr Glu Tyr Asp Glu Glu
50 55 60
Thr Phe Glu Lys Ile Phe Arg Arg Ile Tyr Ser Thr Phe Gly Ser Ala
65 70 75 80
Ala Pro Tyr Ser Xaa Phe Gln Asp Ser Gln Pro Phe Leu Arg Trp Ala
85 90 95
Arg Arg Lys Gly Leu Ile Val Gly Leu Val Ser Asn Ala Glu Tyr Arg
100 105 110
Tyr Gln Glu Val Ile Leu Pro Ser Phe Gly Leu Ser Lys Ala Glu Trp
115 120 125

Asp Phe Gly Val Phe Ser Gly Ile Glu Gly Ile Glu Lys Pro Asp Pro
130 135 140
Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala Gly Asn Asn Ile Ala Pro
145 150 155 160
Glu Glu Val Leu His Ile Gly Asp Ser Met Arg Lys Asp Tyr Val Pro
165 170 175
Ala Lys Ser Ile Gly Met His Ala Leu Leu Val Asp Arg Phe Lys Thr
180 185 190
Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly Ala Ile Val Leu Pro Asp
195 200 205
Leu Val Ala Val Gln Gln Leu Leu Glu Ser Asp Lys Leu Lys Cys
210 215 220

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:

Met Ala Gln Lys Tyr Pro Cys Phe Gly Phe His Ala Lys Met Pro Asn
1 5 10 15
Ile Val Trp Trp Lys Thr Cys Val Arg Asp Ser Phe Val Lys Ala Gly
20 25 30
Tyr Glu Tyr Asp Glu Glu Thr Phe Glu Lys Ile Phe Arg Arg Ile Tyr
35 40 45
Ser Thr Phe Gly Ser Ala Ala Pro Tyr Ser Xaa Phe Gln Asp Ser Gln
50 55 60
Pro Phe Leu Arg Trp Ala Arg Arg Lys Gly Leu Ile Val Gly Leu Val
65 70 75 80
Ser Asn Ala Glu Tyr Arg Tyr Gln Glu Val Ile Leu Pro Ser Phe Gly
85 90 95
Leu Ser Lys Ala Glu Trp Asp Phe Gly Val Phe Ser Gly Ile Glu Gly
100 105 110
Ile Glu Lys Pro Asp Pro Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala
115 120 125
Gly Asn Asn Ile Ala Pro Glu Glu Val Leu His Ile Gly Asp Ser Met
130 135 140
Arg Lys Asp Tyr Val Pro Ala Lys Ser Ile Gly Met His Ala Leu Leu
145 150 155 160
Val Asp Arg Phe Lys Thr Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly
165 170 175
Ala Ile Val Leu Pro Asp Leu Val Ala Val Gln Gln Leu Leu Glu Ser
180 185 190
Asp Lys Leu Lys Cys
195

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571687

atttttagatc	cgatatattat	agaaagcaac	caaactccgg	ctccggttac	tcgggaggttc	60
aagtttttga	ttttgatggg	tcattgctga	actcgtaccg	gtatcatctc	cgtcgctttt	120
aaattcttca	ggtctctggt	ccctcgccat	caccgtacta	acagcatgaa	gataaaaaca	180
ggaacgtttt	tgggggtttc	gatatcattg	attctttataa	acttagctgc	gatcatggaa	240
cgtgcagacg	agaatctatt	gccttcgggt	tataaagaag	tgagtgaagc	atttaacgca	300
ggaccatcag	atttaggcta	cttaacattc	gttagaaaact	ttgttcaagg	acttgcattc	360
ccatttagcag	gagttcttgt	cattacctat	gatcgtccca	ttgttcttgc	aataggctact	420
gtctgtttggg	cttttatcaac	tgtctcagtt	ggagccagca	gctacttcatt	tcaggttgct	480
ttatggagag	cagtgaattg	ttttggattg	gcaattgtta	taccgcgcgt	tcaatcgttt	540
attgcagata	gttataagga	tggtcgcaga	ggagctggtt	tcggaatggt	gaacctcatt	600
ggtacaatcg	gtggtatagg	aggaggtggt	gtagcaactg	ttatggctgg	ttcagagttt	660
tggggcatac	cgggatggcg	ttgtgctttt	ataatgatgg	cagcgctcag	cgcagtgatc	720
ggattacttg	tctttctctt	cgttggtgac	ccgagaaaaga	acattgaacg	agaggaacta	780
atggctcata	agatgaattc	gaactcgggt	tggaatgatt	cattagcagc	tgcaaaatct	840
gtcgtcaaag	taagtacctt	tcagataaat	gtcgcgcaag	gaatcattgg	ttcgtttccg	900
tggaccgcga	tggtttttct	tacaatgttg	tttgagctta	ttggcttcga	tcataaccag	960
actcgcagct	tgcttggggg	atttgtctaca	ggaggagcga	taggaacctt	aatgggaggg	1020
ataatagcgg	ataaaatgtc	cgggatatat	ccgaattcgg	gtagagtgat	gtgtgcgcag	1080
ttcagtgcat	tcatgggaat	cccatctctt	attattcttc	tgaaagtaat	cccacaaagc	1140
acaagcagct	actcaatctt	ctcgataaact	ctcttctctga	tgggtcttac	cataacttgg	1200
tgcggatcag	cgggttaatgc	accgatgttt	gcagaagtgg	ttcctccaag	gcaccgtaca	1260
atgatctacg	cgtttgacgg	tgctttcgaa	gggtcattct	catcttttGc	tgcgcccttg	1320
gtgggaatth	tgtctgagaa	aatgtttggg	tatgactcaa	gagggtattga	tcctttgaaa	1380
ggttcctctg	ttcgtgaggc	tgtatgccct	tcaaaggggc	ttctgtcaat	gatggctggt	1440
ccgtttgggc	tctgttgtct	ctgttacact	ccgttgcat	ttgttttcca	gaaagatcga	1500
gaaaacgcga	aaatgcgcag	ctctaaagaa	actgaaatga	tctgagagac	ttgctcatgt	1560
agtcattgtt	tqattctttt	tataccacaa	acgattttta	aacc		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..514
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1571688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Asp | Pro | Ile | Phe | Ile | Glu | Ser | Asn | Gln | Thr | Pro | Ala | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Arg | Glu | Phe | Lys | Phe | Trp | Ile | Leu | Met | Gly | His | Ala | Arg | Thr | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Gly | Ile | Ile | Ser | Val | Ala | Phe | Lys | Phe | Phe | Arg | Ser | Leu | Phe | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | His | His | Arg | Thr | Asn | Ser | Met | Lys | Ile | Lys | Thr | Gly | Thr | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Val | Ser | Ile | Ser | Leu | Ile | Leu | Ile | Asn | Leu | Ala | Ala | Ile | Met | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ala | Asp | Glu | Asn | Leu | Leu | Pro | Ser | Val | Tyr | Lys | Glu | Val | Ser | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Phe | Asn | Ala | Gly | Pro | Ser | Asp | Leu | Gly | Tyr | Leu | Thr | Phe | Val | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Phe | Val | Gln | Gly | Leu | Ala | Ser | Pro | Leu | Ala | Gly | Val | Leu | Val | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Tyr | Asp | Arg | Pro | Ile | Val | Leu | Ala | Ile | Gly | Thr | Val | Cys | Trp | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Thr | Ala | Ala | Val | Gly | Ala | Ser | Ser | Tyr | Phe | Ile | Gln | Val | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Trp | Arg | Ala | Val | Asn | Gly | Phe | Gly | Leu | Ala | Ile | Val | Ile | Pro | Ala |

165 170 175  
Leu Gln Ser Phe Ile Ala Asp Ser Tyr Lys Asp Gly Ala Arg Gly Ala  
180 185 190  
Gly Phe Gly Met Leu Asn Leu Ile Gly Thr Ile Gly Gly Ile Gly Gly  
195 200 205  
Gly Val Val Ala Thr Val Met Ala Gly Ser Glu Phe Trp Gly Ile Pro  
210 215 220  
Gly Trp Arg Cys Ala Phe Ile Met Met Ala Ala Leu Ser Ala Val Ile  
225 230 235 240  
Gly Leu Leu Val Phe Leu Phe Val Val Asp Pro Arg Lys Asn Ile Glu  
245 250 255  
Arg Glu Glu Leu Met Ala His Lys Met Asn Ser Asn Ser Val Trp Asn  
260 265 270  
Asp Ser Leu Ala Ala Ala Lys Ser Val Val Lys Val Ser Thr Phe Gln  
275 280 285  
Ile Ile Val Ala Gln Gly Ile Ile Gly Ser Phe Pro Trp Thr Ala Met  
290 295 300  
Val Phe Phe Thr Met Trp Phe Glu Leu Ile Gly Phe Asp His Asn Gln  
305 310 315 320  
Thr Ala Ala Leu Leu Gly Val Phe Ala Thr Gly Gly Ala Ile Gly Thr  
325 330 335  
Leu Met Gly Gly Ile Ile Ala Asp Lys Met Ser Arg Ile Tyr Pro Asn  
340 345 350  
Ser Gly Arg Val Met Cys Ala Gln Phe Ser Ala Phe Met Gly Ile Pro  
355 360 365  
Phe Ser Ile Ile Leu Leu Lys Val Ile Pro Gln Ser Thr Ser Ser Tyr  
370 375 380  
Ser Ile Phe Ser Ile Thr Leu Phe Leu Met Gly Leu Thr Ile Thr Trp  
385 390 395 400  
Cys Gly Ser Ala Val Asn Ala Pro Met Phe Ala Glu Val Val Pro Pro  
405 410 415  
Arg His Arg Thr Met Ile Tyr Ala Phe Asp Arg Ala Phe Glu Gly Ser  
420 425 430  
Phe Ser Ser Phe Ala Ala Pro Leu Val Gly Ile Leu Ser Glu Lys Met  
435 440 445  
Phe Gly Tyr Asp Ser Arg Gly Ile Asp Pro Leu Lys Gly Ser Ser Val  
450 455 460  
Arg Glu Ala Asp Ala Leu Ser Lys Gly Leu Leu Ser Met Met Ala Val  
465 470 475 480  
Pro Phe Gly Leu Cys Cys Leu Cys Tyr Thr Pro Leu His Phe Val Phe  
485 490 495  
Gln Lys Asp Arg Glu Asn Ala Lys Ile Ala Ser Ser Lys Glu Thr Glu  
500 505 510  
Met Ile

(2) INFORMATION FOR SEQ ID NO:2054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..489
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

Met Gly His Ala Arg Thr Arg Thr Gly Ile Ile Ser Val Ala Phe Lys  
1 5 10 15  
Phe Phe Arg Ser Leu Phe Pro Arg His His Arg Thr Asn Ser Met Lys  
20 25 30



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Ile Lys Thr Gly Thr Phe Leu Gly Val Ser Ile Ser Leu Ile Leu Ile
 35 40 45
Asn Leu Ala Ala Ile Met Glu Arg Ala Asp Glu Asn Leu Leu Pro Ser
 50 55 60
Val Tyr Lys Glu Val Ser Glu Ala Phe Asn Ala Gly Pro Ser Asp Leu
 65 70 75 80
Gly Tyr Leu Thr Phe Val Arg Asn Phe Val Gln Gly Leu Ala Ser Pro
 85 90 95
Leu Ala Gly Val Leu Val Ile Thr Tyr Asp Arg Pro Ile Val Leu Ala
 100 105 110
Ile Gly Thr Val Cys Trp Ala Leu Ser Thr Ala Ala Val Gly Ala Ser
 115 120 125
Ser Tyr Phe Ile Gln Val Ala Leu Trp Arg Ala Val Asn Gly Phe Gly
 130 135 140
Leu Ala Ile Val Ile Pro Ala Leu Gln Ser Phe Ile Ala Asp Ser Tyr
 145 150 155 160
Lys Asp Gly Ala Arg Gly Ala Gly Phe Gly Met Leu Asn Leu Ile Gly
 165 170 175
Thr Ile Gly Gly Ile Gly Gly Gly Val Val Ala Thr Val Met Ala Gly
 180 185 190
Ser Glu Phe Trp Gly Ile Pro Gly Trp Arg Cys Ala Phe Ile Met Met
 195 200 205
Ala Ala Leu Ser Ala Val Ile Gly Leu Leu Val Phe Leu Phe Val Val
 210 215 220
Asp Pro Arg Lys Asn Ile Glu Arg Glu Glu Leu Met Ala His Lys Met
 225 230 235 240
Asn Ser Asn Ser Val Trp Asn Asp Ser Leu Ala Ala Ala Lys Ser Val
 245 250 255
Val Lys Val Ser Thr Phe Gln Ile Ile Val Ala Gln Gly Ile Ile Gly
 260 265 270
Ser Phe Pro Trp Thr Ala Met Val Phe Phe Thr Met Trp Phe Glu Leu
 275 280 285
Ile Gly Phe Asp His Asn Gln Thr Ala Ala Leu Leu Gly Val Phe Ala
 290 295 300
Thr Gly Gly Ala Ile Gly Thr Leu Met Gly Gly Ile Ile Ala Asp Lys
 305 310 315 320
Met Ser Arg Ile Tyr Pro Asn Ser Gly Arg Val Met Cys Ala Gln Phe
 325 330 335
Ser Ala Phe Met Gly Ile Pro Phe Ser Ile Ile Leu Leu Lys Val Ile
 340 345 350
Pro Gln Ser Thr Ser Ser Tyr Ser Ile Phe Ser Ile Thr Leu Phe Leu
 355 360 365
Met Gly Leu Thr Ile Thr Trp Cys Gly Ser Ala Val Asn Ala Pro Met
 370 375 380
Phe Ala Glu Val Val Pro Pro Arg His Arg Thr Met Ile Tyr Ala Phe
 385 390 395 400
Asp Arg Ala Phe Glu Gly Ser Phe Ser Ser Phe Ala Ala Pro Leu Val
 405 410 415
Gly Ile Leu Ser Glu Lys Met Phe Gly Tyr Asp Ser Arg Gly Ile Asp
 420 425 430
Pro Leu Lys Gly Ser Ser Val Arg Glu Ala Asp Ala Leu Ser Lys Gly
 435 440 445
Leu Leu Ser Met Met Ala Val Pro Phe Gly Leu Cys Cys Leu Cys Tyr
 450 455 460
Thr Pro Leu His Phe Val Phe Gln Lys Asp Arg Glu Asn Ala Lys Ile
 465 470 475 480
Ala Ser Ser Lys Glu Thr Glu Met Ile
 485

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(2) INFORMATION FOR SEQ ID NO:2055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

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(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..459  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571690  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Lys | Thr | Gly | Thr | Phe | Leu | Gly | Val | Ser | Ile | Ser | Leu | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Asn | Leu | Ala | Ala | Ile | Met | Glu | Arg | Ala | Asp | Glu | Asn | Leu | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Val | Tyr | Lys | Glu | Val | Ser | Glu | Ala | Phe | Asn | Ala | Gly | Pro | Ser |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Leu | Gly | Tyr | Leu | Thr | Phe | Val | Arg | Asn | Phe | Val | Gln | Gly | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Pro | Leu | Ala | Gly | Val | Leu | Val | Ile | Thr | Tyr | Asp | Arg | Pro | Ile | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ala | Ile | Gly | Thr | Val | Cys | Trp | Ala | Leu | Ser | Thr | Ala | Ala | Val | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Ser | Tyr | Phe | Ile | Gln | Val | Ala | Leu | Trp | Arg | Ala | Val | Asn | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Leu | Ala | Ile | Val | Ile | Pro | Ala | Leu | Gln | Ser | Phe | Ile | Ala | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Tyr | Lys | Asp | Gly | Ala | Arg | Gly | Ala | Gly | Phe | Gly | Met | Leu | Asn | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Gly | Thr | Ile | Gly | Gly | Ile | Gly | Gly | Gly | Val | Val | Ala | Thr | Val | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Gly | Ser | Glu | Phe | Trp | Gly | Ile | Pro | Gly | Trp | Arg | Cys | Ala | Phe | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Met | Ala | Ala | Leu | Ser | Ala | Val | Ile | Gly | Leu | Leu | Val | Phe | Leu | Phe |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Val | Asp | Pro | Arg | Lys | Asn | Ile | Glu | Arg | Glu | Glu | Leu | Met | Ala | His |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Met | Asn | Ser | Asn | Ser | Val | Trp | Asn | Asp | Ser | Leu | Ala | Ala | Ala | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Val | Val | Lys | Val | Ser | Thr | Phe | Gln | Ile | Ile | Val | Ala | Gln | Gly | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Gly | Ser | Phe | Pro | Trp | Thr | Ala | Met | Val | Phe | Phe | Thr | Met | Trp | Phe |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Leu | Ile | Gly | Phe | Asp | His | Asn | Gln | Thr | Ala | Ala | Leu | Leu | Gly | Val |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Ala | Thr | Gly | Gly | Ala | Ile | Gly | Thr | Leu | Met | Gly | Gly | Ile | Ile | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Lys | Met | Ser | Arg | Ile | Tyr | Pro | Asn | Ser | Gly | Arg | Val | Met | Cys | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Gln | Phe | Ser | Ala | Phe | Met | Gly | Ile | Pro | Phe | Ser | Ile | Ile | Leu | Leu | Lys |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Val | Ile | Pro | Gln | Ser | Thr | Ser | Ser | Tyr | Ser | Ile | Phe | Ser | Ile | Thr | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Phe | Leu | Met | Gly | Leu | Thr | Ile | Thr | Trp | Cys | Gly | Ser | Ala | Val | Asn | Ala |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Pro | Met | Phe | Ala | Glu | Val | Val | Pro | Pro | Arg | His | Arg | Thr | Met | Ile | Tyr |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Phe | Asp | Arg | Ala | Phe | Glu | Gly | Ser | Phe | Ser | Ser | Phe | Ala | Ala | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Leu | Val | Gly | Ile | Leu | Ser | Glu | Lys | Met | Phe | Gly | Tyr | Asp | Ser | Arg | Gly |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Ile | Asp | Pro | Leu | Lys | Gly | Ser | Ser | Val | Arg | Glu | Ala | Asp | Ala | Leu | Ser |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |

Lys Gly Leu Leu Ser Met Met Ala Val Pro Phe Gly Leu Cys Cys Leu  
420 425 430  
Cys Tyr Thr Pro Leu His Phe Val Phe Gln Lys Asp Arg Glu Asn Ala  
435 440 445  
Lys Ile Ala Ser Ser Lys Glu Thr Glu Met Ile  
450 455

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

aatggaatca cactatcaca atcataacca caaaaacaaa cactatggga cacctcaaaa 60  
gtctcttcac tattcttttc ctaatagcta tgtcgtcaac cgtaacattt gcccgtaaaa 120  
taccgcgat catcgtgttt ggcgactctt ccgttgatgc cgggaacaac aactatatcc 180  
caactgttgc tagaagcaac tttagaccat atggacggga ctttgttggg ggaaagccga 240  
ccggacgggt ttgtaacgga aagattgcga cggattttat gtccgaagcc ttagggctta 300  
aaccaatcat tccggcctac ttggatcctt cttataacat ttcagacttt gcaacagggtg 360  
ttacctttgc ttctgtgtgc actggctatg acaacgccac ttctgatgtt ctgtcgggtac 420  
tacctctatg gaaacaactt gaatactaca aagaatacca aacaaaactt aaagcatacc 480  
aaggaaaaga cagagccaca gagactatag aaagctctct ctacctcata agcataggga 540  
ccaacgattt cctcgagaat tactttgtct ttccgggccg ttcttcgcaa tattccgtca 600  
gtctttacca agattttcta gccggaatcg cgaaagaatt tgtgaagaag ttgcatggac 660  
ttggtgctag aaagatctca ctaggtgggt tacctccaat gggatgcatg cctttagaga 720  
gagccaccaa cattggcact ggaggtgagt gcgtaggacg gtacaacgac atagccgtcc 780  
agttcaacag caagcttgat aagatggttg agaagctgaa caaagagctt cctggttcca 840  
acctcgtttt ctcaaatcca tatgagccat ttatgcggtat catcaagaac ccttcctcct 900  
ttgggttcga ggtggtggga gcggcatgCt gcgcgacagg gatgttcgag atgggatatg 960  
gttgtaaaag gaataaccca ttacatgta caaacgcaga caagtatgtg ttttgggact 1020  
catttcaccc aacacagaag actaatcaca tcatggccaa tgctctcatg aacagcacat 1080  
tcctcactt cctctaaatg atttttatgt ttgtgtgtgg aaactaaata gatataagag 1140  
taatattatt attagggtt gcttttgata tgcactctgt atgtatttat atttaagtag 1200  
attttgctct tgtgttagtt agcgaaacct acgtttcttt tctagattat ggtgtgccta 1260  
tttatgtagc ttattttatc ctctttagtt attctcaata tatcc

(2) INFORMATION FOR SEQ ID NO:2057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

Trp Asn His Thr Ile Thr Ile Ile Thr Thr Lys Thr Asn Thr Met Gly  
1 5 10 15  
His Leu Lys Ser Leu Phe Thr Ile Leu Phe Leu Ile Ala Met Ser Ser  
20 25 30  
Thr Val Thr Phe Ala Gly Lys Ile Pro Ala Ile Ile Val Phe Gly Asp  
35 40 45  
Ser Ser Val Asp Ala Gly Asn Asn Asn Tyr Ile Pro Thr Val Ala Arg  
50 55 60  
Ser Asn Phe Glu Pro Tyr Gly Arg Asp Phe Val Gly Gly Lys Pro Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Arg | Phe | Cys | Asn | Gly | Lys | Ile | Ala | Thr | Asp | Phe | Met | Ser | Glu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Gly | Leu | Lys | Pro | Ile | Ile | Pro | Ala | Tyr | Leu | Asp | Pro | Ser | Tyr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ser | Asp | Phe | Ala | Thr | Gly | Val | Thr | Phe | Ala | Ser | Ala | Ala | Thr | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Tyr | Asp | Asn | Ala | Thr | Ser | Asp | Val | Leu | Ser | Val | Leu | Pro | Leu | Trp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Leu | Glu | Tyr | Tyr | Lys | Glu | Tyr | Gln | Thr | Lys | Leu | Lys | Ala | Tyr | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Lys | Asp | Arg | Ala | Thr | Glu | Thr | Ile | Glu | Ser | Ser | Leu | Tyr | Leu | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Ile | Gly | Thr | Asn | Asp | Phe | Leu | Glu | Asn | Tyr | Phe | Val | Phe | Pro | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ser | Ser | Gln | Tyr | Ser | Val | Ser | Leu | Tyr | Gln | Asp | Phe | Leu | Ala | Gly |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ile | Ala | Lys | Glu | Phe | Val | Lys | Lys | Leu | His | Gly | Leu | Gly | Ala | Arg | Lys |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Ser | Leu | Gly | Gly | Leu | Pro | Pro | Met | Gly | Cys | Met | Pro | Leu | Glu | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Thr | Asn | Ile | Gly | Thr | Gly | Gly | Glu | Cys | Val | Gly | Arg | Tyr | Asn | Asp |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ile | Ala | Val | Gln | Phe | Asn | Ser | Lys | Leu | Asp | Lys | Met | Val | Glu | Lys | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Lys | Glu | Leu | Pro | Gly | Ser | Asn | Leu | Val | Phe | Ser | Asn | Pro | Tyr | Glu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Phe | Met | Arg | Ile | Ile | Lys | Asn | Pro | Ser | Ser | Phe | Gly | Phe | Glu | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Gly | Ala | Ala | Cys | Cys | Ala | Thr | Gly | Met | Phe | Glu | Met | Gly | Tyr | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Cys | Gln | Arg | Asn | Asn | Pro | Phe | Thr | Cys | Thr | Asn | Ala | Asp | Lys | Tyr | Val |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Phe | Trp | Asp | Ser | Phe | His | Pro | Thr | Gln | Lys | Thr | Asn | His | Ile | Met | Ala |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Asn | Ala | Leu | Met | Asn | Ser | Thr | Phe | Pro | His | Phe | Leu |     |     |     |     |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | His | Leu | Lys | Ser | Leu | Phe | Thr | Ile | Leu | Phe | Leu | Ile | Ala | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Thr | Val | Thr | Phe | Ala | Gly | Lys | Ile | Pro | Ala | Ile | Ile | Val | Phe |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ser | Ser | Val | Asp | Ala | Gly | Asn | Asn | Asn | Tyr | Ile | Pro | Thr | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Ser | Asn | Phe | Glu | Pro | Tyr | Gly | Arg | Asp | Phe | Val | Gly | Gly | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Thr | Gly | Arg | Phe | Cys | Asn | Gly | Lys | Ile | Ala | Thr | Asp | Phe | Met | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ala | Leu | Gly | Leu | Lys | Pro | Ile | Ile | Pro | Ala | Tyr | Leu | Asp | Pro | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

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Tyr Asn Ile Ser Asp Phe Ala Thr Gly Val Thr Phe Ala Ser Ala Ala
 100 105 110
Thr Gly Tyr Asp Asn Ala Thr Ser Asp Val Leu Ser Val Leu Pro Leu
 115 120 125
Trp Lys Gln Leu Glu Tyr Tyr Lys Glu Tyr Gln Thr Lys Leu Lys Ala
 130 135 140
Tyr Gln Gly Lys Asp Arg Ala Thr Glu Thr Ile Glu Ser Ser Leu Tyr
 145 150 155 160
Leu Ile Ser Ile Gly Thr Asn Asp Phe Leu Glu Asn Tyr Phe Val Phe
 165 170 175
Pro Gly Arg Ser Ser Gln Tyr Ser Val Ser Leu Tyr Gln Asp Phe Leu
 180 185 190
Ala Gly Ile Ala Lys Glu Phe Val Lys Lys Leu His Gly Leu Gly Ala
 195 200 205
Arg Lys Ile Ser Leu Gly Gly Leu Pro Pro Met Gly Cys Met Pro Leu
 210 215 220
Glu Arg Ala Thr Asn Ile Gly Thr Gly Gly Glu Cys Val Gly Arg Tyr
 225 230 235 240
Asn Asp Ile Ala Val Gln Phe Asn Ser Lys Leu Asp Lys Met Val Glu
 245 250 255
Lys Leu Asn Lys Glu Leu Pro Gly Ser Asn Leu Val Phe Ser Asn Pro
 260 265 270
Tyr Glu Pro Phe Met Arg Ile Ile Lys Asn Pro Ser Ser Phe Gly Phe
 275 280 285
Glu Val Val Gly Ala Ala Cys Cys Ala Thr Gly Met Phe Glu Met Gly
 290 295 300
Tyr Gly Cys Gln Arg Asn Asn Pro Phe Thr Cys Thr Asn Ala Asp Lys
 305 310 315 320
Tyr Val Phe Trp Asp Ser Phe His Pro Thr Gln Lys Thr Asn His Ile
 325 330 335
Met Ala Asn Ala Leu Met Asn Ser Thr Phe Pro His Phe Leu
 340 345 350

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(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

```

Met Ser Ser Thr Val Thr Phe Ala Gly Lys Ile Pro Ala Ile Ile Val
1 5 10 15
Phe Gly Asp Ser Ser Val Asp Ala Gly Asn Asn Asn Tyr Ile Pro Thr
 20 25 30
Val Ala Arg Ser Asn Phe Glu Pro Tyr Gly Arg Asp Phe Val Gly Gly
 35 40 45
Lys Pro Thr Gly Arg Phe Cys Asn Gly Lys Ile Ala Thr Asp Phe Met
 50 55 60
Ser Glu Ala Leu Gly Leu Lys Pro Ile Ile Pro Ala Tyr Leu Asp Pro
 65 70 75 80
Ser Tyr Asn Ile Ser Asp Phe Ala Thr Gly Val Thr Phe Ala Ser Ala
 85 90 95
Ala Thr Gly Tyr Asp Asn Ala Thr Ser Asp Val Leu Ser Val Leu Pro
 100 105 110
Leu Trp Lys Gln Leu Glu Tyr Tyr Lys Glu Tyr Gln Thr Lys Leu Lys
 115 120 125
Ala Tyr Gln Gly Lys Asp Arg Ala Thr Glu Thr Ile Glu Ser Ser Leu

```

SEQUENCE 1571694

130 135 140  
Tyr Leu Ile Ser Ile Gly Thr Asn Asp Phe Leu Glu Asn Tyr Phe Val  
145 150 155 160  
Phe Pro Gly Arg Ser Ser Gln Tyr Ser Val Ser Leu Tyr Gln Asp Phe  
165 170 175  
Leu Ala Gly Ile Ala Lys Glu Phe Val Lys Lys Leu His Gly Leu Gly  
180 185 190  
Ala Arg Lys Ile Ser Leu Gly Gly Leu Pro Pro Met Gly Cys Met Pro  
195 200 205  
Leu Glu Arg Ala Thr Asn Ile Gly Thr Gly Gly Glu Cys Val Gly Arg  
210 215 220  
Tyr Asn Asp Ile Ala Val Gln Phe Asn Ser Lys Leu Asp Lys Met Val  
225 230 235 240  
Glu Lys Leu Asn Lys Glu Leu Pro Gly Ser Asn Leu Val Phe Ser Asn  
245 250 255  
Pro Tyr Glu Pro Phe Met Arg Ile Ile Lys Asn Pro Ser Ser Phe Gly  
260 265 270  
Phe Glu Val Val Gly Ala Ala Cys Cys Ala Thr Gly Met Phe Glu Met  
275 280 285  
Gly Tyr Gly Cys Gln Arg Asn Asn Pro Phe Thr Cys Thr Asn Ala Asp  
290 295 300  
Lys Tyr Val Phe Trp Asp Ser Phe His Pro Thr Gln Lys Thr Asn His  
305 310 315 320  
Ile Met Ala Asn Ala Leu Met Asn Ser Thr Phe Pro His Phe Leu  
325 330 335

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atagattacg taagagtctc tctctctctc tctctggaag agggccttgk gattgttttc   | 60   |
| ttcttctctcT ttagcttctc atcgaattcg ttatcgaatt gaaagtctcg accttctgct  | 120  |
| gttgctccctc aatacgtctc attcttttga ttagcatccc taaaactaaa atcgacagaga | 180  |
| gaatttctcc gtttggatct ctaccaaatt ggggcgcttt tgggaataat gccaccgttt   | 240  |
| atgtccggtc tcagagctgt atcttctcta ctttcatgtc gaaacgcgat tagcaggaaa   | 300  |
| ctcgttagtc gttctgggat ctctcgaggg agttttgtat cagatcaaatt taggagattt  | 360  |
| ggttctcttt cgggcgtcga gagatgttct tctaattggg tgatgtccaa tgatgacgct   | 420  |
| agagtctctt tccggagatt gcctggctct gtgagcctac ttcagagacg gcattttctg   | 480  |
| gggtgcggag atggggaaga aggtggtggt gagttatcaa agatctatga agagagacgt   | 540  |
| gtcttagggt atactccgga gcaaagtgtt aacgtagttg cagctgtaga cttgtacat    | 600  |
| ggatttggtc cttgggtgtc gcgctctgag gttcttaaag aataccctga tgggtcattt   | 660  |
| gatgctgaat tggagattgg tttcaagttt ctcgttgaga gttacatttc ccatgtcgaa   | 720  |
| tccgagagggc cgaaatggat taagactaca gcgagggaca ctggcctgtt tgaccatttg  | 780  |
| ataaacctct ggcaatttaa gccagggccc attcctggaa cctgcgacct tcacttccat   | 840  |
| gtagatttca aattcaattc acctctctat cgccaggtgg cgtcaatgtt cttcaaggag   | 900  |
| gtagcatcaa gacttggtgg ggcattcagt gatcgatgcc gactagtgtg tgggtccagga  | 960  |
| gtccgagtag atgaaaacgc atatgagcaa agagcttgag acatatctat atatatatat   | 1020 |
| catggaagta acaacacatc agtttagttt tcatcttggt ttctagagag cgattgcgca   | 1080 |
| tagcatgttt tgttttctta aatatatatg aatgcttttg cataagaaga tgaacacatt   | 1140 |
| agatgtttgt ttaaatgtaa aagcagaaaa ataaacacat ccatttctct gttggagtca   | 1200 |
| ttttttcac tcc                                                       |      |

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..256
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571704
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

Met Pro Pro Phe Met Ser Gly Leu Arg Ala Val Ser Ser Leu Leu Ser  
1 5 10 15  
Cys Arg Asn Ala Ile Ser Arg Lys Leu Val Ser Arg Ser Gly Ile Ser  
20 25 30  
Arg Gly Ser Phe Val Ser Asp Gln Ile Arg Arg Phe Gly Ser Leu Ser  
35 40 45  
Gly Val Glu Arg Cys Ser Ser Asn Trp Leu Met Ser Asn Asp Asp Ala  
50 55 60  
Arg Val Ser Phe Arg Arg Leu Pro Gly Ser Val Ser Leu Leu Gln Arg  
65 70 75 80  
Arg His Phe Leu Gly Cys Gly Asp Gly Glu Gly Gly Gly Glu Leu  
85 90 95  
Ser Lys Ile Tyr Glu Glu Arg Arg Val Leu Gly Tyr Thr Pro Glu Gln  
100 105 110  
Met Phe Asn Val Val Ala Ala Val Asp Leu Tyr His Gly Phe Val Pro  
115 120 125  
Trp Cys Gln Arg Ser Glu Val Leu Lys Glu Tyr Pro Asp Gly Ser Phe  
130 135 140  
Asp Ala Glu Leu Glu Ile Gly Phe Lys Phe Leu Val Glu Ser Tyr Ile  
145 150 155 160  
Ser His Val Glu Ser Glu Arg Pro Lys Trp Ile Lys Thr Thr Ala Arg  
165 170 175  
Asp Thr Gly Leu Phe Asp His Leu Ile Asn Leu Trp Gln Phe Lys Pro  
180 185 190  
Gly Pro Ile Pro Gly Thr Cys Asp Leu His Phe His Val Asp Phe Lys  
195 200 205  
Phe Asn Ser Pro Leu Tyr Arg Gln Val Ala Ser Met Phe Phe Lys Glu  
210 215 220  
Val Ala Ser Arg Leu Val Gly Ala Phe Ser Asp Arg Cys Arg Leu Val  
225 230 235 240  
Tyr Gly Pro Gly Val Arg Val Asp Glu Asn Ala Tyr Glu Gln Arg Ala  
245 250 255

(2) INFORMATION FOR SEQ ID NO:2062:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 252 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..252
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571705
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Met Ser Gly Leu Arg Ala Val Ser Ser Leu Ser Cys Arg Asn Ala  
1 5 10 15  
Ile Ser Arg Lys Leu Val Ser Arg Ser Gly Ile Ser Arg Gly Ser Phe  
20 25 30  
Val Ser Asp Gln Ile Arg Arg Phe Gly Ser Leu Ser Gly Val Glu Arg  
35 40 45

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Ser | Asn | Trp | Leu | Met | Ser | Asn | Asp | Asp | Ala | Arg | Val | Ser | Phe |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Leu | Pro | Gly | Ser | Val | Ser | Leu | Leu | Gln | Arg | Arg | His | Phe | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Cys | Gly | Asp | Gly | Glu | Glu | Gly | Gly | Gly | Glu | Leu | Ser | Lys | Ile | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Glu | Arg | Arg | Val | Leu | Gly | Tyr | Thr | Pro | Glu | Gln | Met | Phe | Asn | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ala | Ala | Val | Asp | Leu | Tyr | His | Gly | Phe | Val | Pro | Trp | Cys | Gln | Arg |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Glu | Val | Leu | Lys | Glu | Tyr | Pro | Asp | Gly | Ser | Phe | Asp | Ala | Glu | Leu |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ile | Gly | Phe | Lys | Phe | Leu | Val | Glu | Ser | Tyr | Ile | Ser | His | Val | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Glu | Arg | Pro | Lys | Trp | Ile | Lys | Thr | Thr | Ala | Arg | Asp | Thr | Gly | Leu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Asp | His | Leu | Ile | Asn | Leu | Trp | Gln | Phe | Lys | Pro | Gly | Pro | Ile | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Thr | Cys | Asp | Leu | His | Phe | His | Val | Asp | Phe | Lys | Phe | Asn | Ser | Pro |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Tyr | Arg | Gln | Val | Ala | Ser | Met | Phe | Phe | Lys | Glu | Val | Ala | Ser | Arg |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Val | Gly | Ala | Phe | Ser | Asp | Arg | Cys | Arg | Leu | Val | Tyr | Gly | Pro | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Arg | Val | Asp | Glu | Asn | Ala | Tyr | Glu | Gln | Arg | Ala |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1571706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Asp | Asp | Ala | Arg | Val | Ser | Phe | Arg | Arg | Leu | Pro | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Leu | Leu | Gln | Arg | Arg | His | Phe | Leu | Gly | Cys | Gly | Asp | Gly | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Gly | Gly | Gly | Glu | Leu | Ser | Lys | Ile | Tyr | Glu | Glu | Arg | Arg | Val | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Tyr | Thr | Pro | Glu | Gln | Met | Phe | Asn | Val | Val | Ala | Ala | Val | Asp | Leu |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | His | Gly | Phe | Val | Pro | Trp | Cys | Gln | Arg | Ser | Glu | Val | Leu | Lys | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Pro | Asp | Gly | Ser | Phe | Asp | Ala | Glu | Leu | Glu | Ile | Gly | Phe | Lys | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Val | Glu | Ser | Tyr | Ile | Ser | His | Val | Glu | Ser | Glu | Arg | Pro | Lys | Trp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Lys | Thr | Thr | Ala | Arg | Asp | Thr | Gly | Leu | Phe | Asp | His | Leu | Ile | Asn |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Trp | Gln | Phe | Lys | Pro | Gly | Pro | Ile | Pro | Gly | Thr | Cys | Asp | Leu | His |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Phe | His | Val | Asp | Phe | Lys | Phe | Asn | Ser | Pro | Leu | Tyr | Arg | Gln | Val | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Met | Phe | Phe | Lys | Glu | Val | Ala | Ser | Arg | Leu | Val | Gly | Ala | Phe | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asp | Arg | Cys | Arg | Leu | Val | Tyr | Gly | Pro | Gly | Val | Arg | Val | Asp | Glu | Asn |



180  
Ala Tyr Glu Gln Arg Ala  
195

185

190

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

gatttcgatac ttactatcct gggatgtgtt caattcttct tcatcttctt ccttcagttc 60  
gtgttctgtg tctgattgat tactctcaca aaactcatct ttccattgtc taaaggtcta 120  
atcttttagct ataactcaaa atctgtttct aagttctgac aagtttctga aacgaaattc 180  
aagttttttg atacatatgt tcatcttctc gaacagggtt taattaaaca agagatgtca 240  
attttggcga tggttttcgt aacataaaca tgagatttga ttgttctgtg cagatctcat 300  
agttaattctg gtttgagttct agaaatttct agtgatgcag ctctgacgcc attgttaccc 360  
actgagaaga tagataccat ggctcaagat ttcaacctga actcaagaac ttcttcttca 420  
agaaaacgaa gattgcgtcg ctctagaagt gctcctcgtg gtgattgtat gtacaatgat 480  
gatgtcaaaa tcgacgaacc acctcctcat ccgagtaaaa tccaatgtt cagtgtatcta 540  
aaccgcgaatc tcaggcgagt gatcatgttc ttggctttat atcttaccat tggtagtctc 600  
tgtttctacc tcgtgagaga ccagatctcc ggtcataaaa ccagtgggtg ggtagatgct 660  
ctctatttct gtatagtaac gatgacaact gttggatacg gtgacctgtt ccctaatagt 720  
tccgcctcaa ggctacttgc ttgtgccttc gtcttctcgg gaatggctct cgttggtcac 780  
ctcttaagtc gagcggcgga ttatctagtg gagaaacaag aggctttgct cgttagggct 840  
ttccatttgc gtcaaagctt tgggtccaaca gacattctca aggagttgca tactaacaag 900  
ttgagataca aatgctatgc tacatgcctt gtcttcttag tcctcttcat tgttggcacg 960  
attttccttg taatgggtga gaaaatgccg gttatctcag ctttctactg cgtctgctcc 1020  
acggttacaa cattgggtta tggagataag agttttaact cggaagccgg acgccttttt 1080  
gctgtgtttt ggatcttgac gagcaccata tgtttTTggc tcagtttttc ctctatgtaA 1140  
gctgagctaa atacagaaaa caaacagagg gcgttgggtga aatgggtttt aacgcgaaga 1200  
atcacaaaca atgatctcga agcagctgat ctcgatgaag atggmgttgt tggagctgca 1260  
gagtttattg tgtataaact gaaagaaatg ggtaagattg atgagaaaga tatttctggg 1320  
ataatgggat agttcgagca acttgattac gatgaatcag gaactctcac gacttctgac 1380  
atcgtttttag ctcagaccac gtcctagatt caaaggtaag cctcattatc atcatcatca 1440  
tcattcttgcg aagacgaatc agaattcttg tttagttata ccttcacaca acaaaaagcc 1500  
aaagagagtg aacagttttt tggaaatttt gtttgttttt cctgtttgtg tttgtaatgt 1560  
aatgccacag tctaactctt tgatcgtttc tc

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

Met Ala Gln Asp Phe Asn Leu Asn Ser Arg Thr Ser Ser Arg Lys  
1 5 10 15  
Arg Arg Leu Arg Arg Ser Arg Ser Ala Pro Arg Gly Asp Cys Met Tyr  
20 25 30  
Asn Asp Asp Val Lys Ile Asp Glu Pro Pro Pro His Pro Ser Lys Ile  
35 40 45  
Pro Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile Met Phe

50 55 60  
Leu Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu Val Arg  
65 70 75 80  
Asp Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala Leu Tyr  
85 90 95  
Phe Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu Val Pro  
100 105 110  
Asn Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe Ser Gly  
115 120 125  
Met Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr Leu Val  
130 135 140  
Glu Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg Gln Ser  
145 150 155 160  
Phe Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys Leu Arg  
165 170 175  
Tyr Lys Cys Tyr Ala Thr Cys Leu Val Leu Val Val Leu Phe Ile Val  
180 185 190  
Gly Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile Ser Ala  
195 200 205  
Phe Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly Asp Lys  
210 215 220  
Ser Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp Ile Leu  
225 230 235 240  
Thr Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met  
245 250

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1571709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

Met Tyr Asn Asp Asp Val Lys Ile Asp Glu Pro Pro Pro His Pro Ser  
1 5 10 15  
Lys Ile Pro Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile  
20 25 30  
Met Phe Leu Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu  
35 40 45  
Val Arg Asp Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala  
50 55 60  
Leu Tyr Phe Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu  
65 70 75 80  
Val Pro Asn Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe  
85 90 95  
Ser Gly Met Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr  
100 105 110  
Leu Val Glu Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg  
115 120 125  
Gln Ser Phe Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys  
130 135 140  
Leu Arg Tyr Lys Cys Tyr Ala Thr Cys Leu Val Leu Val Val Leu Phe  
145 150 155 160  
Ile Val Gly Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile  
165 170 175  
Ser Ala Phe Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly  
180 185 190

Asp Lys Ser Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp  
195 200 205  
Ile Leu Thr Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile Met Phe Leu  
1 5 10 15  
Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu Val Arg Asp  
20 25 30  
Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala Leu Tyr Phe  
35 40 45  
Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu Val Pro Asn  
50 55 60  
Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe Ser Gly Met  
65 70 75 80  
Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr Leu Val Glu  
85 90 95  
Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg Gln Ser Phe  
100 105 110  
Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys Leu Arg Tyr  
115 120 125  
Lys Cys Tyr Ala Thr Cys Leu Val Leu Val Val Leu Phe Ile Val Gly  
130 135 140  
Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile Ser Ala Phe  
145 150 155 160  
Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly Asp Lys Ser  
165 170 175  
Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp Ile Leu Thr  
180 185 190  
Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met  
195 200

(2) INFORMATION FOR SEQ ID NO:2068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1324
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ctatcgaaac tctctctgac ttgtttgtgt tctctcaaat cctctgataa gaatcaatgg  | 60  |
| cgaaggaatt agcagagaaa gctaaagaag ctYttctaga tgatgacttc gatgttgctg  | 120 |
| ttgacttata ctccaaagcc attgacttgg atcccaattg cgccgccttc ttgcgcgatc  | 180 |
| gtgctcaggc caacatcaaa atcgataact tcaactgaagc tgtttagatg gcgaacaaag | 240 |
| ccattgagtt ggagccaacg ttggcaaaag cctatctcag aaagggcact gcttgtatga  | 300 |
| agctagaaga atatagtact gctaaagcag ccctggaaaa gggagcttct gttgcaccga  | 360 |
| atgaaccaa gtttaagaag atgatagatg aatgcgatct tcgtattgca gaagaagaga   | 420 |

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| aagattttggt | tcagccgatg | ccaccgagtt  | tgccttcaag  | ctctacaaca | ccactagcaa  | 480  |
| cggaagctga  | tgctcctcct | gttccaattc  | ctgcagcacc  | tgccaaaccg | atgttcaggc  | 540  |
| acgagttcta  | ccagaaacca | gaagaagcgg  | tggtgacaat  | tttcgccaaa | aaagtaccta  | 600  |
| aggagaacgt  | aactgtcgag | tttgggtgagc | agatttctgag | tggtgtcatt | gatgttgctg  | 660  |
| gagaggaagc  | ttatcatctc | cagccgagat  | tggtcgggaa  | gataatacca | gagaagtgca  | 720  |
| gatttgaagt  | attgtcgacc | aaagttgaga  | tccgtcttgc  | gaaagcagag | ataatcacct  | 780  |
| gggcctccct  | tgaatatggt | aaagggcaaa  | gtgttttgcc  | caaacccaat | gtctcatcag  | 840  |
| cgctgtcgca  | gagaccagtg | tacccatctt  | ctaagccagc  | aaaagactgg | gacaagttgg  | 900  |
| aagctgaagt  | gaagaaacag | gagaaggatg  | agaagcttga  | tggagatgca | gctatgaaca  | 960  |
| aatttttcag  | cgacatatac | tcgagtgcag  | atgaagacat  | gaggcgggca | atgaacaaat  | 1020 |
| cattttgcaga | gtcgaatggg | acggtactgt  | cgacaaactg  | gaaagaagtt | gggactaaga  | 1080 |
| aagtggagag  | cactccacca | gatggcatgg  | agctcaagaa  | gtgggagtat | tgatcttctt  | 1140 |
| aaaatcccct  | tttctggttt | ttgttaaaaa  | aaagtctgac  | aaatcttttg | aactttttaag | 1200 |
| gtgttttttt  | ttttggtttc | tgctcgaatt  | tgtctctctc  | cattcttgcg | ttgtgggtctc | 1260 |
| aaagaacggt  | ctgatacttt | gattttgtat  | tagaaaacta  | aaactcgcaa | gtctgttggt  | 1320 |
| ttgg        |            |             |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..358
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Glu | Leu | Ala | Glu | Lys | Ala | Lys | Glu | Ala | Xaa | Leu | Asp | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Phe | Asp | Val | Ala | Val | Asp | Leu | Tyr | Ser | Lys | Ala | Ile | Asp | Leu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Cys | Ala | Ala | Phe | Phe | Ala | Asp | Arg | Ala | Gln | Ala | Asn | Ile | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asp | Asn | Phe | Thr | Glu | Ala | Val | Val | Asp | Ala | Asn | Lys | Ala | Ile | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Pro | Thr | Leu | Ala | Lys | Ala | Tyr | Leu | Arg | Lys | Gly | Thr | Ala | Cys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | Lys | Leu | Glu | Glu | Tyr | Ser | Thr | Ala | Lys | Ala | Ala | Leu | Glu | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ser | Val | Ala | Pro | Asn | Glu | Pro | Lys | Phe | Lys | Lys | Met | Ile | Asp | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Asp | Leu | Arg | Ile | Ala | Glu | Glu | Glu | Lys | Asp | Leu | Val | Gln | Pro | Met |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Pro | Pro | Ser | Leu | Pro | Ser | Ser | Ser | Thr | Thr | Pro | Leu | Ala | Thr | Glu | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asp | Ala | Pro | Pro | Val | Pro | Ile | Pro | Ala | Ala | Pro | Ala | Lys | Pro | Met | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | His | Glu | Phe | Tyr | Gln | Lys | Pro | Glu | Glu | Ala | Val | Val | Thr | Ile | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Lys | Lys | Val | Pro | Lys | Glu | Asn | Val | Thr | Val | Glu | Phe | Gly | Glu | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Leu | Ser | Val | Val | Ile | Asp | Val | Ala | Gly | Glu | Glu | Ala | Tyr | His | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Pro | Arg | Leu | Phe | Gly | Lys | Ile | Ile | Pro | Glu | Lys | Cys | Arg | Phe | Glu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Val | Leu | Ser | Thr | Lys | Val | Glu | Ile | Arg | Leu | Ala | Lys | Ala | Glu | Ile | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Trp | Ala | Ser | Leu | Glu | Tyr | Gly | Lys | Gly | Gln | Ser | Val | Leu | Pro | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Asn | Val | Ser | Ser | Ala | Leu | Ser | Gln | Arg | Pro | Val | Tyr | Pro | Ser | Ser |

(2) INFORMATION FOR SEQ ID NO:2070:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1571736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1571737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

Met Ile Asp Glu Cys Asp Leu Arg Ile Ala Glu Glu Glu Lys Asp Leu  
1 5 10 15  
Val Gln Pro Met Pro Pro Ser Leu Pro Ser Ser Ser Thr Thr Pro Leu  
20 25 30  
Ala Thr Glu Ala Asp Ala Pro Pro Val Pro Ile Pro Ala Ala Pro Ala  
35 40 45  
Lys Pro Met Phe Arg His Glu Phe Tyr Gln Lys Pro Glu Glu Ala Val  
50 55 60  
Val Thr Ile Phe Ala Lys Lys Val Pro Lys Glu Asn Val Thr Val Glu  
65 70 75 80  
Phe Gly Glu Gln Ile Leu Ser Val Val Ile Asp Val Ala Gly Glu Glu  
85 90 95  
Ala Tyr His Leu Gln Pro Arg Leu Phe Gly Lys Ile Ile Pro Glu Lys  
100 105 110  
Cys Arg Phe Glu Val Leu Ser Thr Lys Val Glu Ile Arg Leu Ala Lys  
115 120 125  
Ala Glu Ile Ile Thr Trp Ala Ser Leu Glu Tyr Gly Lys Gly Gln Ser  
130 135 140  
Val Leu Pro Lys Pro Asn Val Ser Ser Ala Leu Ser Gln Arg Pro Val  
145 150 155 160  
Tyr Pro Ser Ser Lys Pro Ala Lys Asp Trp Asp Lys Leu Glu Ala Glu  
165 170 175  
Val Lys Lys Gln Glu Lys Asp Glu Lys Leu Asp Gly Asp Ala Ala Met  
180 185 190  
Asn Lys Phe Phe Ser Asp Ile Tyr Ser Ser Ala Asp Glu Asp Met Arg  
195 200 205  
Arg Ala Met Asn Lys Ser Phe Ala Glu Ser Asn Gly Thr Val Leu Ser  
210 215 220  
Thr Asn Trp Lys Glu Val Gly Thr Lys Lys Val Glu Ser Thr Pro Pro  
225 230 235 240  
Asp Gly Met Glu Leu Lys Lys Trp Glu Tyr  
245 250

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 767 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..767

(D) OTHER INFORMATION: / Ceres Seq. ID 1571750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

atcatcacia ctactatcac accaaactca aaaaacacaa accacaagag gatcatttca 60  
ttttttattg tttcgtttta atcatcatca tcagaagaaa aatgggttgcg atatcggaga 120  
tcaagtcgac ggtggatgtc acggcggcga attgtttgat gcttttatct agagttggac 180  
aagaaaacgt tgacggtggc gatcaaaaac gcgttttcac atgtaaaacg tgtttgaagc 240  
agtttcatto gttccaagcc ttaggaggtc accgtgcgag tcacaagaag cctaacaacg 300

acgctttgtc gtctagattg atgaagaagg tgaaaacgtc gtcgcctcct tgtcccatat 360  
gtggagtggg gtttccgatg ggacaagcct tgggaggaca catgaggaga cacaggaacg 420  
agagtggNgg ctgctgggtg cgcgttggtt acacgcgctt tgttgccgga gccacagggtg 480  
actacgttga agaaatctav cagtgggaag agagtggctt gtttggatct gagtctaggg 540  
atggtggaca atttgaatct caagttggag cttggaagaa cagtttattg attttattta 600  
ttttccttaa attttctgaa tataattggtt tctctcattc tttgaatttt tcttaatttt 660  
ctagattata catacatccg cagatttagg aaactttcat agagtgtaat cttttctttc 720  
tgtaaaaata tattttactt gtagcattgg agatttggtta tgagatc

(2) INFORMATION FOR SEQ ID NO:2073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1571751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

His His Asn Tyr Tyr His Thr Lys Leu Lys Lys His Lys Pro Gln Glu  
1 5 10 15  
Asp His Phe Ile Phe Tyr Cys Phe Val Leu Ile Ile Ile Ile Arg Arg  
20 25 30  
Lys Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala  
35 40 45  
Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp  
50 55 60  
Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln  
65 70 75 80  
Phe His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys  
85 90 95  
Pro Asn Asn Asp Ala Leu Ser Ser Arg Leu Met Lys Lys Val Lys Thr  
100 105 110  
Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln  
115 120 125  
Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Xaa Gly Cys  
130 135 140  
Trp Trp Arg Val Gly Tyr Thr Arg Phe Val Ala Gly Ala His Gly Asp  
145 150 155 160  
Tyr Val Glu Glu Ile Xaa Gln Trp Glu Glu Ser Gly Leu Phe Gly Ser  
165 170 175  
Glu Ser Arg Asp Gly Gly Gln Phe Glu Ser Gln Val Gly Ala Trp Lys  
180 185 190  
Asn Ser Leu Leu Ile Leu Phe Ile Phe Leu Lys Phe Ser Glu Tyr Ile  
195 200 205  
Cys Phe Ser His Ser Leu Asn Phe Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1571752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala

1 5 10 15  
Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly  
20 25 30  
Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe  
35 40 45  
His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro  
50 55 60  
Asn Asn Asp Ala Leu Ser Ser Arg Leu Met Lys Lys Val Lys Thr Ser  
65 70 75 80  
Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala  
85 90 95  
Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Xaa Gly Cys Trp  
100 105 110  
Trp Arg Val Gly Tyr Thr Arg Phe Val Ala Gly Ala His Gly Asp Tyr  
115 120 125  
Val Glu Glu Ile Xaa Gln Trp Glu Glu Ser Gly Leu Phe Gly Ser Glu  
130 135 140  
Ser Arg Asp Gly Gly Gln Phe Glu Ser Gln Val Gly Ala Trp Lys Asn  
145 150 155 160  
Ser Leu Leu Ile Leu Phe Ile Phe Leu Lys Phe Ser Glu Tyr Ile Cys  
165 170 175  
Phe Ser His Ser Leu Asn Phe Ser  
180

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1571753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp Gly Gly Asp Gln  
1 5 10 15  
Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln Phe His Ser Phe  
20 25 30  
Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Pro Asn Asn Asp  
35 40 45  
Ala Leu Ser Ser Arg Leu Met Lys Lys Val Lys Thr Ser Ser His Pro  
50 55 60  
Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala Leu Gly Gly  
65 70 75 80  
His Met Arg Arg His Arg Asn Glu Ser Xaa Gly Cys Trp Trp Arg Val  
85 90 95  
Gly Tyr Thr Arg Phe Val Ala Gly Ala His Gly Asp Tyr Val Glu Glu  
100 105 110  
Ile Xaa Gln Trp Glu Glu Ser Gly Leu Phe Gly Ser Glu Ser Arg Asp  
115 120 125  
Gly Gly Gln Phe Glu Ser Gln Val Gly Ala Trp Lys Asn Ser Leu Leu  
130 135 140  
Ile Leu Phe Ile Phe Leu Lys Phe Ser Glu Tyr Ile Cys Phe Ser His  
145 150 155 160  
Ser Leu Asn Phe Ser  
165

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 949 base pairs

(B) TYPE: nucleic acid



- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..949  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571770  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

```
ctccaacgatt ctgacacaaa aaaggagaag gaataagaga aaagtgaagt tgttgtttgt 60
atcgatcaga aaatggcgac gtcgatgata cagaggatgt tcaagcaagg gacgaaaatc 120
gtctgcgtcg gccgtaacta cgccgctcac gccaaagaac taggcaacgc cgtccccaag 180
gaaccagtta tattcttgaa gccaacatca tcatacttag aaaatggagg aacaattgag 240
atccacatc ctttgattc acttcacat gaagtagaac tcgctttagt gattggacag 300
aaagctagag atgtacctga atcaatagcc atggattaca ttggaggata tgcggttgct 360
cttgatatga ctgctaggGa actccaagct tctgctaagg catctgggtct cccatggacg 420
gttgcgaaaag gacaagatac cttcactcct atcagctctg ttctgccaaa ggcgatgggtg 480
cgtgatcccg ataacttaga actttggctc aagggttgatg gtgaaacaag acagaagggt 540
ttgaccaaag atatgatatt caaggcccc tacctcatta gctacataag ttctataatg 600
accctttacg aaggagatgt catcttgaca ggcacaccag aagggtgttg acctgtaaag 660
ataggtcaga agataacggc cggaatcacc ggtctatctg aagttcaatt cgatgtggag 720
aggcgtgtaa agcccttgag ctaataagtg gttttattta tctttcatac aaaaatgtca 780
attttataaa agcatctcta aaattttcat cacttactgt gtttcctaag gaaggagaa 840
ataaaaactcg ttactcattt tatttgtaat ctctataaca atggctctaa gaccggttta 900
aattgtttat atgggagagt atttgtaaag ttgtgatatt tactgttgc
```

(2) INFORMATION FOR SEQ ID NO:2077:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..223  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571771  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

```
Met Ala Thr Ser Met Ile Gln Arg Met Phe Lys Gln Gly Thr Lys Ile
1 5 10 15
Val Cys Val Gly Arg Asn Tyr Ala Ala His Ala Lys Glu Leu Gly Asn
20 25 30
Ala Val Pro Lys Glu Pro Val Ile Phe Leu Lys Pro Thr Ser Ser Tyr
35 40 45
Leu Glu Asn Gly Gly Thr Ile Glu Ile Pro His Pro Leu Asp Ser Leu
50 55 60
His His Glu Val Glu Leu Ala Leu Val Ile Gly Gln Lys Ala Arg Asp
65 70 75 80
Val Pro Glu Ser Ile Ala Met Asp Tyr Ile Gly Gly Tyr Ala Val Ala
85 90 95
Leu Asp Met Thr Ala Arg Glu Leu Gln Ala Ser Ala Lys Ala Ser Gly
100 105 110
Leu Pro Trp Thr Val Ala Lys Gly Gln Asp Thr Phe Thr Pro Ile Ser
115 120 125
Ser Val Leu Pro Lys Ala Met Val Arg Asp Pro Asp Asn Leu Glu Leu
130 135 140
Trp Leu Lys Val Asp Gly Glu Thr Arg Gln Lys Gly Leu Thr Lys Asp
145 150 155 160
Met Ile Phe Lys Val Pro Tyr Leu Ile Ser Tyr Ile Ser Ser Ile Met
165 170 175
Thr Leu Tyr Glu Gly Asp Val Ile Leu Thr Gly Thr Pro Glu Gly Val
180 185 190
Gly Pro Val Lys Ile Gly Gln Lys Ile Thr Ala Gly Ile Thr Gly Leu
```

195 200 205  
Ser Glu Val Gln Phe Asp Val Glu Arg Arg Val Lys Pro Leu Ser  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

Met Ile Gln Arg Met Phe Lys Gln Gly Thr Lys Ile Val Cys Val Gly  
1 5 10 15  
Arg Asn Tyr Ala Ala His Ala Lys Glu Leu Gly Asn Ala Val Pro Lys  
20 25 30  
Glu Pro Val Ile Phe Leu Lys Pro Thr Ser Ser Tyr Leu Glu Asn Gly  
35 40 45  
Gly Thr Ile Glu Ile Pro His Pro Leu Asp Ser Leu His His Glu Val  
50 55 60  
Glu Leu Ala Leu Val Ile Gly Gln Lys Ala Arg Asp Val Pro Glu Ser  
65 70 75 80  
Ile Ala Met Asp Tyr Ile Gly Gly Tyr Ala Val Ala Leu Asp Met Thr  
85 90 95  
Ala Arg Glu Leu Gln Ala Ser Ala Lys Ala Ser Gly Leu Pro Trp Thr  
100 105 110  
Val Ala Lys Gly Gln Asp Thr Phe Thr Pro Ile Ser Ser Val Leu Pro  
115 120 125  
Lys Ala Met Val Arg Asp Pro Asp Asn Leu Glu Leu Trp Leu Lys Val  
130 135 140  
Asp Gly Glu Thr Arg Gln Lys Gly Leu Thr Lys Asp Met Ile Phe Lys  
145 150 155 160  
Val Pro Tyr Leu Ile Ser Tyr Ile Ser Ser Ile Met Thr Leu Tyr Glu  
165 170 175  
Gly Asp Val Ile Leu Thr Gly Thr Pro Glu Gly Val Gly Pro Val Lys  
180 185 190  
Ile Gly Gln Lys Ile Thr Ala Gly Ile Thr Gly Leu Ser Glu Val Gln  
195 200 205  
Phe Asp Val Glu Arg Arg Val Lys Pro Leu Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Met Phe Lys Gln Gly Thr Lys Ile Val Cys Val Gly Arg Asn Tyr Ala  
1 5 10 15  
Ala His Ala Lys Glu Leu Gly Asn Ala Val Pro Lys Glu Pro Val Ile  
20 25 30  
Phe Leu Lys Pro Thr Ser Ser Tyr Leu Glu Asn Gly Gly Thr Ile Glu  
35 40 45

Ile Pro His Pro Leu Asp Ser Leu His His Glu Val Glu Leu Ala Leu  
50 55 60  
Val Ile Gly Gln Lys Ala Arg Asp Val Pro Glu Ser Ile Ala Met Asp  
65 70 75 80  
Tyr Ile Gly Gly Tyr Ala Val Ala Leu Asp Met Thr Ala Arg Glu Leu  
85 90 95  
Gln Ala Ser Ala Lys Ala Ser Gly Leu Pro Trp Thr Val Ala Lys Gly  
100 105 110  
Gln Asp Thr Phe Thr Pro Ile Ser Ser Val Leu Pro Lys Ala Met Val  
115 120 125  
Arg Asp Pro Asp Asn Leu Glu Leu Trp Leu Lys Val Asp Gly Glu Thr  
130 135 140  
Arg Gln Lys Gly Leu Thr Lys Asp Met Ile Phe Lys Val Pro Tyr Leu  
145 150 155 160  
Ile Ser Tyr Ile Ser Ser Ile Met Thr Leu Tyr Glu Gly Asp Val Ile  
165 170 175  
Leu Thr Gly Thr Pro Glu Gly Val Gly Pro Val Lys Ile Gly Gln Lys  
180 185 190  
Ile Thr Ala Gly Ile Thr Gly Leu Ser Glu Val Gln Phe Asp Val Glu  
195 200 205  
Arg Arg Val Lys Pro Leu Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

|             |             |            |            |             |            |      |
|-------------|-------------|------------|------------|-------------|------------|------|
| gtttctaatt  | gctttcgacg  | acaatcgatc | gtagagaagt | ctacctcgta  | gacatctctc | 60   |
| tcacaaatcc  | aattcaatta  | ccattgtttg | ttattatctg | atgtcgaata  | tgcaattctc | 120  |
| tcgtggtttt  | aatccctttg  | ttatottctt | ctgtctcgcc | gtggttgcac  | caattatctc | 180  |
| ggctgatgtc  | gctatcttga  | gaacggacta | ttaccaaaaa | acatgtcctg  | atttccacaa | 240  |
| aattgtgcgt  | gaagccgtta  | caaccaaaaa | agtccaacaa | ccaacaactg  | cggccgggac | 300  |
| cctccgtctc  | tttttccatg  | attgtttcct | tgaaggttgt | gatgcactct  | tcttgatcgc | 360  |
| gaccaactcg  | ttcaacaaag  | cggaaacgvg | tgatgatctc | aatgattccc  | tcccgggaga | 420  |
| tgcttttgac  | atcgtcaccc  | gcataagac  | agctctcgag | ttgtcttgct  | ctggtgtagt | 480  |
| atcatgcgcg  | gatattctag  | cgcaggctac | acgtgacctt | gtcacaatgg  | taggaggacc | 540  |
| ttactttgac  | gtaaagcttg  | gtcgtaaaga | cggattcgaa | tccaaagctc  | ataaagtcag | 600  |
| aggaaatgtc  | ccaatggcaa  | accagactgt | tcctgacatc | cacgggatat  | tcaagaaaaa | 660  |
| cgttttttagt | cttcgcgaga  | tggtagcatt | aagcggggct | cacaccattg  | gattctctca | 720  |
| ctgcaaaag   | ttttccgaca  | ggctctacgg | atcccgtgct | gataaaagaa  | tcaaccgcgc | 780  |
| attcgcagcc  | gctctcaaa   | atctttgcaa | aaaccacacc | gtggatgata  | caatcgccgc | 840  |
| gtttaacgac  | gtgatgactc  | caggaaagtt | cgacaacatg | tacttcaaga  | acctaagcgc | 900  |
| agggtctagg  | cttttagcgt  | ctgaccacat | ccttattaaa | gacaacagca  | ccaagccgtt | 960  |
| tgtggatcta  | tacgcaacta  | acgagacagc | attctttgag | gatttcgctc  | gtgcgatgga | 1020 |
| gaaacttggc  | acggtcggcg  | tcaagggcga | taaagatgga | gaagtgcgac  | gtaggtgcga | 1080 |
| ccacttcaac  | aattctcaacg | tttaagaaga | aaaagaaaac | acaaaaccat  | ataaatataa | 1140 |
| tattattttct | gttttatttg  | cggaggagtt | gaggagaaga | aaggtttggt  | tggtatatat | 1200 |
| gtttaataac  | tacctattat  | aagcaagatc | ttgtaacaac | tcaagttggg  | atgtttaatt | 1260 |
| tttccatgaa  | aattcaaaact | gttgatttga | aagtatatag | ataaaaataac | atattatata | 1320 |
| tcg         |             |            |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..334  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571789  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Met Ser Asn Met Gln Phe Ser Arg Gly Phe Asn Pro Phe Val Ile Phe  
1 5 10 15  
Phe Cys Leu Ala Val Val Ala Pro Ile Ile Ser Ala Asp Val Ala Ile  
20 25 30  
Leu Arg Thr Asp Tyr Tyr Gln Lys Thr Cys Pro Asp Phe His Lys Ile  
35 40 45  
Val Arg Glu Ala Val Thr Thr Lys Gln Val Gln Gln Pro Thr Thr Ala  
50 55 60  
Ala Gly Thr Leu Arg Leu Phe Phe His Asp Cys Phe Leu Glu Gly Cys  
65 70 75 80  
Asp Ala Ser Val Leu Ile Ala Thr Asn Ser Phe Asn Lys Ala Glu Xaa  
85 90 95  
Asp Asp Asp Leu Asn Asp Ser Leu Pro Gly Asp Ala Phe Asp Ile Val  
100 105 110  
Thr Arg Ile Lys Thr Ala Leu Glu Leu Ser Cys Pro Gly Val Val Ser  
115 120 125  
Cys Ala Asp Ile Leu Ala Gln Ala Thr Arg Asp Leu Val Thr Met Val  
130 135 140  
Gly Gly Pro Tyr Phe Asp Val Lys Leu Gly Arg Lys Asp Gly Phe Glu  
145 150 155 160  
Ser Lys Ala His Lys Val Arg Gly Asn Val Pro Met Ala Asn Gln Thr  
165 170 175  
Val Pro Asp Ile His Gly Ile Phe Lys Lys Asn Gly Phe Ser Leu Arg  
180 185 190  
Glu Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Phe Ser His Cys  
195 200 205  
Lys Glu Phe Ser Asp Arg Leu Tyr Gly Ser Arg Ala Asp Lys Glu Ile  
210 215 220  
Asn Pro Arg Phe Ala Ala Ala Leu Lys Asp Leu Cys Lys Asn His Thr  
225 230 235  
Val Asp Asp Thr Ile Ala Ala Phe Asn Asp Val Met Thr Pro Gly Lys  
245 250 255  
Phe Asp Asn Met Tyr Phe Lys Asn Leu Lys Arg Gly Leu Gly Leu Leu  
260 265 270  
Ala Ser Asp His Ile Leu Ile Lys Asp Asn Ser Thr Lys Pro Phe Val  
275 280 285  
Asp Leu Tyr Ala Thr Asn Glu Thr Ala Phe Phe Glu Asp Phe Ala Arg  
290 295 300  
Ala Met Glu Lys Leu Gly Thr Val Gly Val Lys Gly Asp Lys Asp Gly  
305 310 315 320  
Glu Val Arg Arg Arg Cys Asp His Phe Asn Asn Leu Asn Val  
325 330

- (2) INFORMATION FOR SEQ ID NO:2082:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 331 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..331  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571790

00000000-00000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

Met Gln Phe Ser Arg Gly Phe Asn Pro Phe Val Ile Phe Phe Cys Leu  
1 5 10 15  
Ala Val Val Ala Pro Ile Ile Ser Ala Asp Val Ala Ile Leu Arg Thr  
20 25 30  
Asp Tyr Tyr Gln Lys Thr Cys Pro Asp Phe His Lys Ile Val Arg Glu  
35 40 45  
Ala Val Thr Thr Lys Gln Val Gln Gln Pro Thr Thr Ala Ala Gly Thr  
50 55 60  
Leu Arg Leu Phe Phe His Asp Cys Phe Leu Glu Gly Cys Asp Ala Ser  
65 70 75 80  
Val Leu Ile Ala Thr Asn Ser Phe Asn Lys Ala Glu Xaa Asp Asp Asp  
85 90 95  
Leu Asn Asp Ser Leu Pro Gly Asp Ala Phe Asp Ile Val Thr Arg Ile  
100 105 110  
Lys Thr Ala Leu Glu Leu Ser Cys Pro Gly Val Val Ser Cys Ala Asp  
115 120 125  
Ile Leu Ala Gln Ala Thr Arg Asp Leu Val Thr Met Val Gly Gly Pro  
130 135 140  
Tyr Phe Asp Val Lys Leu Gly Arg Lys Asp Gly Phe Glu Ser Lys Ala  
145 150 155 160  
His Lys Val Arg Gly Asn Val Pro Met Ala Asn Gln Thr Val Pro Asp  
165 170 175  
Ile His Gly Ile Phe Lys Lys Asn Gly Phe Ser Leu Arg Glu Met Val  
180 185 190  
Ala Leu Ser Gly Ala His Thr Ile Gly Phe Ser His Cys Lys Glu Phe  
195 200 205  
Ser Asp Arg Leu Tyr Gly Ser Arg Ala Asp Lys Glu Ile Asn Pro Arg  
210 215 220  
Phe Ala Ala Ala Leu Lys Asp Leu Cys Lys Asn His Thr Val Asp Asp  
225 230 235 240  
Thr Ile Ala Ala Phe Asn Asp Val Met Thr Pro Gly Lys Phe Asp Asn  
245 250 255  
Met Tyr Phe Lys Asn Leu Lys Arg Gly Leu Gly Leu Leu Ala Ser Asp  
260 265 270  
His Ile Leu Ile Lys Asp Asn Ser Thr Lys Pro Phe Val Asp Leu Tyr  
275 280 285  
Ala Thr Asn Glu Thr Ala Phe Phe Glu Asp Phe Ala Arg Ala Met Glu  
290 295 300  
Lys Leu Gly Thr Val Gly Val Lys Gly Asp Lys Asp Gly Glu Val Arg  
305 310 315 320  
Arg Arg Cys Asp His Phe Asn Asn Leu Asn Val  
325 330

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

Met Val Gly Gly Pro Tyr Phe Asp Val Lys Leu Gly Arg Lys Asp Gly  
1 5 10 15  
Phe Glu Ser Lys Ala His Lys Val Arg Gly Asn Val Pro Met Ala Asn  
20 25 30  
Gln Thr Val Pro Asp Ile His Gly Ile Phe Lys Lys Asn Gly Phe Ser  
35 40 45

Leu Arg Glu Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Phe Ser  
50 55 60  
His Cys Lys Glu Phe Ser Asp Arg Leu Tyr Gly Ser Arg Ala Asp Lys  
65 70 75 80  
Glu Ile Asn Pro Arg Phe Ala Ala Ala Leu Lys Asp Leu Cys Lys Asn  
85 90 95  
His Thr Val Asp Asp Thr Ile Ala Ala Phe Asn Asp Val Met Thr Pro  
100 105 110  
Gly Lys Phe Asp Asn Met Tyr Phe Lys Asn Leu Lys Arg Gly Leu Gly  
115 120 125  
Leu Leu Ala Ser Asp His Ile Leu Ile Lys Asp Asn Ser Thr Lys Pro  
130 135 140  
Phe Val Asp Leu Tyr Ala Thr Asn Glu Thr Ala Phe Phe Glu Asp Phe  
145 150 155 160  
Ala Arg Ala Met Glu Lys Leu Gly Thr Val Gly Val Lys Gly Asp Lys  
165 170 175  
Asp Gly Glu Val Arg Arg Arg Cys Asp His Phe Asn Asn Leu Asn Val  
180 185 190

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| acattgcaac  | actttctaca | aaaacaagat | gaagattgca | aagttttctg | ttctactctt | 60   |
| gcttttattt  | attttccccg | tggcattagc | gcagCtgaaa | tttaagtttt | acagtgaatc | 120  |
| gtgcccta    | at         | gcagagacta | tcgtagaaaa | cctggttcgc | cagcagtttg | 180  |
| ttcaatcacg  | gccgccttga | ctcgtagtgc | ttttcacgac | tgttttgtcc | agggctgcca | 240  |
| cgcttctctc  | ctcatagacc | caacgacgct | tcaactatcg | gaaaaaacg  | ccggcccaaa | 300  |
| ctttagcggtg | agagggttcg | agctgatcga | cgagatcaag | acggcactcg | aagctcaatg | 360  |
| tccctctacg  | gtctcgtgct | ccgatatagt | cacgctcgcc | acacgtgacg | ccgtgttctt | 420  |
| aggtggagga  | ccaagctacg | tggccccac  | cggacgtcgc | gatggctttg | tgctgaatcc | 480  |
| tgaagacgcc  | aatgatgacc | tccctccacc | attcatatcc | gtcgaaggca | tgtaagttt  | 540  |
| tttcggcaac  | aaaggaatga | atgtttttga | ttccgtagct | cttttggggg | cgcacacggt | 600  |
| tgggatcgcg  | tcttgttgga | atgtttgtga | ccgggtcacg | aactttcaag | gaaccggact | 660  |
| gcccgaacca  | tccatggacc | ccactttggc | tggcaggcta | aggaacacat | gtgcggttcc | 720  |
| aggcggcttc  | gcggcactgg | accagtcgat | gccagtaacg | ccggtctcat | tcgacaactt | 780  |
| gttctttggt  | cagatcagag | agaggaaagg | aattttgctt | attgaccaac | tgatcgcaag | 840  |
| cgacccggcc  | acttctggtg | ttgtacttca | gtatgcgtcc | aacaacgaac | tattcaaacg | 900  |
| tcagttcgca  | atcgcaatgg | tgaagatggg | agccgttgac | gtgcttaccg | gttcagctgg | 960  |
| tgagatcagg  | acgaattgta | gagcattcaa | ctaaagcttt | ataacaagtt | tctatatctg | 1020 |
| attattgatt  | gtttttccct | taatttccgc | ttctgatgat | gaattgtgaa | tggtgattgt | 1080 |
| ttgcctatat  | atgtatgtac | gtatatcttt | aaaataaggt | ttggc      |            |      |

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1571793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

His Cys Asn Thr Phe Tyr Lys Asn Lys Met Lys Ile Ala Lys Phe Ser  
1 5 10 15  
Val Leu Leu Leu Leu Phe Ile Phe Pro Val Ala Leu Ala Gln Leu  
20 25 30  
Lys Phe Lys Phe Tyr Ser Glu Ser Cys Pro Asn Ala Glu Thr Ile Val  
35 40 45  
Glu Asn Leu Val Arg Gln Gln Phe Ala Arg Asp Pro Ser Ile Thr Ala  
50 55 60  
Ala Leu Thr Arg Met His Phe His Asp Cys Phe Val Gln Gly Cys Asp  
65 70 75 80  
Ala Ser Leu Leu Ile Asp Pro Thr Thr Ser Gln Leu Ser Glu Lys Asn  
85 90 95  
Ala Gly Pro Asn Phe Ser Val Arg Gly Phe Glu Leu Ile Asp Glu Ile  
100 105 110  
Lys Thr Ala Leu Glu Ala Gln Cys Pro Ser Thr Val Ser Cys Ser Asp  
115 120 125  
Ile Val Thr Leu Ala Thr Arg Asp Ala Val Phe Leu Gly Gly Gly Pro  
130 135 140  
Ser Tyr Val Val Pro Thr Gly Arg Arg Asp Gly Phe Val Ser Asn Pro  
145 150 155 160  
Glu Asp Ala Asn Glu Ile Leu Pro Pro Pro Phe Ile Ser Val Glu Gly  
165 170 175  
Met Leu Ser Phe Phe Gly Asn Lys Gly Met Asn Val Phe Asp Ser Val  
180 185 190  
Ala Leu Leu Gly Ala His Thr Val Gly Ile Ala Ser Cys Gly Asn Phe  
195 200 205  
Val Asp Arg Val Thr Asn Phe Gln Gly Thr Gly Leu Pro Asp Pro Ser  
210 215 220  
Met Asp Pro Thr Leu Ala Gly Arg Leu Arg Asn Thr Cys Ala Val Pro  
225 230 235 240  
Gly Gly Phe Ala Ala Leu Asp Gln Ser Met Pro Val Thr Pro Val Ser  
245 250 255  
Phe Asp Asn Leu Phe Phe Gly Gln Ile Arg Glu Arg Lys Gly Ile Leu  
260 265 270  
Leu Ile Asp Gln Leu Ile Ala Ser Asp Pro Ala Thr Ser Gly Val Val  
275 280 285  
Leu Gln Tyr Ala Ser Asn Asn Glu Leu Phe Lys Arg Gln Phe Ala Ile  
290 295 300  
Ala Met Val Lys Met Gly Ala Val Asp Val Leu Thr Gly Ser Ala Gly  
305 310 315 320  
Glu Ile Arg Thr Asn Cys Arg Ala Phe Asn  
325 330

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1571794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

Met Lys Ile Ala Lys Phe Ser Val Leu Leu Leu Leu Phe Ile Phe  
1 5 10 15  
Pro Val Ala Leu Ala Gln Leu Lys Phe Lys Phe Tyr Ser Glu Ser Cys  
20 25 30  
Pro Asn Ala Glu Thr Ile Val Glu Asn Leu Val Arg Gln Gln Phe Ala

(2) INFORMATION FOR SEO ID NO:2087:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1571795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Phe | His | Asp | Cys | Phe | Val | Gln | Gly | Cys | Asp | Ala | Ser | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asp | Pro | Thr | Thr | Ser | Gln | Leu | Ser | Glu | Lys | Asn | Ala | Gly | Pro | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Val | Arg | Gly | Phe | Glu | Leu | Ile | Asp | Glu | Ile | Lys | Thr | Ala | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Gln | Cys | Pro | Ser | Thr | Val | Ser | Cys | Ser | Asp | Ile | Val | Thr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Arg | Asp | Ala | Val | Phe | Leu | Gly | Gly | Gly | Pro | Ser | Tyr | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Pro | Thr | Gly | Arg | Arg | Asp | Gly | Phe | Val | Ser | Asn | Pro | Glu | Asp | Ala | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |



Glu Ile Leu Pro Pro Phe Ile Ser Val Glu Gly Met Leu Ser Phe  
100 105 110  
Phe Gly Asn Lys Gly Met Asn Val Phe Asp Ser Val Ala Leu Leu Gly  
115 120 125  
Ala His Thr Val Gly Ile Ala Ser Cys Gly Asn Phe Val Asp Arg Val  
130 135 140  
Thr Asn Phe Gln Gly Thr Gly Leu Pro Asp Pro Ser Met Asp Pro Thr  
145 150 155 160  
Leu Ala Gly Arg Leu Arg Asn Thr Cys Ala Val Pro Gly Gly Phe Ala  
165 170 175  
Ala Leu Asp Gln Ser Met Pro Val Thr Pro Val Ser Phe Asp Asn Leu  
180 185 190  
Phe Phe Gly Gln Ile Arg Glu Arg Lys Gly Ile Leu Leu Ile Asp Gln  
195 200 205  
Leu Ile Ala Ser Asp Pro Ala Thr Ser Gly Val Val Leu Gln Tyr Ala  
210 215 220  
Ser Asn Asn Glu Leu Phe Lys Arg Gln Phe Ala Ile Ala Met Val Lys  
225 230 235 240  
Met Gly Ala Val Asp Val Leu Thr Gly Ser Ala Gly Glu Ile Arg Thr  
245 250 255  
Asn Cys Arg Ala Phe Asn  
260

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gttgcggttat tcttctggat aagagcttcg tgatgggttg aaacctctga gtgaagaaga | 60   |
| agcgccatgg ctgggattac cagcagcacc gttggattca acgccgtctt caccggaata  | 120  |
| acaaaaacag tatcatcaca ttcaactctt tctgttgatt ccaaactctg tagtcttcgt  | 180  |
| ctctccaaaa ccgaactgtc tttaactaat ctcaactcct ctctctgccg tgctttcgcc  | 240  |
| gtcacttgcc gcttcggcgg tgggtggtgga gggtatcgat tctctggaga caatagaaga | 300  |
| ggtaggccga aagaagctga aattgatgaa gctcttgata tctcctcaat taggtcagct  | 360  |
| actgttaggc ttatcgatgg gcaacaaaa acatgcttggt tagtgtctaa agacgaagcc  | 420  |
| gttcgaatgg ctgatgatgc tgaacttgat ctggtKatac tatcgctga tgcagatcct   | 480  |
| ccggttggtt aaatgatgga ctacagtaaa tacagatacg aacagcaaaa gaggaaaaaa  | 540  |
| gatcagcaaa agaaaacaac tcgcatggat ttaaaggagc ttaaaatggg ttataatatt  | 600  |
| gatcagcatg attattccgt tcgtctaagg gctgccc aaa agttcttgca agatggtgac | 660  |
| aagggttaagg tgattgtgag catgaaagga cgagaaaacg agttcagaaa tatcgctatt | 720  |
| gaactcctca gacgttttca aaccgaaata ggggagcttg caactgaaga gagcaaaaaa  | 780  |
| ttcagggaca gaaatatgtt cattatcttg gtcccaaca aagaaatgat tcggaaacca   | 840  |
| caagaaccac ccacaagaaa gaagaaaaaa acagcgaaa acgaagcttc agcttcagct   | 900  |
| gcagaaataa cagctgagcc tgagcctgag cctgaacctg agcctgagcc tgagcctgag  | 960  |
| cctgagcctg agcctgagcc agagcctcta cagatcgatt cttgagttta aaatcttggt  | 1020 |
| gtaggatttt cagagctaaa gtaaagtttt gtatatattac ttttctacca tgtctcaaga | 1080 |
| gagccaagag ctgtataaca aatagagtta gtcctatttg aatgatgttc ttcgtttgta  | 1140 |
| gatcttttct ctaatctatt tttttgttta act                               |      |

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1571797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

Met Ala Gly Ile Thr Ser Ser Thr Val Gly Phe Asn Ala Val Phe Thr  
1 5 10 15  
Gly Ile Thr Lys Thr Val Ser Ser His Ser Leu Phe Ser Val Asp Ser  
20 25 30  
Lys Leu Cys Ser Leu Arg Leu Ser Lys Thr Glu Leu Ser Phe Thr Asn  
35 40 45  
Leu Thr Pro Ser Pro Arg Arg Ala Phe Ala Val Thr Cys Arg Phe Gly  
50 55 60  
Gly Gly Gly Gly Gly Tyr Arg Phe Ser Gly Asp Asn Arg Arg Gly Arg  
65 70 75 80  
Pro Lys Glu Ala Glu Ile Asp Glu Ala Leu Asp Ile Ser Ser Ile Arg  
85 90 95  
Ser Ala Thr Val Arg Leu Ile Asp Gly Gln Gln Asn Met Leu Gly Leu  
100 105 110  
Val Ser Lys Asp Glu Ala Val Arg Met Ala Asp Asp Ala Glu Leu Asp  
115 120 125  
Leu Xaa Ile Leu Ser Pro Asp Ala Asp Pro Pro Val Val Lys Met Met  
130 135 140  
Asp Tyr Ser Lys Tyr Arg Tyr Glu Gln Gln Lys Arg Lys Lys Asp Gln  
145 150 155 160  
Gln Lys Lys Thr Thr Arg Met Asp Leu Lys Glu Leu Lys Met Gly Tyr  
165 170 175  
Asn Ile Asp Gln His Asp Tyr Ser Val Arg Leu Arg Ala Ala Gln Lys  
180 185 190  
Phe Leu Gln Asp Gly Asp Lys Val Lys Val Ile Val Ser Met Lys Gly  
195 200 205  
Arg Glu Asn Glu Phe Arg Asn Ile Ala Ile Glu Leu Leu Arg Arg Phe  
210 215 220  
Gln Thr Glu Ile Gly Glu Leu Ala Thr Glu Glu Ser Lys Asn Phe Arg  
225 230 235 240  
Asp Arg Asn Met Phe Ile Ile Leu Val Pro Asn Lys Glu Met Ile Arg  
245 250 255  
Lys Pro Gln Glu Pro Pro Thr Arg Lys Lys Lys Thr Ala Glu Asn  
260 265 270  
Glu Ala Ser Ala Ser Ala Ala Glu Ile Thr Ala Glu Pro Glu Pro Glu  
275 280 285  
Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu  
290 295 300  
Pro Glu Pro Leu Gln Ile Asp Ser  
305 310

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

Met Leu Gly Leu Val Ser Lys Asp Glu Ala Val Arg Met Ala Asp Asp  
1 5 10 15  
Ala Glu Leu Asp Leu Xaa Ile Leu Ser Pro Asp Ala Asp Pro Pro Val  
20 25 30

Val Lys Met Met Asp Tyr Ser Lys Tyr Arg Tyr Glu Gln Gln Lys Arg  
35 40 45  
Lys Lys Asp Gln Gln Lys Lys Thr Thr Arg Met Asp Leu Lys Glu Leu  
50 55 60  
Lys Met Gly Tyr Asn Ile Asp Gln His Asp Tyr Ser Val Arg Leu Arg  
65 70 75 80  
Ala Ala Gln Lys Phe Leu Gln Asp Gly Asp Lys Val Lys Val Ile Val  
85 90 95  
Ser Met Lys Gly Arg Glu Asn Glu Phe Arg Asn Ile Ala Ile Glu Leu  
100 105 110  
Leu Arg Arg Phe Gln Thr Glu Ile Gly Glu Leu Ala Thr Glu Glu Ser  
115 120 125  
Lys Asn Phe Arg Asp Arg Asn Met Phe Ile Ile Leu Val Pro Asn Lys  
130 135 140  
Glu Met Ile Arg Lys Pro Gln Glu Pro Pro Thr Arg Lys Lys Lys Lys  
145 150 155 160  
Thr Ala Glu Asn Glu Ala Ser Ala Ser Ala Ala Glu Ile Thr Ala Glu  
165 170 175  
Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu  
180 185 190  
Pro Glu Pro Glu Pro Glu Pro Leu Gln Ile Asp Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:2091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

Met Ala Asp Asp Ala Glu Leu Asp Leu Xaa Ile Leu Ser Pro Asp Ala  
1 5 10 15  
Asp Pro Pro Val Val Lys Met Met Asp Tyr Ser Lys Tyr Arg Tyr Glu  
20 25 30  
Gln Gln Lys Arg Lys Lys Asp Gln Lys Lys Thr Thr Arg Met Asp  
35 40 45  
Leu Lys Glu Leu Lys Met Gly Tyr Asn Ile Asp Gln His Asp Tyr Ser  
50 55 60  
Val Arg Leu Arg Ala Ala Gln Lys Phe Leu Gln Asp Gly Asp Lys Val  
65 70 75 80  
Lys Val Ile Val Ser Met Lys Gly Arg Glu Asn Glu Phe Arg Asn Ile  
85 90 95  
Ala Ile Glu Leu Leu Arg Arg Phe Gln Thr Glu Ile Gly Glu Leu Ala  
100 105 110  
Thr Glu Glu Ser Lys Asn Phe Arg Asp Arg Asn Met Phe Ile Ile Leu  
115 120 125  
Val Pro Asn Lys Glu Met Ile Arg Lys Pro Gln Glu Pro Pro Thr Arg  
130 135 140  
Lys Lys Lys Lys Thr Ala Glu Asn Glu Ala Ser Ala Ser Ala Ala Glu  
145 150 155 160  
Ile Thr Ala Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu  
165 170 175  
Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Leu Gln Ile Asp Ser  
180 185 190

(2) INFORMATION FOR SEQ ID NO:2092:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1185 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1185  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571800  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

```
gacgatgacg atgatgatga tgatgatgaa gttgatggag atgataatga gaaggagaaa 60
attggggttat acgagctcaa gaagggaat ctaactgtca aattcacaaa ttgggggtgct 120
tcaatcatat ctctccattt cccagacaaa aatggtaaaa tggacgatat tgttcttggc 180
tatgatagcg tcaaaaccta caagaccgac aaggtttatt tcggagcaac cgttggccga 240
gtagcaaata gaataggaaa gggcaaattc aagttgaatg gtaaagagta caagacaagt 300
gtcaacgaNt ggaaaaaaca cactccatgg tggcaagaaa gggtttgggg atgttgtgtg 360
ggcagttgca aaacaccagt acgatggcaa gaaaccacac attgtcttca ctcacacaag 420
tcctgacggc gatcaagggt ttccgggaga actcagtgtc acggtgacat ataaacttgt 480
caaagacaat gaattgagtg tggatgatga ggcaaagCct aaggataaag caactccggg 540
gaacttagct catcatagtt attggaatct tggatggtcat aattccggag atattttgtc 600
tgaagaaatt caaatcctcg gctcgggtta taccgccgtc gacggtgagc tcattcccac 660
cgggaaaatc aatccggtga aaggaacagc atacgatttt ctccaactcc gtctatttaa 720
agataatatg aaggatctta aaacaggata tgatataaat tattgcttag atggtaaggc 780
aaaaaagatg agaaaaatag ttgaactcgt agataagaaa tcaggaggga aaatggagtt 840
atccggaaac caagcgggtt tgcaattcta taccggaggg atgttaaagg atgtcaaagg 900
gaagaatggg gcagtttacc aagctttcgg gggattatgt ttagaaacac aaagtatcc 960
agacgcattg aaccatccca aatttccttc acagattgtc gagccaggga aaaaatacaa 1020
acacactatg ctcttcaagt tttctattgt ttcatagatt gttttagatg ttgttacatg 1080
aacacccttg gaaccatgtc caatgttcat gaacaagaaa ctaaatacat tgtaatatatt 1140
tgtaacaatg cttaaattat caaattatat aaacctaacg tgaac
```

(2) INFORMATION FOR SEQ ID NO:2093:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 141 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..141  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571801  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

```
Asp Asp Asp Asp Asp Asp Asp Asp Asp Glu Val Asp Gly Asp Asp Asn
1 5 10 15
Glu Lys Glu Lys Ile Gly Leu Tyr Glu Leu Lys Lys Gly Asn Leu Thr
20 25 30
Val Lys Phe Thr Asn Trp Gly Ala Ser Ile Ile Ser Leu His Phe Pro
35 40 45
Asp Lys Asn Gly Lys Met Asp Asp Ile Val Leu Gly Tyr Asp Ser Val
50 55 60
Lys Thr Tyr Lys Thr Asp Lys Val Tyr Phe Gly Ala Thr Val Gly Arg
65 70 75 80
Val Ala Asn Arg Ile Gly Lys Gly Lys Phe Lys Leu Asn Gly Lys Glu
85 90 95
Tyr Lys Thr Ser Val Asn Xaa Trp Lys Lys His Thr Pro Trp Trp Gln
100 105 110
Glu Arg Val Trp Gly Cys Cys Val Gly Ser Cys Lys Thr Pro Val Arg
115 120 125
Trp Gln Glu Thr Thr His Cys Leu His Ser His Lys Ser
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:2094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1571802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

Met Val Lys Ser Thr Arg Gln Val Ser Thr Xaa Gly Lys Asn Thr Leu  
1 5 10 15  
His Gly Gly Lys Lys Gly Phe Gly Asp Val Val Trp Ala Val Ala Lys  
20 25 30  
His Gln Tyr Asp Gly Lys Lys Pro His Ile Val Phe Thr His Thr Ser  
35 40 45  
Pro Asp Gly Asp Gln Gly Phe Pro Gly Glu Leu Ser Val Thr Val Thr  
50 55 60  
Tyr Lys Leu Val Lys Asp Asn Glu Leu Ser Val Val Met Glu Ala Lys  
65 70 75 80  
Pro Lys Asp Lys Ala Thr Pro Val Asn Leu Ala His His Ser Tyr Trp  
85 90 95  
Asn Leu Gly Gly His Asn Ser Gly Asp Ile Leu Ser Glu Glu Ile Gln  
100 105 110  
Ile Leu Gly Ser Gly Tyr Thr Pro Val Asp Gly Glu Leu Ile Pro Thr  
115 120 125  
Gly Lys Ile Asn Pro Val Lys Gly Thr Ala Tyr Asp Phe Leu Gln Leu  
130 135 140  
Arg Pro Ile Lys Asp Asn Met Lys Asp Leu Lys Thr Gly Tyr Asp Ile  
145 150 155 160  
Asn Tyr Cys Leu Asp Gly Lys Ala Lys Lys Met Arg Lys Ile Val Glu  
165 170 175  
Leu Val Asp Lys Lys Ser Gly Arg Lys Met Glu Leu Ser Gly Asn Gln  
180 185 190  
Ala Gly Leu Gln Phe Tyr Thr Gly Met Leu Lys Asp Val Lys Gly  
195 200 205  
Lys Asn Gly Ala Val Tyr Gln Ala Phe Gly Gly Leu Cys Leu Glu Thr  
210 215 220  
Gln Ser Tyr Pro Asp Ala Leu Asn His Pro Lys Phe Pro Ser Gln Ile  
225 230 235 240  
Val Glu Pro Gly Lys Lys Tyr Lys His Thr Met Leu Phe Lys Phe Ser  
245 250 255  
Ile Val Ser

(2) INFORMATION FOR SEQ ID NO:2095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1571803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:

Met Glu Ala Lys Pro Lys Asp Lys Ala Thr Pro Val Asn Leu Ala His  
1 5 10 15  
His Ser Tyr Trp Asn Leu Gly Gly His Asn Ser Gly Asp Ile Leu Ser

20 25 30  
Glu Glu Ile Gln Ile Leu Gly Ser Gly Tyr Thr Pro Val Asp Gly Glu  
35 40 45  
Leu Ile Pro Thr Gly Lys Ile Asn Pro Val Lys Gly Thr Ala Tyr Asp  
50 55 60  
Phe Leu Gln Leu Arg Pro Ile Lys Asp Asn Met Lys Asp Leu Lys Thr  
65 70 75 80  
Gly Tyr Asp Ile Asn Tyr Cys Leu Asp Gly Lys Ala Lys Lys Met Arg  
85 90 95  
Lys Ile Val Glu Leu Val Asp Lys Lys Ser Gly Arg Lys Met Glu Leu  
100 105 110  
Ser Gly Asn Gln Ala Gly Leu Gln Phe Tyr Thr Gly Gly Met Leu Lys  
115 120 125  
Asp Val Lys Gly Lys Asn Gly Ala Val Tyr Gln Ala Phe Gly Gly Leu  
130 135 140  
Cys Leu Glu Thr Gln Ser Tyr Pro Asp Ala Leu Asn His Pro Lys Phe  
145 150 155 160  
Pro Ser Gln Ile Val Glu Pro Gly Lys Lys Tyr Lys His Thr Met Leu  
165 170 175  
Phe Lys Phe Ser Ile Val Ser  
180

(2) INFORMATION FOR SEQ ID NO:2096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..554
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

tctatcagat gaaaccccttg agttatgggt ctatcaccaa aagtcctagt gataacaagg 60  
aagatgccaa atgcagcatc tgccaggaag aatatacgat tggagatgaa gttgggaggc 120  
tacactgtga gcacacatac catgtgaagt gtgtgcaaga gtggttgcgg atgaagagtt 180  
ggtgcccaat ctgcaaagcc acagccgaaa cctcctctaa ataaccgtct tcttcttctt 240  
cctcgttcgt tgtattagtt ctttcatcta aagcctgtga acaacaatgg aacctgcgta 300  
aaaaaggcct caccatttcc tttgtgtaca taccaattca caccggctct gtctctctct 360  
cccttttgtc taatgacaaa gctatcctgt gtttctcttg tcttttcctc tctttactgt 420  
ttgacttccg taatgtaaag tgggaaagac ggaaacgatt tcatttgaac tttgaagatc 480  
aagtaaacat gatctKttta attcttaaaa ttggacaatt tgttgaaaag caacaaagag 540  
cgtggttctt tggt

(2) INFORMATION FOR SEQ ID NO:2097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

Tyr Gln Met Lys Pro Leu Ser Tyr Gly Ser Ile Thr Lys Ser Pro Ser  
1 5 10 15  
Asp Asn Lys Glu Asp Ala Lys Cys Ser Ile Cys Gln Glu Glu Tyr Thr  
20 25 30  
Ile Gly Asp Glu Val Gly Arg Leu His Cys Glu His Thr Tyr His Val  
35 40 45

Lys Cys Val Gln Glu Trp Leu Arg Met Lys Ser Trp Cys Pro Ile Cys  
50 55 60  
Lys Ala Thr Ala Glu Thr Ser Ser Lys  
65 70

- (2) INFORMATION FOR SEQ ID NO:2098:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..71
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1571814
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Lys Pro Leu Ser Tyr Gly Ser Ile Thr Lys Ser Pro Ser Asp Asn  
1 5 10 15  
Lys Glu Asp Ala Lys Cys Ser Ile Cys Gln Glu Glu Tyr Thr Ile Gly  
20 25 30  
Asp Glu Val Gly Arg Leu His Cys Glu His Thr Tyr His Val Lys Cys  
35 40 45  
Val Gln Glu Trp Leu Arg Met Lys Ser Trp Cys Pro Ile Cys Lys Ala  
50 55 60  
Thr Ala Glu Thr Ser Ser Lys  
65 70

- (2) INFORMATION FOR SEQ ID NO:2099:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..40
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1571815
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

Met Gly Leu Ser Pro Lys Val Leu Val Ile Thr Arg Lys Met Pro Asn  
1 5 10 15  
Ala Ala Ser Ala Arg Lys Asn Ile Arg Leu Glu Met Lys Leu Gly Gly  
20 25 30  
Tyr Thr Val Ser Thr His Thr Met  
35 40

- (2) INFORMATION FOR SEQ ID NO:2100:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1617 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..1617
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1571820
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cccgacagta gcaagcaaaa attcttcata gactcaaatt caaaaaactca tctctctcta | 60  |
| tctctatttc tctggttcca tagctcaccg tcgcatcgca gatctactcc ttccgcaata  | 120 |
| aattttaccg gcggaggtat cagatctcgc cgatctgttg tagcagctac tgtattttgg  | 180 |
| gcttctcatt tgatattggg gaaacgagga gtagaggacg atggaaaatc tgatctctct  | 240 |
| ggttaacaag atacagagag cttgcacggc tttaggagac catggagact ccagcgcttt  | 300 |

acctactctt tgggattcct tgcctgcat cgccgtcggt ggtggtcaga gctcagggaa 360  
gtcttcagtc ctggagagca tctgtggaaa ggacttttta ccccgtagat ctggcattgt 420  
tactgaagg ccccttgtct tacagttgca aaagatcgat gatggaaCcc gggagtatgc 480  
agagtttctt cactcccgga ggaaaaagtt tactgatttt gctgctgtga ggaaggagat 540  
tcaagatgag actgacagag agactggacg cagcaaggct atttctagtg ttccattca 600  
ccttagcata tactctocca atgttgtcaa cttgacactg atagatcttc cagggcttac 660  
aaaagtgtgt gttgatggac aatctgatag tatagtgaag gacattgaaa acatggttcg 720  
gtcctacatt gaaaagccca actgcatcat tttggcaatc tcacctgcaa accaagatct 780  
tgctacctca gatgcaatta aaatttcccg tgaggttgat ccacggggg acagaacatt 840  
tggtgtcttg acaaagattg atcttatgga caaggggacg gatgcagtgg aaattctgga 900  
aggagatct tttaaactta aatatccgtg ggttggtgtc gtcaaccgtt cccaagcaga 960  
tattaacaag aatgtcgaca tgattgctgc tcggaaaaga gagaggagat acttttccaa 1020  
tactactgag tataggcacc ttgctaataa aatgggttcc gagcatttgg caaagatgct 1080  
ctccaagcat ctagaacgtg tgatcaagtc gagaattcct ggcattcagt cacttattaa 1140  
caaaacagta ttagagctgg aaactgaact aagtcgcctt ggaaagccta ttgcagctga 1200  
tgcagggggg aagttgtact caataatgga gatatgtcgg ctttttgatc aaatattcaa 1260  
agagcatctt gatggagtgc gtgctggtgg tgaaaaagtg tacaacgtgt ttgataacca 1320  
ccttctgctg gctctgaaga gactocaatt tgacaagcag ctagcgatgg acaacatccg 1380  
gaagctggtc actgaggctg atggttacca gcctcacttg attgctcctg agcaaggtta 1440  
ccgtcgtctc attgagtctt ctattgtctc catcagaggc cctgctgaag catctgttga 1500  
caccgtatga actctttact ttcatctcta aaaagatgta tcaaaaacct aacacaaaac 1560  
aataagcttc tctctccgtt tttttttttt ttctatggtt aaatattagg ttcatgc

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1571821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

Met Glu Asn Leu Ile Ser Leu Val Asn Lys Ile Gln Arg Ala Cys Thr  
1 5 10 15  
Ala Leu Gly Asp His Gly Asp Ser Ser Ala Leu Pro Thr Leu Trp Asp  
20 25 30  
Ser Leu Pro Ala Ile Ala Val Val Gly Gln Ser Ser Gly Lys Ser  
35 40 45  
Ser Val Leu Glu Ser Ile Val Gly Lys Asp Phe Leu Pro Arg Gly Ser  
50 55 60  
Gly Ile Val Thr Arg Arg Pro Leu Val Leu Gln Leu Gln Lys Ile Asp  
65 70 75 80  
Asp Gly Thr Arg Glu Tyr Ala Glu Phe Leu His Leu Pro Arg Lys Lys  
85 90 95  
Phe Thr Asp Phe Ala Ala Val Arg Lys Glu Ile Gln Asp Glu Thr Asp  
100 105 110  
Arg Glu Thr Gly Arg Ser Lys Ala Ile Ser Ser Val Pro Ile His Leu  
115 120 125  
Ser Ile Tyr Ser Pro Asn Val Val Asn Leu Thr Leu Ile Asp Leu Pro  
130 135 140  
Gly Leu Thr Lys Val Ala Val Asp Gly Gln Ser Asp Ser Ile Val Lys  
145 150 155 160  
Asp Ile Glu Asn Met Val Arg Ser Tyr Ile Glu Lys Pro Asn Cys Ile  
165 170 175  
Ile Leu Ala Ile Ser Pro Ala Asn Gln Asp Leu Ala Thr Ser Asp Ala  
180 185 190  
Ile Lys Ile Ser Arg Glu Val Asp Pro Ser Gly Asp Arg Thr Phe Gly  
195 200 205  
Val Leu Thr Lys Ile Asp Leu Met Asp Lys Gly Thr Asp Ala Val Glu



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 210                                                             | 215 | 220 |
| Ile Leu Glu Gly Arg Ser Phe Lys Leu Lys Tyr Pro Trp Val Gly Val |     |     |
| 225                                                             | 230 | 235 |
| Val Asn Arg Ser Gln Ala Asp Ile Asn Lys Asn Val Asp Met Ile Ala |     | 240 |
|                                                                 | 245 | 250 |
| Ala Arg Lys Arg Glu Arg Glu Tyr Phe Ser Asn Thr Thr Glu Tyr Arg |     | 255 |
|                                                                 | 260 | 265 |
| His Leu Ala Asn Lys Met Gly Ser Glu His Leu Ala Lys Met Leu Ser |     | 270 |
|                                                                 | 275 | 280 |
| Lys His Leu Glu Arg Val Ile Lys Ser Arg Ile Pro Gly Ile Gln Ser |     | 285 |
|                                                                 | 290 | 295 |
| Leu Ile Asn Lys Thr Val Leu Glu Leu Glu Thr Glu Leu Ser Arg Leu |     | 300 |
| 305                                                             | 310 | 315 |
| Gly Lys Pro Ile Ala Ala Asp Ala Gly Gly Lys Leu Tyr Ser Ile Met |     | 320 |
|                                                                 | 325 | 330 |
| Glu Ile Cys Arg Leu Phe Asp Gln Ile Phe Lys Glu His Leu Asp Gly |     | 335 |
|                                                                 | 340 | 345 |
| Val Arg Ala Gly Gly Glu Lys Val Tyr Asn Val Phe Asp Asn His Leu |     | 350 |
|                                                                 | 355 | 360 |
| Pro Ala Ala Leu Lys Arg Leu Gln Phe Asp Lys Gln Leu Ala Met Asp |     | 365 |
|                                                                 | 370 | 375 |
| Asn Ile Arg Lys Leu Val Thr Glu Ala Asp Gly Tyr Gln Pro His Leu |     | 380 |
| 385                                                             | 390 | 395 |
| Ile Ala Pro Glu Gln Gly Tyr Arg Arg Leu Ile Glu Ser Ser Ile Val |     | 400 |
|                                                                 | 405 | 410 |
| Ser Ile Arg Gly Pro Ala Glu Ala Ser Val Asp Thr Val             |     | 415 |
|                                                                 | 420 | 425 |

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1571822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Val Arg Ser Tyr Ile Glu Lys Pro Asn Cys Ile Ile Leu Ala Ile |     |
| 1                                                               | 5   |
| Ser Pro Ala Asn Gln Asp Leu Ala Thr Ser Asp Ala Ile Lys Ile Ser |     |
|                                                                 | 20  |
| Arg Glu Val Asp Pro Ser Gly Asp Arg Thr Phe Gly Val Leu Thr Lys |     |
|                                                                 | 35  |
| Ile Asp Leu Met Asp Lys Gly Thr Asp Ala Val Glu Ile Leu Glu Gly |     |
|                                                                 | 50  |
| Arg Ser Phe Lys Leu Lys Tyr Pro Trp Val Gly Val Val Asn Arg Ser |     |
| 65                                                              | 70  |
| Gln Ala Asp Ile Asn Lys Asn Val Asp Met Ile Ala Ala Arg Lys Arg |     |
|                                                                 | 85  |
| Glu Arg Glu Tyr Phe Ser Asn Thr Thr Glu Tyr Arg His Leu Ala Asn |     |
|                                                                 | 100 |
| Lys Met Gly Ser Glu His Leu Ala Lys Met Leu Ser Lys His Leu Glu |     |
|                                                                 | 115 |
| Arg Val Ile Lys Ser Arg Ile Pro Gly Ile Gln Ser Leu Ile Asn Lys |     |
|                                                                 | 130 |
| Thr Val Leu Glu Leu Glu Thr Glu Leu Ser Arg Leu Gly Lys Pro Ile |     |
| 145                                                             | 150 |
| Ala Ala Asp Ala Gly Gly Lys Leu Tyr Ser Ile Met Glu Ile Cys Arg |     |
|                                                                 | 165 |
|                                                                 | 170 |
|                                                                 | 175 |

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Leu Phe Asp Gln Ile Phe Lys Glu His Leu Asp Gly Val Arg Ala Gly  
180 185 190  
Gly Glu Lys Val Tyr Asn Val Phe Asp Asn His Leu Pro Ala Ala Leu  
195 200 205  
Lys Arg Leu Gln Phe Asp Lys Gln Leu Ala Met Asp Asn Ile Arg Lys  
210 215 220  
Leu Val Thr Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala Pro Glu  
225 230 235 240  
Gln Gly Tyr Arg Arg Leu Ile Glu Ser Ser Ile Val Ser Ile Arg Gly  
245 250 255  
Pro Ala Glu Ala Ser Val Asp Thr Val  
260 265

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1571823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Met Asp Lys Gly Thr Asp Ala Val Glu Ile Leu Glu Gly Arg Ser Phe  
1 5 10 15  
Lys Leu Lys Tyr Pro Trp Val Gly Val Val Asn Arg Ser Gln Ala Asp  
20 25 30  
Ile Asn Lys Asn Val Asp Met Ile Ala Ala Arg Lys Arg Glu Arg Glu  
35 40 45  
Tyr Phe Ser Asn Thr Thr Glu Tyr Arg His Leu Ala Asn Lys Met Gly  
50 55 60  
Ser Glu His Leu Ala Lys Met Leu Ser Lys His Leu Glu Arg Val Ile  
65 70 75 80  
Lys Ser Arg Ile Pro Gly Ile Gln Ser Leu Ile Asn Lys Thr Val Leu  
85 90 95  
Glu Leu Glu Thr Glu Leu Ser Arg Leu Gly Lys Pro Ile Ala Ala Asp  
100 105 110  
Ala Gly Gly Lys Leu Tyr Ser Ile Met Glu Ile Cys Arg Leu Phe Asp  
115 120 125  
Gln Ile Phe Lys Glu His Leu Asp Gly Val Arg Ala Gly Gly Glu Lys  
130 135 140  
Val Tyr Asn Val Phe Asp Asn His Leu Pro Ala Ala Leu Lys Arg Leu  
145 150 155 160  
Gln Phe Asp Lys Gln Leu Ala Met Asp Asn Ile Arg Lys Leu Val Thr  
165 170 175  
Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala Pro Glu Gln Gly Tyr  
180 185 190  
Arg Arg Leu Ile Glu Ser Ser Ile Val Ser Ile Arg Gly Pro Ala Glu  
195 200 205  
Ala Ser Val Asp Thr Val  
210

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1476

(D) OTHER INFORMATION: / Ceres Seq. ID 1571824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| aaaaagttgc | gaaGctctct | cattgagtaa  | actaacggct  | atattctctc  | tgatattcaa  | 60   |
| aatttgctcg | aagaaacgac | gatggcagcc  | gaaacgaagg  | ttcagggtttc | agatccagag  | 120  |
| gcagagtttc | ttaattcgaa | gcaggagact  | ggatacgagt  | gggagctttt  | caaggagaac  | 180  |
| gtccggccat | tgaagagagg | tcgcaatggt  | ggtattctca  | accacgctct  | caaattctcac | 240  |
| tctgaccacc | aattgagaaa | gaatctcatc  | gagaaacgca  | ggaatttgat  | tgaagccatt  | 300  |
| gatgagtatg | aaggagatga | cccttttatct | ccatggatag  | agtgtataaa  | atgggtacaa  | 360  |
| gaggcttttc | caccaggagg | agaatgttca  | ggactgttag  | tgatatatga  | gcaatgtgtt  | 420  |
| cgtaaatttt | ggcactctga | acgtttacaag | gatgatcttc  | gttatcttaa  | agtctggttg  | 480  |
| gaatatgcgg | agcattgcgc | tgatgcggaa  | gtgattttaca | agtttttgga  | ggtcaatgag  | 540  |
| attggaaaga | cacatgctgt | ctactatata  | gcttatgctt  | tgacattga   | gtttaagaat  | 600  |
| aaggtcaaaa | ctgctaata  | gatcttcaat  | cttggaaatct | ctagggatgc  | aaagccagtg  | 660  |
| gaaaagttga | atgacgcgta | caagaagttt  | atggtgagaa  | cgatgagaag  | gtccaacaca  | 720  |
| gctgatgaag | aaccaaagga | gaataatgac  | ttaccgtcaa  | gaagcttttg  | cactttattg  | 780  |
| tccaggggag | ataataatgc | aagaaggcag  | gcgtaggaa   | gttctaacc   | acaagccaaa  | 840  |
| aagctaaagc | caaataatc  | atccaagaca  | ccttttgcta  | tctacgcaga  | tgacgtttca  | 900  |
| gacaccacat | cagggaatca | accagagtca  | gacaagtcaa  | gaccagagtt  | tggtagttgg  | 960  |
| ctcatgcttg | gaggcagagc | agagaggaac  | aaagaaaaca  | attctttacc  | tagaaaatgg  | 1020 |
| gcacattcca | aggttcctca | gaaacccatt  | gtgagaactg  | ttgcagcagc  | atctgctttc  | 1080 |
| acctttgagg | ttttgtcga  | tgaagaagaa  | tgtacagaag  | aggaagaaga  | aaagaagaag  | 1140 |
| aatgatgaaa | ctatctcatc | atcatcaaac  | gttctgcccc  | ttaatggcgg  | ccgtgagata  | 1200 |
| aaaaaagaaa | cagagctgct | acgacagaac  | cctttaagac  | atttcccacc  | caacagcttc  | 1260 |
| ctacgatgat | gatattggac | tttcttctct  | acacgatctt  | atggtttgag  | atttgagctt  | 1320 |
| ttgtctataa | agctccttgt | gtgtttttgc  | ctatttggat  | ttgtttttgt  | gatgtactgg  | 1380 |
| gatatactat | cctactatgt | accatgatgt  | gcotttcatg  | ttttgaaatt  | aatgtgactt  | 1440 |
| gtcttgtttc | aatccttata | tgatttggtt  | ctcctg      |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1571825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Glu | Thr | Lys | Val | Gln | Val | Ser | Asp | Pro | Glu | Ala | Glu | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Asn | Ser | Lys | Gln | Glu | Thr | Gly | Tyr | Glu | Trp | Glu | Leu | Phe | Lys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Arg | Pro | Leu | Lys | Arg | Gly | Arg | Asn | Val | Gly | Ile | Leu | Asn | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Lys | Ser | His | Ser | Asp | His | Gln | Leu | Arg | Lys | Asn | Leu | Ile | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Arg | Asn | Leu | Ile | Glu | Ala | Ile | Asp | Glu | Tyr | Glu | Gly | Asp | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Leu | Ser | Pro | Trp | Ile | Glu | Cys | Ile | Lys | Trp | Val | Gln | Glu | Ala | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Gly | Gly | Glu | Cys | Ser | Gly | Leu | Leu | Val | Ile | Tyr | Glu | Gln | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Lys | Phe | Trp | His | Ser | Glu | Arg | Tyr | Lys | Asp | Asp | Leu | Arg | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Leu | Lys | Val | Trp | Leu | Glu | Tyr | Ala | Glu | His | Cys | Ala | Asp | Ala | Glu | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Tyr | Lys | Phe | Leu | Glu | Val | Asn | Glu | Ile | Gly | Lys | Thr | His | Ala | Val |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Tyr | Tyr | Ile | Ala | Tyr | Ala | Leu | His | Ile | Glu | Phe | Lys | Asn | Lys | Val | Lys |

(2) INFORMATION FOR SEO ID NO:2106:

(A) LENGTH: 1641 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1641

(D) OTHER INFORMATION: / Ceres Seq. ID 1571826

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2106:

|            |            |             |             |             |            |      |
|------------|------------|-------------|-------------|-------------|------------|------|
| ataagattca | cacatacgct | tactcttttg  | gctatttcca  | acccccctta  | tgttatttct | 60   |
| ttccttttca | ggcatttgga | cagccttgga  | actgttgtgg  | gcatacacaac | accaggaggt | 120  |
| taagaaacca | tataaggata | ctctgatcaa  | tgtaaagag   | cttgatttct  | caaaaccaga | 180  |
| aggttcttcg | ggtacatctc | tagatctggg  | tgaagacca   | cccggctctca | acgactttgg | 240  |
| aatggttgcc | tggtgcctag | atatgtcgac  | cccagagttt  | cctatggggc  | ggaaacttct | 300  |
| cgtgattgcg | aatgatgtca | ccttcaaagc  | tggttctttt  | ggtcctagag  | aggacgcgtt | 360  |
| tttccttgct | gttactgaac | tcgcttggtc  | caagaagctt  | cccttgattt  | acttggcagc | 420  |
| aaattctctg | gcccgaactt | gggttgctga  | agaagtcaaa  | gctcgcttca  | aagttggatg | 480  |
| tcggagtga  | atttcccttg | agaattggtt  | tcagatatata | taacctaaagc | ctgaagacca | 540  |
| cgaaggtatt | ggatcatctg | tcaattggcca | tgaagtaaag  | ctccctagtg  | ctgaaactag | 600  |
| gtgggtgatt | gatacgatcg | ttggcaaaga  | agatggtatt  | ggtgtagaga  | acttaacagg | 660  |
| aagtggggcc | atagcgggtg | cttactcaaa  | ggcatacaat  | gaaactttta  | ctttaacctt | 720  |
| tgttagtga  | agaacggttg | gaattggtgc  | ttatcttgcc  | cgctaggtta  | tcgggtgcat | 780  |
| acagagactt | gatcagccga | tcattcttgac | tggcttctct  | acactcaaca  | agttacttgg | 840  |
| gcgtgaggtc | tatagctctc | acatgcaact  | gggtggcccg  | aaaatcatgg  | gcacaaatgg | 900  |
| tgttgttcat | cttagactct | cagatgatct  | tgaaggcgta  | tcagcaattc  | tcaactggct | 960  |
| cagctacatt | cctgcgttac | tgggtgggtc  | tcttctctgt  | cttgcccctt  | tagatccacc | 1020 |
| ggagagaatt | gtggagtatg | tcccagagaa  | ctcttgcgac  | ccacgacggc  | ctatagctgg | 1080 |
| ggtcaaagac | aataccggta | aatggcttgg  | aggtatcttt  | gataaaaata  | gtttcattga | 1140 |
| gactcttgaa | ggctgggcaa | ggacggtagt  | gactggtaga  | gccaaagctcg | ggggaatacc | 1200 |

cgttggagtt gttgcagttg agacacagac tgtcatgcag atcatcccag cagatcctgg 1260  
acagcttgac tctcatgaaa gagtggttcc gcaagcaggg caagtctggt ttcctgattc 1320  
agcggccaag actgctcaag cacttatgga tttcaaccgg gaagagcttc cattgtttat 1380  
cctagcgaac tggagagggg tttcaggtgg gcagagagat cttttcgaag gaatacttca 1440  
ggcaggttca actatagtag aaaatctgag aacctatcgt cagccagtgt ttgtgtacat 1500  
cccaatgatg ggagaGctgc gcggtggagc gtgggttgtt gttgacagcc agataaatcc 1560  
ggattatgtt gaaatgtatg ctgatgaaac agctcgtgga aatgtgctcg agccagaagg 1620  
gacaatagag ataaaattta g

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..530

(D) OTHER INFORMATION: / Ceres Seq. ID 1571827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

Met Leu Phe Leu Ser Phe Ser Gly Ile Trp Thr Ala Leu Glu Leu Leu  
1 5 10 15  
Trp Ala Ser Gln His Pro Gly Val Lys Lys Pro Tyr Lys Asp Thr Leu  
20 25 30  
Ile Asn Val Lys Glu Leu Val Phe Ser Lys Pro Glu Gly Ser Ser Gly  
35 40 45  
Thr Ser Leu Asp Leu Val Glu Arg Pro Pro Gly Leu Asn Asp Phe Gly  
50 55 60  
Met Val Ala Trp Cys Leu Asp Met Ser Thr Pro Glu Phe Pro Met Gly  
65 70 75 80  
Arg Lys Leu Leu Val Ile Ala Asn Asp Val Thr Phe Lys Ala Gly Ser  
85 90 95  
Phe Gly Pro Arg Glu Asp Ala Phe Phe Leu Ala Val Thr Glu Leu Ala  
100 105 110  
Cys Ala Lys Lys Leu Pro Leu Ile Tyr Leu Ala Ala Asn Ser Gly Ala  
115 120 125  
Arg Leu Gly Val Ala Glu Glu Val Lys Ala Cys Phe Lys Val Gly Trp  
130 135 140  
Ser Asp Glu Ile Ser Pro Glu Asn Gly Phe Gln Tyr Ile Tyr Leu Ser  
145 150 155 160  
Pro Glu Asp His Glu Arg Ile Gly Ser Ser Val Ile Ala His Glu Val  
165 170 175  
Lys Leu Pro Ser Gly Glu Thr Arg Trp Val Ile Asp Thr Ile Val Gly  
180 185 190  
Lys Glu Asp Gly Ile Gly Val Glu Asn Leu Thr Gly Ser Gly Ala Ile  
195 200 205  
Ala Gly Ala Tyr Ser Lys Ala Tyr Asn Glu Thr Phe Thr Leu Thr Phe  
210 215 220  
Val Ser Gly Arg Thr Val Gly Ile Gly Ala Tyr Leu Ala Arg Leu Gly  
225 230 235 240  
Met Arg Cys Ile Gln Arg Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe  
245 250 255  
Ser Thr Leu Asn Lys Leu Leu Gly Arg Glu Val Tyr Ser Ser His Met  
260 265 270  
Gln Leu Gly Gly Pro Lys Ile Met Gly Thr Asn Gly Val Val His Leu  
275 280 285  
Thr Val Ser Asp Asp Leu Glu Gly Val Ser Ala Ile Leu Asn Trp Leu  
290 295 300  
Ser Tyr Ile Pro Ala Tyr Val Gly Gly Pro Leu Pro Val Leu Ala Pro  
305 310 315 320  
Leu Asp Pro Pro Glu Arg Ile Val Glu Tyr Val Pro Glu Asn Ser Cys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Asp | Pro | Arg | Ala | Ile | Ala | Gly | Val | Lys | Asp | Asn | Thr | Gly | Lys | Trp |     |  |  |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |  |  |
| Leu | Gly | Gly | Ile | Phe | Asp | Lys | Asn | Ser | Phe | Ile | Glu | Thr | Leu | Glu | Gly |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Trp | Ala | Arg | Thr | Val | Val | Thr | Gly | Arg | Ala | Lys | Leu | Gly | Gly | Ile | Pro |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |
| Val | Gly | Val | Val | Ala | Val | Glu | Thr | Gln | Thr | Val | Met | Gln | Ile | Ile | Pro |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Ala | Asp | Pro | Gly | Gln | Leu | Asp | Ser | His | Glu | Arg | Val | Val | Pro | Gln | Ala |  |  |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |  |  |
| Gly | Gln | Val | Trp | Phe | Pro | Asp | Ser | Ala | Ala | Lys | Thr | Ala | Gln | Ala | Leu |  |  |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Met | Asp | Phe | Asn | Arg | Glu | Glu | Leu | Pro | Leu | Phe | Ile | Leu | Ala | Asn | Trp |  |  |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |
| Arg | Gly | Phe | Ser | Gly | Gly | Gln | Arg | Asp | Leu | Phe | Glu | Gly | Ile | Leu | Gln |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |
| Ala | Gly | Ser | Thr | Ile | Val | Glu | Asn | Leu | Arg | Thr | Tyr | Arg | Gln | Pro | Val |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |
| Phe | Val | Tyr | Ile | Pro | Met | Met | Gly | Glu | Leu | Arg | Gly | Gly | Ala | Trp | Val |  |  |
|     |     |     |     | 485 |     |     |     | 490 |     |     |     |     |     | 495 |     |  |  |
| Val | Val | Asp | Ser | Gln | Ile | Asn | Ser | Asp | Tyr | Val | Glu | Met | Tyr | Ala | Asp |  |  |
|     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |
| Glu | Thr | Ala | Arg | Gly | Asn | Val | Leu | Glu | Pro | Glu | Gly | Thr | Ile | Glu | Ile |  |  |
|     |     | 515 |     |     |     | 520 |     |     |     |     |     | 525 |     |     |     |  |  |
| Lys | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     | 530 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 466 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..466

(D) OTHER INFORMATION: / Ceres Seq. ID 1571828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Val | Ala | Trp | Cys | Leu | Asp | Met | Ser | Thr | Pro | Glu | Phe | Pro | Met | Gly |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Arg | Lys | Leu | Leu | Val | Ile | Ala | Asn | Asp | Val | Thr | Phe | Lys | Ala | Gly | Ser |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Phe | Gly | Pro | Arg | Glu | Asp | Ala | Phe | Phe | Leu | Ala | Val | Thr | Glu | Leu | Ala |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Cys | Ala | Lys | Lys | Leu | Pro | Leu | Ile | Tyr | Leu | Ala | Ala | Asn | Ser | Gly | Ala |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Arg | Leu | Gly | Val | Ala | Glu | Glu | Val | Lys | Ala | Cys | Phe | Lys | Val | Gly | Trp |  |  |
| 65  |     |     |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |  |  |
| Ser | Asp | Glu | Ile | Ser | Pro | Glu | Asn | Gly | Phe | Gln | Tyr | Ile | Tyr | Leu | Ser |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Pro | Glu | Asp | His | Glu | Arg | Ile | Gly | Ser | Ser | Val | Ile | Ala | His | Glu | Val |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Lys | Leu | Pro | Ser | Gly | Glu | Thr | Arg | Trp | Val | Ile | Asp | Thr | Ile | Val | Gly |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |  |
| Lys | Glu | Asp | Gly | Ile | Gly | Val | Glu | Asn | Leu | Thr | Gly | Ser | Gly | Ala | Ile |  |  |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |  |
| Ala | Gly | Ala | Tyr | Ser | Lys | Ala | Tyr | Asn | Glu | Thr | Phe | Thr | Leu | Thr | Phe |  |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |  |
| Val | Ser | Gly | Arg | Thr | Val | Gly | Ile | Gly | Ala | Tyr | Leu | Ala | Arg | Leu | Gly |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |

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Met Arg Cys Ile Gln Arg Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe
 180 185 190
Ser Thr Leu Asn Lys Leu Leu Gly Arg Glu Val Tyr Ser Ser His Met
 195 200 205
Gln Leu Gly Gly Pro Lys Ile Met Gly Thr Asn Gly Val Val His Leu
 210 215 220
Thr Val Ser Asp Asp Leu Glu Gly Val Ser Ala Ile Leu Asn Trp Leu
 225 230 235 240
Ser Tyr Ile Pro Ala Tyr Val Gly Gly Pro Leu Pro Val Leu Ala Pro
 245 250 255
Leu Asp Pro Pro Glu Arg Ile Val Glu Tyr Val Pro Glu Asn Ser Cys
 260 265 270
Asp Pro Arg Ala Ala Ile Ala Gly Val Lys Asp Asn Thr Gly Lys Trp
 275 280 285
Leu Gly Gly Ile Phe Asp Lys Asn Ser Phe Ile Glu Thr Leu Glu Gly
 290 295 300
Trp Ala Arg Thr Val Val Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro
 305 310 315 320
Val Gly Val Val Ala Val Glu Thr Gln Thr Val Met Gln Ile Ile Pro
 325 330 335
Ala Asp Pro Gly Gln Leu Asp Ser His Glu Arg Val Val Pro Gln Ala
 340 345 350
Gly Gln Val Trp Phe Pro Asp Ser Ala Ala Lys Thr Ala Gln Ala Leu
 355 360 365
Met Asp Phe Asn Arg Glu Glu Leu Pro Leu Phe Ile Leu Ala Asn Trp
 370 375 380
Arg Gly Phe Ser Gly Gly Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln
 385 390 395 400
Ala Gly Ser Thr Ile Val Glu Asn Leu Arg Thr Tyr Arg Gln Pro Val
 405 410 415
Phe Val Tyr Ile Pro Met Met Gly Glu Leu Arg Gly Gly Ala Trp Val
 420 425 430
Val Val Asp Ser Gln Ile Asn Ser Asp Tyr Val Glu Met Tyr Ala Asp
 435 440 445
Glu Thr Ala Arg Gly Asn Val Leu Glu Pro Glu Gly Thr Ile Glu Ile
 450 455 460
Lys Phe
465

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(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

```

Met Ser Thr Pro Glu Phe Pro Met Gly Arg Lys Leu Leu Val Ile Ala
1 5 10 15
Asn Asp Val Thr Phe Lys Ala Gly Ser Phe Gly Pro Arg Glu Asp Ala
 20 25 30
Phe Phe Leu Ala Val Thr Glu Leu Ala Cys Ala Lys Lys Leu Pro Leu
 35 40 45
Ile Tyr Leu Ala Ala Asn Ser Gly Ala Arg Leu Gly Val Ala Glu Glu
 50 55 60
Val Lys Ala Cys Phe Lys Val Gly Trp Ser Asp Glu Ile Ser Pro Glu
 65 70 75 80
Asn Gly Phe Gln Tyr Ile Tyr Leu Ser Pro Glu Asp His Glu Arg Ile

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| 85  |     |     |     |     |     |     |     |     |     | 90  |     |     |     |     | 95  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Gly | Ser | Ser | Val | Ile | Ala | His | Glu | Val | Lys | Leu | Pro | Ser | Gly | Glu | Thr |  |  |  |  |
| 100 |     |     |     |     |     |     |     |     |     | 105 |     |     |     |     | 110 |  |  |  |  |
| Arg | Trp | Val | Ile | Asp | Thr | Ile | Val | Gly | Lys | Glu | Asp | Gly | Ile | Gly | Val |  |  |  |  |
| 115 |     |     |     |     |     |     |     |     |     | 120 |     |     |     |     | 125 |  |  |  |  |
| Glu | Asn | Leu | Thr | Gly | Ser | Gly | Ala | Ile | Ala | Gly | Ala | Tyr | Ser | Lys | Ala |  |  |  |  |
| 130 |     |     |     |     |     |     |     |     |     | 135 |     |     |     |     | 140 |  |  |  |  |
| Tyr | Asn | Glu | Thr | Phe | Thr | Leu | Thr | Phe | Val | Ser | Gly | Arg | Thr | Val | Gly |  |  |  |  |
| 145 |     |     |     |     |     |     |     |     |     | 150 |     |     |     |     | 155 |  |  |  |  |
| Ile | Gly | Ala | Tyr | Leu | Ala | Arg | Leu | Gly | Met | Arg | Cys | Ile | Gln | Arg | Leu |  |  |  |  |
| 165 |     |     |     |     |     |     |     |     |     | 170 |     |     |     |     | 175 |  |  |  |  |
| Asp | Gln | Pro | Ile | Ile | Leu | Thr | Gly | Phe | Ser | Thr | Leu | Asn | Lys | Leu | Leu |  |  |  |  |
| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |  |  |  |  |
| Gly | Arg | Glu | Val | Tyr | Ser | Ser | His | Met | Gln | Leu | Gly | Gly | Pro | Lys | Ile |  |  |  |  |
| 195 |     |     |     |     |     |     |     |     |     | 200 |     |     |     |     | 205 |  |  |  |  |
| Met | Gly | Thr | Asn | Gly | Val | Val | His | Leu | Thr | Val | Ser | Asp | Asp | Leu | Glu |  |  |  |  |
| 210 |     |     |     |     |     |     |     |     |     | 215 |     |     |     |     | 220 |  |  |  |  |
| Gly | Val | Ser | Ala | Ile | Leu | Asn | Trp | Leu | Ser | Tyr | Ile | Pro | Ala | Tyr | Val |  |  |  |  |
| 225 |     |     |     |     |     |     |     |     |     | 230 |     |     |     |     | 235 |  |  |  |  |
| Gly | Gly | Pro | Leu | Pro | Val | Leu | Ala | Pro | Leu | Asp | Pro | Pro | Glu | Arg | Ile |  |  |  |  |
| 245 |     |     |     |     |     |     |     |     |     | 250 |     |     |     |     | 255 |  |  |  |  |
| Val | Glu | Tyr | Val | Pro | Glu | Asn | Ser | Cys | Asp | Pro | Arg | Ala | Ala | Ile | Ala |  |  |  |  |
| 260 |     |     |     |     |     |     |     |     |     | 265 |     |     |     |     | 270 |  |  |  |  |
| Gly | Val | Lys | Asp | Asn | Thr | Gly | Lys | Trp | Leu | Gly | Gly | Ile | Phe | Asp | Lys |  |  |  |  |
| 275 |     |     |     |     |     |     |     |     |     | 280 |     |     |     |     | 285 |  |  |  |  |
| Asn | Ser | Phe | Ile | Glu | Thr | Leu | Glu | Gly | Trp | Ala | Arg | Thr | Val | Val | Thr |  |  |  |  |
| 290 |     |     |     |     |     |     |     |     |     | 295 |     |     |     |     | 300 |  |  |  |  |
| Gly | Arg | Ala | Lys | Leu | Gly | Gly | Ile | Pro | Val | Gly | Val | Val | Ala | Val | Glu |  |  |  |  |
| 305 |     |     |     |     |     |     |     |     |     | 310 |     |     |     |     | 315 |  |  |  |  |
| Thr | Gln | Thr | Val | Met | Gln | Ile | Ile | Pro | Ala | Asp | Pro | Gly | Gln | Leu | Asp |  |  |  |  |
| 325 |     |     |     |     |     |     |     |     |     | 330 |     |     |     |     | 335 |  |  |  |  |
| Ser | His | Glu | Arg | Val | Val | Pro | Gln | Ala | Gly | Gln | Val | Trp | Phe | Pro | Asp |  |  |  |  |
| 340 |     |     |     |     |     |     |     |     |     | 345 |     |     |     |     | 350 |  |  |  |  |
| Ser | Ala | Ala | Lys | Thr | Ala | Gln | Ala | Leu | Met | Asp | Phe | Asn | Arg | Glu | Glu |  |  |  |  |
| 355 |     |     |     |     |     |     |     |     |     | 360 |     |     |     |     | 365 |  |  |  |  |
| Leu | Pro | Leu | Phe | Ile | Leu | Ala | Asn | Trp | Arg | Gly | Phe | Ser | Gly | Gly | Gln |  |  |  |  |
| 370 |     |     |     |     |     |     |     |     |     | 375 |     |     |     |     | 380 |  |  |  |  |
| Arg | Asp | Leu | Phe | Glu | Gly | Ile | Leu | Gln | Ala | Gly | Ser | Thr | Ile | Val | Glu |  |  |  |  |
| 385 |     |     |     |     |     |     |     |     |     | 390 |     |     |     |     | 395 |  |  |  |  |
| Asn | Leu | Arg | Thr | Tyr | Arg | Gln | Pro | Val | Phe | Val | Tyr | Ile | Pro | Met | Met |  |  |  |  |
| 405 |     |     |     |     |     |     |     |     |     | 410 |     |     |     |     | 415 |  |  |  |  |
| Gly | Glu | Leu | Arg | Gly | Gly | Ala | Trp | Val | Val | Val | Asp | Ser | Gln | Ile | Asn |  |  |  |  |
| 420 |     |     |     |     |     |     |     |     |     | 425 |     |     |     |     | 430 |  |  |  |  |
| Ser | Asp | Tyr | Val | Glu | Met | Tyr | Ala | Asp | Glu | Thr | Ala | Arg | Gly | Asn | Val |  |  |  |  |
| 435 |     |     |     |     |     |     |     |     |     | 440 |     |     |     |     | 445 |  |  |  |  |
| Leu | Glu | Pro | Glu | Gly | Thr | Ile | Glu | Ile | Lys | Phe |     |     |     |     |     |  |  |  |  |
| 450 |     |     |     |     |     |     |     |     |     | 455 |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:

aaaattcaca ctatgaaact cgccaaacta attccaaaac gtttcttcat cagatccaaa  
gatcgttcca ctgtctctaa gtccccacg gctttttcCt tcggatccgc ttcctcatct

60  
120



tccggccaag actgtaaaaa ctccggtggt gatggcggtg gcggttccgt taccgccact 180  
agcattctcc cggagggttcc ttctccttat tcctacgtcg agattctcca agcggtttaag 240  
ttgatagaca gagacaacga cggagctgtc tctagacacg atcttgagtc gttacttagc 300  
cggctaggtc ctgattccttt gacggaggag gagatcaacg ttatgcttaa agaggtggac 360  
tgcgacggcg acggtacgat ccgtcttgaa gagcttgcca gtcgtgtagt ctctttagat 420  
ccggctcgtg actcgactga gctgaaggag actttcgagt tctttgacgc ggatcgtaac 480  
ggtttgatct cggctgatga gcttctacga gttttctcga ccattggaga tgaRcggtgc 540  
acgtagatg attgtaagcg tatgatagca gatgttgatg aggacggtga t

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1571831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

Lys Ile His Thr Met Lys Leu Ala Lys Leu Ile Pro Lys Arg Phe Phe  
1 5 10 15  
Ile Arg Ser Lys Asp Arg Ser Thr Val Ser Lys Ser Pro Thr Ala Phe  
20 25 30  
Ser Phe Gly Ser Ala Ser Ser Ser Ser Gly Gln Asp Cys Lys Asn Ser  
35 40 45  
Gly Gly Asp Gly Gly Gly Gly Ser Val Thr Pro Thr Ser Ile Leu Pro  
50 55 60  
Glu Val Pro Ser Pro Tyr Ser Tyr Val Glu Ile Leu Gln Ala Phe Lys  
65 70 75 80  
Leu Ile Asp Arg Asp Asn Asp Gly Ala Val Ser Arg His Asp Leu Glu  
85 90 95  
Ser Leu Leu Ser Arg Leu Gly Pro Asp Pro Leu Thr Glu Glu Glu Ile  
100 105 110  
Asn Val Met Leu Lys Glu Val Asp Cys Asp Gly Asp Gly Thr Ile Arg  
115 120 125  
Leu Glu Glu Leu Ala Ser Arg Val Val Ser Leu Asp Pro Ala Arg Asp  
130 135 140  
Ser Thr Glu Leu Lys Glu Thr Phe Glu Phe Phe Asp Ala Asp Arg Asn  
145 150 155 160  
Gly Leu Ile Ser Ala Asp Glu Leu Leu Arg Val Phe Ser Thr Ile Gly  
165 170 175  
Asp Xaa Arg Cys Thr Leu Asp Asp Cys Lys Arg Met Ile Ala Asp Val  
180 185 190  
Asp Glu Asp Gly Asp  
195

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

Met Lys Leu Ala Lys Leu Ile Pro Lys Arg Phe Phe Ile Arg Ser Lys  
1 5 10 15  
Asp Arg Ser Thr Val Ser Lys Ser Pro Thr Ala Phe Ser Phe Gly Ser

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 20                                                              | 25  | 30  |
| Ala Ser Ser Ser Ser Gly Gln Asp Cys Lys Asn Ser Gly Gly Asp Gly |     |     |
| 35                                                              | 40  | 45  |
| Gly Gly Gly Ser Val Thr Pro Thr Ser Ile Leu Pro Glu Val Pro Ser |     |     |
| 50                                                              | 55  | 60  |
| Pro Tyr Ser Tyr Val Glu Ile Leu Gln Ala Phe Lys Leu Ile Asp Arg |     |     |
| 65                                                              | 70  | 75  |
| Asp Asn Asp Gly Ala Val Ser Arg His Asp Leu Glu Ser Leu Leu Ser |     |     |
| 85                                                              | 90  | 95  |
| Arg Leu Gly Pro Asp Pro Leu Thr Glu Glu Glu Ile Asn Val Met Leu |     |     |
| 100                                                             | 105 | 110 |
| Lys Glu Val Asp Cys Asp Gly Asp Gly Thr Ile Arg Leu Glu Glu Leu |     |     |
| 115                                                             | 120 | 125 |
| Ala Ser Arg Val Val Ser Leu Asp Pro Ala Arg Asp Ser Thr Glu Leu |     |     |
| 130                                                             | 135 | 140 |
| Lys Glu Thr Phe Glu Phe Phe Asp Ala Asp Arg Asn Gly Leu Ile Ser |     |     |
| 145                                                             | 150 | 155 |
| Ala Asp Glu Leu Leu Arg Val Phe Ser Thr Ile Gly Asp Xaa Arg Cys |     |     |
| 165                                                             | 170 | 175 |
| Thr Leu Asp Asp Cys Lys Arg Met Ile Ala Asp Val Asp Glu Asp Gly |     |     |
| 180                                                             | 185 | 190 |
| Asp                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:2113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| atattaaaaa | taaagattct  | taaggctctt  | catattttgc  | tttttgtcaa  | ctctttcttt  | 60   |
| gccatctgtt | acaaacacca  | aactctcctg  | attcatcagt  | tttaagtctt  | cttcaagtcc  | 120  |
| cagggatcat | caatccaatg  | gctcagatct  | tagcagcttc  | tccaacatgt  | cagatgagag  | 180  |
| tgccataaca | ctcatcagtc  | attgcatcat  | catccaagtt  | atggagctct  | gttgtgttga  | 240  |
| aacagaagaa | gcagagcaac  | aacaaagtca  | gaggcttttag | agttcttgct  | ctccaatctg  | 300  |
| ataacagtac | tgtcaataga  | gttgagactc  | ttctcaattt  | agacacccaa  | ccttactctg  | 360  |
| acaggatcat | tgctgaatac  | atttg gatcg | gaggatctgg  | aattgacctt  | agaagcaagt  | 420  |
| caaggactat | cgaaaagccg  | gtggaggatc  | cttctgagct  | acctaagtgg  | aactatgatg  | 480  |
| gttcgagtac | cgg tcaagca | cctggtgaag  | atagtgaagt  | gattctatac  | ccgcaagcta  | 540  |
| tcttcagaga | tcctttccgt  | ggaggcaata  | acatcttggg  | tatctgtgat  | acttggaacac | 600  |
| cagctggtga | gccaatcca   | acaaacaaac  | gtgctaaagc  | tgctgagatc  | ttcagtaaca  | 660  |
| agaaggtctc | tggcgaggtt  | ccatggttcg  | gcattgaaca  | agagtacact  | ttacttcagc  | 720  |
| aaaacgtcaa | atggccttta  | ggttggcctg  | ttggagcggt  | ccctggtcct  | cagggtcctt  | 780  |
| actactgtgg | agttggagct  | gacaagattt  | gggggcgtga  | catttcagat  | gctcattaca  | 840  |
| aagcttggtt | atatgctgga  | attaacatta  | gtgg tactaa | tggtgaagtt  | atgcctggac  | 900  |
| agtgggagtt | ccaagttggc  | ccgagcgtag  | gaattgatgc  | aggtgatcat  | gtttgggtgtg | 960  |
| ctagatacct | tcttgagaga  | atcacagaac  | aagctgggtg  | tgctctaaca  | cttgatccca  | 1020 |
| aaccgataga | gggtgactgg  | aacggtgctg  | gttgccacac  | caattacagt  | accaagagca  | 1080 |
| tgagagagga | aggaggattt  | gaagtgatca  | agaaggctat  | cttgaacctc  | tgcTttcgcc  | 1140 |
| acaaggagca | catcagtgCc  | tacggtgaag  | gaaacgagag  | aagggttgacc | ggaaagcacg  | 1200 |
| agacagctag | tattgaccag  | ttctcatggg  | gcgtggctaa  | ccgtggatgc  | tctattcgtg  | 1260 |
| tgggacgtga | caccgaggcg  | aaaggaaaag  | gttacttaga  | agatcgccgt  | ccagcatcta  | 1320 |
| acatggaccc | atacattgtg  | acctcacttt  | tggcagagac  | cacactcctg  | tgggagccaa  | 1380 |
| ctcttgaggc | tgaagccctt  | gcagctcaaa  | agctttcttt  | gaatgtttta  | aattagtcga  | 1440 |
| aactttcatg | aatctgatga  | acacacgtgt  | ctatgtggtc  | tctcaagttg  | tttaaacatt  | 1500 |
| cggattaaga | cattgtttgt  | tgtcttttca  | tttgcatttt  | taaaactcag  | aattgtatgg  | 1560 |

acaatgttca tccttttata ttggttcttt tgactgtt

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1571838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gln | Ile | Leu | Ala | Ala | Ser | Pro | Thr | Cys | Gln | Met | Arg | Val | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | His | Ser | Ser | Val | Ile | Ala | Ser | Ser | Ser | Lys | Leu | Trp | Ser | Ser | Val |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Lys | Gln | Lys | Lys | Gln | Ser | Asn | Asn | Lys | Val | Arg | Gly | Phe | Arg |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Ala | Leu | Gln | Ser | Asp | Asn | Ser | Thr | Val | Asn | Arg | Val | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Asn | Leu | Asp | Thr | Lys | Pro | Tyr | Ser | Asp | Arg | Ile | Ile | Ala | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | Ile | Trp | Ile | Gly | Gly | Ser | Gly | Ile | Asp | Leu | Arg | Ser | Lys | Ser | Arg |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Ile | Glu | Lys | Pro | Val | Glu | Asp | Pro | Ser | Glu | Leu | Pro | Lys | Trp | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Tyr | Asp | Gly | Ser | Ser | Thr | Gly | Gln | Ala | Pro | Gly | Glu | Asp | Ser | Glu | Val |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ile | Leu | Tyr | Pro | Gln | Ala | Ile | Phe | Arg | Asp | Pro | Phe | Arg | Gly | Gly | Asn |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Asn | Ile | Leu | Val | Ile | Cys | Asp | Thr | Trp | Thr | Pro | Ala | Gly | Glu | Pro | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Thr | Asn | Lys | Arg | Ala | Lys | Ala | Ala | Glu | Ile | Phe | Ser | Asn | Lys | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ser | Gly | Glu | Val | Pro | Trp | Phe | Gly | Ile | Glu | Gln | Glu | Tyr | Thr | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gln | Gln | Asn | Val | Lys | Trp | Pro | Leu | Gly | Trp | Pro | Val | Gly | Ala | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Gly | Pro | Gln | Gly | Pro | Tyr | Tyr | Cys | Gly | Val | Gly | Ala | Asp | Lys | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Trp | Gly | Arg | Asp | Ile | Ser | Asp | Ala | His | Tyr | Lys | Ala | Cys | Leu | Tyr | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Ile | Asn | Ile | Ser | Gly | Thr | Asn | Gly | Glu | Val | Met | Pro | Gly | Gln | Trp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Phe | Gln | Val | Gly | Pro | Ser | Val | Gly | Ile | Asp | Ala | Gly | Asp | His | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Cys | Ala | Arg | Tyr | Leu | Leu | Glu | Arg | Ile | Thr | Glu | Gln | Ala | Gly | Val |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Leu | Thr | Leu | Asp | Pro | Lys | Pro | Ile | Glu | Gly | Asp | Trp | Asn | Gly | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Cys | His | Thr | Asn | Tyr | Ser | Thr | Lys | Ser | Met | Arg | Glu | Glu | Gly | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Glu | Val | Ile | Lys | Lys | Ala | Ile | Leu | Asn | Leu | Ser | Leu | Arg | His | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | His | Ile | Ser | Ala | Tyr | Gly | Glu | Gly | Asn | Glu | Arg | Arg | Leu | Thr | Gly |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Lys | His | Glu | Thr | Ala | Ser | Ile | Asp | Gln | Phe | Ser | Trp | Gly | Val | Ala | Asn |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Gly | Cys | Ser | Ile | Arg | Val | Gly | Arg | Asp | Thr | Glu | Ala | Lys | Gly | Lys |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

(2) INFORMATION FOR SEO ID NO:2115:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..418

(D) OTHER INFORMATION: / Ceres Seq. ID 1571839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

| Variable                          | Mean        | SD   | Min | Max |
|-----------------------------------|-------------|------|-----|-----|
| Age                               | 34.5        | 10.2 | 21  | 55  |
| Gender                            | Male        | 10.5 | 0   | 21  |
| Marital status                    | Married     | 15.2 | 0   | 21  |
| Education                         | High school | 12.5 | 0   | 21  |
| Occupation                        | Unemployed  | 18.5 | 0   | 21  |
| Income                            | Low         | 15.5 | 0   | 21  |
| Health status                     | Good        | 12.5 | 0   | 21  |
| Smoking status                    | Non-smoker  | 10.5 | 0   | 21  |
| Alcohol consumption               | Non-drinker | 10.5 | 0   | 21  |
| Exercise frequency                | Low         | 10.5 | 0   | 21  |
| Stress level                      | Low         | 10.5 | 0   | 21  |
| Sleep quality                     | Good        | 12.5 | 0   | 21  |
| Appetite                          | Good        | 12.5 | 0   | 21  |
| Weight change                     | Stable      | 10.5 | 0   | 21  |
| Blood pressure                    | Normal      | 10.5 | 0   | 21  |
| Blood sugar                       | Normal      | 10.5 | 0   | 21  |
| Cholesterol                       | Normal      | 10.5 | 0   | 21  |
| Triglycerides                     | Normal      | 10.5 | 0   | 21  |
| Hemoglobin A1c                    | Normal      | 10.5 | 0   | 21  |
| Uric acid                         | Normal      | 10.5 | 0   | 21  |
| Creatinine                        | Normal      | 10.5 | 0   | 21  |
| Proteinuria                       | None        | 10.5 | 0   | 21  |
| Diabetes                          | No          | 10.5 | 0   | 21  |
| Hypertension                      | No          | 10.5 | 0   | 21  |
| Heart disease                     | No          | 10.5 | 0   | 21  |
| Stroke                            | No          | 10.5 | 0   | 21  |
| Angina                            | No          | 10.5 | 0   | 21  |
| Myocardial infarction             | No          | 10.5 | 0   | 21  |
| Heart failure                     | No          | 10.5 | 0   | 21  |
| Arrhythmia                        | No          | 10.5 | 0   | 21  |
| Coronary artery disease           | No          | 10.5 | 0   | 21  |
| Peripheral vascular disease       | No          | 10.5 | 0   | 21  |
| Chronic kidney disease            | No          | 10.5 | 0   | 21  |
| Chronic liver disease             | No          | 10.5 | 0   | 21  |
| Chronic lung disease              | No          | 10.5 | 0   | 21  |
| Chronic pain                      | No          | 10.5 | 0   | 21  |
| Chronic mental health issues      | No          | 10.5 | 0   | 21  |
| Chronic substance use             | No          | 10.5 | 0   | 21  |
| Chronic autoimmune disease        | No          | 10.5 | 0   | 21  |
| Chronic infectious disease        | No          | 10.5 | 0   | 21  |
| Chronic cancer                    | No          | 10.5 | 0   | 21  |
| Chronic neurological disease      | No          | 10.5 | 0   | 21  |
| Chronic endocrine disease         | No          | 10.5 | 0   | 21  |
| Chronic dermatological disease    | No          | 10.5 | 0   | 21  |
| Chronic ophthalmological disease  | No          | 10.5 | 0   | 21  |
| Chronic otolaryngological disease | No          | 10.5 | 0   | 21  |
| Chronic rheumatological disease   | No          | 10.5 | 0   | 21  |
| Chronic gastrointestinal disease  | No          | 10.5 | 0   | 21  |
| Chronic urological disease        | No          | 10.5 | 0   | 21  |
| Chronic gynecological disease     | No          | 10.5 | 0   | 21  |
| Chronic pediatric disease         | No          | 10.5 | 0   | 21  |
| Chronic geriatric disease         | No          | 10.5 | 0   | 21  |
| Chronic infectious disease        | No          | 10.5 | 0   | 21  |
| Chronic cancer                    | No          | 10.5 | 0   | 21  |
| Chronic neurological disease      | No          | 10.5 | 0   | 21  |
| Chronic endocrine disease         | No          | 10.5 | 0   | 21  |
| Chronic dermatological disease    | No          | 10.5 | 0   | 21  |
| Chronic ophthalmological disease  | No          | 10.5 | 0   | 21  |
| Chronic otolaryngological disease | No          | 10.5 | 0   | 21  |
| Chronic rheumatological disease   | No          | 10.5 | 0   | 21  |
| Chronic gastrointestinal disease  | No          | 10.5 | 0   | 21  |
| Chronic urological disease        | No          | 10.5 | 0   | 21  |
| Chronic gynecological disease     | No          | 10.5 | 0   | 21  |
| Chronic pediatric disease         | No          | 10.5 | 0   | 21  |
| Chronic geriatric disease         | No          | 10.5 | 0   | 21  |
| Chronic infectious disease        | No          | 10.5 | 0   | 21  |
| Chronic cancer                    | No          | 10.5 | 0   | 21  |
| Chronic neurological disease      | No          | 10.5 | 0   | 21  |
| Chronic endocrine disease         | No          | 10.5 | 0   | 21  |
| Chronic dermatological disease    | No          | 10.5 | 0   | 21  |
| Chronic ophthalmological disease  | No          | 10.5 | 0   | 21  |
| Chronic otolaryngological disease | No          | 10.5 | 0   | 21  |
| Chronic rheumatological disease   | No          | 10.5 | 0   | 21  |
| Chronic gastrointestinal disease  | No          | 10.5 | 0   | 21  |
| Chronic urological disease        | No          | 10.5 | 0   | 21  |
| Chronic gynecological disease     | No          | 10.5 | 0   | 21  |
| Chronic pediatric disease         | No          | 10.5 | 0   | 21  |
| Chronic geriatric disease         | No          | 10.5 | 0   | 21  |
| Chronic infectious disease        | No          | 10.5 | 0   | 21  |
| Chronic cancer                    | No          | 10.5 | 0   | 21  |
| Chronic neurological disease      | No          | 10.5 | 0   | 21  |
| Chronic endocrine disease         | No          | 10.5 | 0   | 21  |
| Chronic dermatological disease    | No          | 10.5 | 0   | 21  |
| Chronic ophthalmological disease  | No          | 1    |     |     |

340 345 350  
Gly Val Ala Asn Arg Gly Cys Ser Ile Arg Val Gly Arg Asp Thr Glu  
355 360 365  
Ala Lys Gly Lys Gly Tyr Leu Glu Asp Arg Arg Pro Ala Ser Asn Met  
370 375 380  
Asp Pro Tyr Ile Val Thr Ser Leu Leu Ala Glu Thr Thr Leu Leu Trp  
385 390 395 400  
Glu Pro Thr Leu Glu Ala Glu Ala Leu Ala Ala Gln Lys Leu Ser Leu  
405 410 415  
Asn Val

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

aataataatt agacttctgc actttctcac gaacctctct gtctcgtcca ttacttaaaa 60  
accaaaatctt tcatcatctt ccttcaccag ttgactctct ttcaatctat ctctgaatct 120  
ctcactctcc taccgaaaa ccatgaactc caacgaccag gatccgattc cggttcagacc 180  
cgaagacaac aacttctcog gttccaaaac ctacgccatg agcggcaaaa tcatgctaag 240  
tgcaatagta atcctcttct tctgctgcat tttaatggtc ttctctccatc tttacgctcg 300  
ttggtatctc ctccgtgctc gtagacgtca tctccgtcgt cgtagccgta accgtcgcg 360  
tacgatgggt ttcttcaccg ctgactcttc caccgccgca acttccgctc tctgttcacg 420  
tggacttgat ccaaacgtta ttaaactctt tctgttttc actttctccg acgagactca 480  
taaagatccg atcgaatgcg ccgtttgttt atcggaattc gaagagagcg agacgggtcg 540  
ggttttgccc aattgtcaac atacttttca tgttgattgt attgatattg ggtttcattc 600  
tcattccact tgtcctcttt gtgatctct cgttgagcct ctgccggga ttgaatcaac 660  
ggcggcgcg agggagaggg aagttgtgat tgcggttgat tctgatccgg ttttggtaat 720  
tgaaccgagt tctagctctg gattgacgga tgaaccacat ggatctggat ctctcagat 780  
gctgagggaa gattccggga gaaaaccggc ggcgattgag gttccgagga ggacttttag 840  
cgagtttgaa gatgagttga ctcgagagaga ctgccggcg agtcagtcgt ttaggtctcc 900  
gatgagtcgg atgttatctt tcatctggat gttgagtga gatagaagaa gcgcttcgtc 960  
tcctatcgcc ggaGctccgc cgctatcgcc gacgttaagc tgccggatac agatgaccga 1020  
gtcagatata gaacggggag gagaagagag taggtgactt gtcacgtgtt ggtgtctgat 1080  
tggtttaatg ttaaccggga gtaaaaaaag gaattactac aagtcaacag gcttttgtct 1140  
aggtgttgat ttcggcgccc aaggacacgt ggcgtaaact gagcttcag gaatcaatat 1200  
tcaccgtcta ttatgattag atagggtaga tagatttgtg taacgatgta caaagtcata 1260  
tacaatattg aatctgtttc catttatatt accatattct ttttttttat aattttcgaa 1320  
gttctacaaa ctcttttatg taaaacacaa tccaatggtc ataattgtga taaagacttt 1380  
gksawwatt

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

Met Asn Ser Asn Asp Gln Asp Pro Ile Pro Phe Arg Pro Glu Asp Asn  
1 5 10 15

```

Asn Phe Ser Gly Ser Lys Thr Tyr Ala Met Ser Gly Lys Ile Met Leu
 20 25 30
Ser Ala Ile Val Ile Leu Phe Phe Val Val Ile Leu Met Val Phe Leu
 35 40 45
His Leu Tyr Ala Arg Trp Tyr Leu Leu Arg Ala Arg Arg Arg His Leu
 50 55 60
Arg Arg Arg Ser Arg Asn Arg Arg Ala Thr Met Val Phe Phe Thr Ala
 65 70 75 80
Asp Pro Ser Thr Ala Ala Thr Ser Val Val Ala Ser Arg Gly Leu Asp
 85 90 95
Pro Asn Val Ile Lys Ser Leu Pro Val Phe Thr Phe Ser Asp Glu Thr
 100 105 110
His Lys Asp Pro Ile Glu Cys Ala Val Cys Leu Ser Glu Phe Glu Glu
 115 120 125
Ser Glu Thr Gly Arg Val Leu Pro Asn Cys Gln His Thr Phe His Val
 130 135 140
Asp Cys Ile Asp Met Trp Phe His Ser His Ser Thr Cys Pro Leu Cys
 145 150 155 160
Arg Ser Leu Val Glu Pro Leu Ala Gly Ile Glu Ser Thr Ala Ala Ala
 165 170 175
Arg Glu Arg Glu Val Val Ile Ala Val Asp Ser Asp Pro Val Leu Val
 180 185 190
Ile Glu Pro Ser Ser Ser Ser Gly Leu Thr Asp Glu Pro His Gly Ser
 195 200 205
Gly Ser Ser Gln Met Leu Arg Glu Asp Ser Gly Arg Lys Pro Ala Ala
 210 215 220
Ile Glu Val Pro Arg Arg Thr Phe Ser Glu Phe Glu Asp Glu Leu Thr
 225 230 235 240
Arg Arg Asp Ser Pro Ala Ser Gln Ser Phe Arg Ser Pro Met Ser Arg
 245 250 255
Met Leu Ser Phe Thr Arg Met Leu Ser Arg Asp Arg Arg Ser Ala Ser
 260 265 270
Ser Pro Ile Ala Gly Ala Pro Pro Leu Ser Pro Thr Leu Ser Cys Arg
 275 280 285
Ile Gln Met Thr Glu Ser Asp Ile Glu Arg Gly Gly Glu Glu Ser Arg
 290 295 300

```

(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1571842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

```

Met Ser Gly Lys Ile Met Leu Ser Ala Ile Val Ile Leu Phe Phe Val
1 5 10 15
Val Ile Leu Met Val Phe Leu His Leu Tyr Ala Arg Trp Tyr Leu Leu
 20 25 30
Arg Ala Arg Arg Arg His Leu Arg Arg Arg Ser Arg Asn Arg Arg Ala
 35 40 45
Thr Met Val Phe Phe Thr Ala Asp Pro Ser Thr Ala Ala Thr Ser Val
 50 55 60
Val Ala Ser Arg Gly Leu Asp Pro Asn Val Ile Lys Ser Leu Pro Val
 65 70 75 80
Phe Thr Phe Ser Asp Glu Thr His Lys Asp Pro Ile Glu Cys Ala Val

```

|            |            |            |            |           |            |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Leu        | Ser        | Ala        | Ile<br>5  | Val        | Ile        | Leu        | Phe        | Phe<br>10  | Val        | Val        | Ile        | Leu        | Met<br>15 | Val        |
| Phe        | Leu        | His        | Leu<br>20  | Tyr       | Ala        | Arg        | Trp        | Tyr<br>25  | Leu        | Leu        | Arg        | Ala        | Arg<br>30  | Arg       | Arg        |
| His        | Leu        | Arg<br>35  | Arg        | Arg       | Ser        | Arg        | Asn<br>40  | Arg        | Arg        | Ala        | Thr        | Met<br>45  | Val        | Phe       | Phe        |
| Thr        | Ala<br>50  | Asp        | Pro        | Ser       | Thr        | Ala<br>55  | Ala        | Thr        | Ser        | Val        | Val<br>60  | Ala        | Ser        | Arg       | Gly        |
| Leu<br>65  | Asp        | Pro        | Asn        | Val<br>70 | Ile        | Lys        | Ser        | Leu        | Pro        | Val<br>75  | Phe        | Thr        | Phe        | Ser       | Asp<br>80  |
| Glu        | Thr        | His        | Lys<br>85  | Asp       | Pro        | Ile        | Glu        | Cys        | Ala<br>90  | Val        | Cys        | Leu        | Ser        | Glu<br>95 | Phe        |
| Glu        | Glu        | Ser        | Glu<br>100 | Thr       | Gly        | Arg        | Val        | Leu<br>105 | Pro        | Asn        | Cys        | Gln        | His<br>110 | Thr       | Phe        |
| His        | Val        | Asp<br>115 | Cys        | Ile       | Asp        | Met        | Trp<br>120 | Phe        | His        | Ser        | His        | Ser<br>125 | Thr        | Cys       | Pro        |
| Leu        | Cys<br>130 | Arg        | Ser        | Leu       | Val        | Glu<br>135 | Pro        | Leu        | Ala        | Gly        | Ile<br>140 | Glu        | Ser        | Thr       | Ala        |
| Ala<br>145 | Ala        | Arg        | Glu        | Arg       | Glu<br>150 | Val        | Val        | Ile        | Ala        | Val<br>155 | Asp        | Ser        | Asp        | Pro       | Val<br>160 |
| Leu        | Val        | Ile        | Glu<br>165 | Pro       | Ser        | Ser        | Ser        | Ser        | Gly<br>170 | Leu        | Thr        | Asp        | Glu        | Pro       | His        |
| Gly        | Ser        | Gly        | Ser<br>180 | Ser       | Gln        | Met        | Leu        | Arg<br>185 | Glu        | Asp        | Ser        | Gly        | Arg<br>190 | Lys       | Pro        |

Ala Ala Ile Glu Val Pro Arg Arg Thr Phe Ser Glu Phe Glu Asp Glu  
195 200 205  
Leu Thr Arg Arg Asp Ser Pro Ala Ser Gln Ser Phe Arg Ser Pro Met  
210 215 220  
Ser Arg Met Leu Ser Phe Thr Arg Met Leu Ser Arg Asp Arg Arg Ser  
225 230 235 240  
Ala Ser Ser Pro Ile Ala Gly Ala Pro Pro Leu Ser Pro Thr Leu Ser  
245 250 255  
Cys Arg Ile Gln Met Thr Glu Ser Asp Ile Glu Arg Gly Gly Glu Glu  
260 265 270  
Ser Arg

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

aaaaaatttta ttagccattc gagaacaag gcattctctat ttttttgctt cttctaataag 60  
acttcttcgt cactgatctc ccacgacgat ctccaaact catttctcta cggtcatcga 120  
tctctctcitt tctcgtttgc tctacgaaaa tcagccatgg atgaagagta cgagggttatt 180  
gttctcggca cgggtctcaa ggagtgtatc ctcagcggtc tcctttccgt cgatgggtgtc 240  
aaggtgcttc acatggacag gaatgactac tatggtggag aatcaacttc tcttaatctc 300  
aatcagcttt ggaagaagtt caggggagaa gagaaggctc ctgagcattt aggtgctagc 360  
cgggattaca atgttgacat gatgcctaag tttatgatgg gaaatggcaa gcttgttcgt 420  
acccttattc atacagatgt tacaaaatgt ttgtccttca aagctgttga tgggaagctat 480  
gttttcgtca aaggaaaggt tcaaaaggtg ccagctactc ctatggaggc cctgaaatct 540  
tctctcatgg gcatatttga gaaacgtcga gccggcaagt ttttcagttt tggtcaggaa 600  
tacgatgaga aggacccaaa aacacacgat ggaatggatt tgaccagagt tacaacaaag 660  
gaactgattg cgaatatatg tcttgatggc aacactattg actttatttg tcacgcagtg 720  
gcactTcaca cgaatgacca acatctcgat caaccgcct ttgatactgt aatgagaatg 780  
aagctctatg cggaatctct tgcacgtttc caaggaacat ctccatatat ttatcctctc 840  
tatgggttgg gagaactacc ccaggcattt gcacgactta gtgctgtcta tgggtggcaca 900  
tatatgttga acaaacctga gtgcaaggta gagtttgacg agggaggtaa ggttatttgt 960  
gtaacatctg agggagagac tgctaaatgc aaaaagattg tgtgtgacct ttcataacctg 1020  
ccgaacaagg ttaggaagat tggcagggtt gctcgggcca tcgccattat gagccacccg 1080  
attccaaaca ccaatgattc tcaactcagt caggtcacat taccacagaa acagttggcc 1140  
cgaaatcgg atatgtatgt cttctgttgt tcgtactccc acaacgttgc tcccaaggga 1200  
aaattcattg catttggtgc tacagatgca gagactgata accctcaaac cgaactaaag 1260  
cctggaactg atcttttggg tcctgttgat gagatattct tcgacatgta tgatagatac 1320  
gagcctgtca acgagccaga gttggacaac tgctttatat caacgagcta tgatgctaca 1380  
acacactttg agacaactgt tgcgg

(2) INFORMATION FOR SEQ ID NO:2121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

Met Asp Glu Glu Tyr Glu Val Ile Val Leu Gly Thr Gly Leu Lys Glu

2025 RELEASE UNDER E.O. 14176



|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Cys | Ile | Leu | Ser | Gly | Leu | Leu |
|     |     | 20  |     | 25  |     | 30  |
| Met | Asp | Arg | Asn | Asp | Tyr | Tyr |
|     |     | 35  |     | 40  |     | 45  |
| Asn | Gln | Leu | Trp | Lys | Lys | Phe |
|     |     | 50  |     | 55  |     | 60  |
| Leu | Gly | Ala | Ser | Arg | Asp | Tyr |
|     |     | 65  |     | 70  |     | 75  |
| Met | Gly | Asn | Gly | Lys | Leu | Val |
|     |     | 85  |     | 90  |     | 95  |
| Lys | Tyr | Leu | Ser | Phe | Lys | Ala |
|     |     | 100 |     | 105 |     | 110 |
| Gly | Lys | Val | Gln | Lys | Val | Pro |
|     |     | 115 |     | 120 |     | 125 |
| Ser | Leu | Met | Gly | Ile | Phe | Glu |
|     |     | 130 |     | 135 |     | 140 |
| Phe | Val | Gln | Glu | Tyr | Asp | Glu |
|     |     | 145 |     | 150 |     | 155 |
| Asp | Leu | Thr | Arg | Val | Thr | Thr |
|     |     | 165 |     | 170 |     | 175 |
| Asp | Gly | Asn | Thr | Ile | Asp | Phe |
|     |     | 180 |     | 185 |     | 190 |
| Asn | Asp | Gln | His | Leu | Asp | Gln |
|     |     | 195 |     | 200 |     | 205 |
| Lys | Leu | Tyr | Ala | Glu | Ser | Leu |
|     |     | 210 |     | 215 |     | 220 |
| Ile | Tyr | Pro | Leu | Tyr | Gly | Leu |
|     |     | 225 |     | 230 |     | 235 |
| Leu | Ser | Ala | Val | Tyr | Gly | Gly |
|     |     | 245 |     | 250 |     | 255 |
| Lys | Val | Glu | Phe | Asp | Glu | Gly |
|     |     | 260 |     | 265 |     | 270 |
| Gly | Glu | Thr | Ala | Lys | Cys | Lys |
|     |     | 275 |     | 280 |     | 285 |
| Pro | Asn | Lys | Val | Arg | Lys | Ile |
|     |     | 290 |     | 295 |     | 300 |
| Met | Ser | His | Pro | Ile | Pro | Asn |
|     |     | 305 |     | 310 |     | 315 |
| Ile | Ile | Pro | Gln | Lys | Gln | Leu |
|     |     | 325 |     | 330 |     | 335 |
| Cys | Cys | Ser | Tyr | Ser | His | Asn |
|     |     | 340 |     | 345 |     | 350 |
| Phe | Val | Ser | Thr | Asp | Ala | Glu |
|     |     | 355 |     | 360 |     | 365 |
| Pro | Gly | Thr | Asp | Leu | Leu | Gly |
|     |     | 370 |     | 375 |     | 380 |
| Tyr | Asp | Arg | Tyr | Glu | Pro | Val |
|     |     | 385 |     | 390 |     | 395 |
| Ile | Ser | Thr | Ser | Tyr | Asp | Ala |
|     |     | 405 |     | 410 |     | 415 |

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1571846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Asn | Asp | Tyr | Tyr | Gly | Gly | Glu | Ser | Thr | Ser | Leu | Asn | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Gln | Leu | Trp | Lys | Lys | Phe | Arg | Gly | Glu | Glu | Lys | Ala | Pro | Glu | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Ala | Ser | Arg | Asp | Tyr | Asn | Val | Asp | Met | Met | Pro | Lys | Phe | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Gly | Asn | Gly | Lys | Leu | Val | Arg | Thr | Leu | Ile | His | Thr | Asp | Val | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Tyr | Leu | Ser | Phe | Lys | Ala | Val | Asp | Gly | Ser | Tyr | Val | Phe | Val | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Lys | Val | Gln | Lys | Val | Pro | Ala | Thr | Pro | Met | Glu | Ala | Leu | Lys | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Met | Gly | Ile | Phe | Glu | Lys | Arg | Arg | Ala | Gly | Lys | Phe | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Val | Gln | Glu | Tyr | Asp | Glu | Lys | Asp | Pro | Lys | Thr | His | Asp | Gly | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Leu | Thr | Arg | Val | Thr | Thr | Lys | Glu | Leu | Ile | Ala | Lys | Tyr | Gly | Leu |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asp | Gly | Asn | Thr | Ile | Asp | Phe | Ile | Gly | His | Ala | Val | Ala | Leu | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Asp | Gln | His | Leu | Asp | Gln | Pro | Ala | Phe | Asp | Thr | Val | Met | Arg | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Leu | Tyr | Ala | Glu | Ser | Leu | Ala | Arg | Phe | Gln | Gly | Thr | Ser | Pro | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Tyr | Pro | Leu | Tyr | Gly | Leu | Gly | Glu | Leu | Pro | Gln | Ala | Phe | Ala | Arg |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Ser | Ala | Val | Tyr | Gly | Gly | Thr | Tyr | Met | Leu | Asn | Lys | Pro | Glu | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Val | Glu | Phe | Asp | Glu | Gly | Gly | Lys | Val | Ile | Gly | Val | Thr | Ser | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Glu | Thr | Ala | Lys | Cys | Lys | Lys | Ile | Val | Cys | Asp | Pro | Ser | Tyr | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Asn | Lys | Val | Arg | Lys | Ile | Gly | Arg | Val | Ala | Arg | Ala | Ile | Ala | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Met | Ser | His | Pro | Ile | Pro | Asn | Thr | Asn | Asp | Ser | His | Ser | Val | Gln | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Ile | Pro | Gln | Lys | Gln | Leu | Ala | Arg | Lys | Ser | Asp | Met | Tyr | Val | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Cys | Cys | Ser | Tyr | Ser | His | Asn | Val | Ala | Pro | Lys | Gly | Lys | Phe | Ile | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Val | Ser | Thr | Asp | Ala | Glu | Thr | Asp | Asn | Pro | Gln | Thr | Glu | Leu | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Gly | Thr | Asp | Leu | Leu | Gly | Pro | Val | Asp | Glu | Ile | Phe | Phe | Asp | Met |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Tyr | Asp | Arg | Tyr | Glu | Pro | Val | Asn | Glu | Pro | Glu | Leu | Asp | Asn | Cys | Phe |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Ser | Thr | Ser | Tyr | Asp | Ala | Thr | Thr | His | Phe | Glu | Thr | Thr | Val | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1571847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Met Pro Lys Phe Met Met Gly Asn Gly Lys Leu Val Arg Thr Leu  
1 5 10 15  
Ile His Thr Asp Val Thr Lys Tyr Leu Ser Phe Lys Ala Val Asp Gly  
20 25 30  
Ser Tyr Val Phe Val Lys Gly Lys Val Gln Lys Val Pro Ala Thr Pro  
35 40 45  
Met Glu Ala Leu Lys Ser Ser Leu Met Gly Ile Phe Glu Lys Arg Arg  
50 55 60  
Ala Gly Lys Phe Phe Ser Phe Val Gln Glu Tyr Asp Glu Lys Asp Pro  
65 70 75 80  
Lys Thr His Asp Gly Met Asp Leu Thr Arg Val Thr Thr Lys Glu Leu  
85 90 95  
Ile Ala Lys Tyr Gly Leu Asp Gly Asn Thr Ile Asp Phe Ile Gly His  
100 105 110  
Ala Val Ala Leu His Thr Asn Asp Gln His Leu Asp Gln Pro Ala Phe  
115 120 125  
Asp Thr Val Met Arg Met Lys Leu Tyr Ala Glu Ser Leu Ala Arg Phe  
130 135 140  
Gln Gly Thr Ser Pro Tyr Ile Tyr Pro Leu Tyr Gly Leu Gly Glu Leu  
145 150 155 160  
Pro Gln Ala Phe Ala Arg Leu Ser Ala Val Tyr Gly Gly Thr Tyr Met  
165 170 175  
Leu Asn Lys Pro Glu Cys Lys Val Glu Phe Asp Glu Gly Gly Lys Val  
180 185 190  
Ile Gly Val Thr Ser Glu Gly Glu Thr Ala Lys Cys Lys Lys Ile Val  
195 200 205  
Cys Asp Pro Ser Tyr Leu Pro Asn Lys Val Arg Lys Ile Gly Arg Val  
210 215 220  
Ala Arg Ala Ile Ala Ile Met Ser His Pro Ile Pro Asn Thr Asn Asp  
225 230 235 240  
Ser His Ser Val Gln Val Ile Ile Pro Gln Lys Gln Leu Ala Arg Lys  
245 250 255  
Ser Asp Met Tyr Val Phe Cys Cys Ser Tyr Ser His Asn Val Ala Pro  
260 265 270  
Lys Gly Lys Phe Ile Ala Phe Val Ser Thr Asp Ala Glu Thr Asp Asn  
275 280 285  
Pro Gln Thr Glu Leu Lys Pro Gly Thr Asp Leu Leu Gly Pro Val Asp  
290 295 300  
Glu Ile Phe Phe Asp Met Tyr Asp Arg Tyr Glu Pro Val Asn Glu Pro  
305 310 315 320  
Glu Leu Asp Asn Cys Phe Ile Ser Thr Ser Tyr Asp Ala Thr Thr His  
325 330 335  
Phe Glu Thr Thr Val Ala  
340

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..884

(D) OTHER INFORMATION: / Ceres Seq. ID 1571867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

```
acacaattca gattccaatt ttctcaaact ctaaaatcaa tctctcaa atctcaaccg 60
tgatcaagat gcagatcttc gttaagactc tcaccggaaa gactatcacc ctcgaggtgg 120
aaagctctga caccatcgac aacgttaagg ccaagatcca ggataaggaa ggtattcttc 180
cggatcagca gaggtttatc ttccgcccga agcagttgga ggatggccgc acgttggcgg 240
attacaatat ccagaaggaa tccaccctcc acttggttct caggctccgt ggtgggtatgc 300
agattttcgt taaaaccCta acgggaaaga cgattactct tgaggtggag agctctgaca 360
ccattgacaa cgtcaaggcc aagatccaag ataaggaggg tattctctccg gaccagcaga 420
ggttgatctt cgccggaaag caacttgagg acggcagaac tttggcggat tacaacatcc 480
agaaggagtc tacgcttcat ttggtcttgc gtctgcgtgg aggtatgcag atcttcgtaa 540
agactttgac cggaaagacc atcactcttg aagttgagag ctccgacacc attgataacg 600
tgaaggctaa gatccaggac aaggaaggca ttctcccgga ccagcagcgt ctcatcttcg 660
ctggaaagca gcttgaggat ggacgtactt tggccgacta caacatccag aaggagtcta 720
ctcttcactt ggtctctcgt ctccgtgggt gtttctaaac cttgtctctc tctcttatgg 780
ttactgaacc aagttcatgt atcgtttcat ctagtacttt ggtggtttat gttttggggc 840
catgtacagc ctctgataaa taattgatcg actatgtttc cgtc
```

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

```
Thr Ile Gln Ile Pro Ile Phe Ser Asn Ser Lys Ile Asn Leu Ser Asn
1 5 10 15
Leu Ser Thr Val Ile Lys Met Gln Ile Phe Val Lys Thr Leu Thr Gly
 20 25 30
Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val
 35 40 45
Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
 50 55 60
Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp
 65 70 75 80
Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
 85 90 95
Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
 100 105 110
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile
 115 120 125
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
 130 135 140
Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln
 145 150 155 160
Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln
 165 170 175
Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu
 180 185 190
Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu
 195 200 205
Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu
 210 215 220
Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr
 225 230 235 240
Leu His Leu Val Leu Arg Leu Arg Gly Gly Phe
 245 250
```

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..229  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571869  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
65 70 75 80  
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile  
100 105 110  
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
115 120 125  
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
130 135 140  
Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu  
145 150 155 160  
Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp  
165 170 175  
Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln  
180 185 190  
Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu  
195 200 205  
Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg  
210 215 220  
Leu Arg Gly Gly Phe  
225

(2) INFORMATION FOR SEQ ID NO:2127:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571870  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe

(2) INFORMATION FOR SEO ID NO:2128:

(A) LENGTH: 833 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..833

(D) OTHER INFORMATION: / Ceres Seq. ID 1571871

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| caaaccaagt | tttcttctaa | gctgtatttg  | aaatgggtata | tatttcacac | accaaacaga | 60  |
| tcagaagcta | aaaggtaata | atataatggc  | ggatttgagg  | gacgaaaaag | gtaaccaat  | 120 |
| ccatctaacc | gacacacagg | gaaacccaat  | tgtcgacctg  | actgatgagc | acggtaacc  | 180 |
| catgtaccta | accggtgttg | ttagctccac  | tcctcagcat  | aaggagagta | ctaccagcga | 240 |
| cattgcagag | caccctacta | gcaccgttgg  | agaaacacat  | ccggcagctg | ctccaactgg | 300 |
| tgctgtgtgt | gccaccgctg | ccactgcgac  | aggagtctct  | gctggtactg | gagcaaccac | 360 |
| cacagggcag | caacaccatg | ggtcgcttga  | agagcatctt  | cgtcgtctg  | gaagttcatc | 420 |
| tagctctagc | tcggaggatg | acgggcaagg  | agggaggagg  | aagaagagca | taaaggagaa | 480 |
| aattaaagag | aagttcagta | gcgggcaaca  | caaggacgaa  | caaacaccaa | ccaccgccac | 540 |
| aacaacagga | cctgccacta | ccgaccaacc  | tcacgagaag  | aagggcattc | tcgagaagat | 600 |
| caaggacaag | cttcccggcc | accataacca  | caaccaccca  | tgaacaccaa | tcatatgacg | 660 |
| tctttgttac | atgaataaat | cgtttgcacg  | aattttCatta | gggcttatga | agaatcaata | 720 |
| tatatgtcta | gtgaagttta | ctaaatttta  | gttgtgtttg  | cttgagttt  | gtgaatgtga | 780 |
| ccatcgtgtt | atcatgtttc | tgtttatttta | taaagaagga  | actgtatttt | gct        |     |

(2) INFORMATION FOR SEQ ID NO:2129:

(A) LENGTH: 185 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1571872

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Leu | Arg | Asp | Glu | Lys | Gly | Asn | Pro | Ile | His | Leu | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gln | Gly | Asn | Pro | Ile | Val | Asp | Leu | Thr | Asp | Glu | His | Gly | Asn | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Tyr | Leu | Thr | Gly | Val | Val | Ser | Ser | Thr | Pro | Gln | His | Lys | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Ser | Asp | Ile | Ala | Glu | His | Pro | Thr | Ser | Thr | Val | Gly | Glu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Pro | Ala | Ala | Ala | Pro | Thr | Gly | Ala | Gly | Ala | Ala | Thr | Ala | Ala | Thr |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ala | Thr | Gly | Val | Ser | Ala | Gly | Thr | Gly | Ala | Thr | Thr | Thr | Gly | Gln | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |

His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser  
100 105 110  
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser  
115 120 125  
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp  
130 135 140  
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp  
145 150 155 160  
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu  
165 170 175  
Pro Gly His His Asn His Asn His Pro  
180 185

(2) INFORMATION FOR SEQ ID NO:2130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:

Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser  
1 5 10 15  
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr  
20 25 30  
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Thr Ala Ala Thr  
35 40 45  
Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Gly Gln Gln  
50 55 60  
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser  
65 70 75 80  
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser  
85 90 95  
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp  
100 105 110  
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp  
115 120 125  
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu  
130 135 140  
Pro Gly His His Asn His Asn His Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:2131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1091
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attttatttt gtcttaaagc ttttggcgag tttgcttggt tgtgagtgtg tggttatgga  | 60  |
| gtctccgttc aaacctgatg tcgtcagagg tcaagtggct ctcaccaccg gtggtggatc  | 120 |
| cggtatcggt tttgagatct cttctcagtt tggcaaaccat ggagcttcta tcgctatcat | 180 |
| gggacgacga aaacaagtcc tcgatgacgc cgtctctgct cttcgatctc ttggaatcca  | 240 |
| ggctattgga ttggaagggtg atgttcgtaa gcaagaagat gcgagaagag ttgtggaagc | 300 |

aacttatcag catttttgga aacttgatat tcttggttaac gccgctgctg ggaattttct 360  
ggctgctgct gaggatttgt ctctaatgg cttcagaaca gtcttagaca ttgatgcggt 420  
aggaacattc aacatgtgtc acgcagctct caagtatctt aagaaaggag cgcctggaag 480  
agactcatca agcgggtggag gttcgattat taacatttagc gcgactttgc actacacggc 540  
ttcttggtac caaatacatg tctctgCagc caaggctgca gttgatgcta ccacaagaaa 600  
cttggcattg gagtggggaa ctgactatga tattagagtg aacgggattg ctccagggtcc 660  
tattggagggt acacctggaa tgagtaaact tgtacctgag gagattgaaa acaaaaccag 720  
agagtacatg cctctttata aagttggaga gaagtgggat atcgctatgg ctgcactcta 780  
cctcagctgt gattctggga aatatgtgag cggactaaca atggtggttag atggaggact 840  
gtggcttagc aaacctcgcc acttgccata agaagcgggtg aagcaactct ctcgctgcggt 900  
ggagaagagg tctagggcca agcctgttgg tctcccaacc agcaagctgt agatcatttg 960  
aatttcagat atcaaataag tgcacattga aaaaatgttt tggttttattg aattacattg 1020  
gagactgaga aaatggtatt aagattatgt agatcaaact atcttatgca caataaagta 1080  
gctttctttg c

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Phe | Val | Leu | Lys | Leu | Leu | Ala | Ser | Leu | Leu | Val | Cys | Glu | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Met | Glu | Ser | Pro | Phe | Lys | Pro | Asp | Val | Val | Arg | Gly | Gln | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ile | Thr | Gly | Gly | Gly | Ser | Gly | Ile | Gly | Phe | Glu | Ile | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Phe | Gly | Lys | His | Gly | Ala | Ser | Ile | Ala | Ile | Met | Gly | Arg | Arg | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Val | Leu | Asp | Asp | Ala | Val | Ser | Ala | Leu | Arg | Ser | Leu | Gly | Ile | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ile | Gly | Leu | Glu | Gly | Asp | Val | Arg | Lys | Gln | Glu | Asp | Ala | Arg | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Val | Glu | Ala | Thr | Tyr | Gln | His | Phe | Gly | Lys | Leu | Asp | Ile | Leu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ala | Ala | Ala | Gly | Asn | Phe | Leu | Ala | Ala | Ala | Glu | Asp | Leu | Ser | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gly | Phe | Arg | Thr | Val | Leu | Asp | Ile | Asp | Ala | Val | Gly | Thr | Phe | Asn |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Cys | His | Ala | Ala | Leu | Lys | Tyr | Leu | Lys | Lys | Gly | Ala | Pro | Gly | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ser | Ser | Ser | Gly | Gly | Gly | Ser | Ile | Ile | Asn | Ile | Ser | Ala | Thr | Leu |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| His | Tyr | Thr | Ala | Ser | Trp | Tyr | Gln | Ile | His | Val | Ser | Ala | Ala | Lys | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Val | Asp | Ala | Thr | Thr | Arg | Asn | Leu | Ala | Leu | Glu | Trp | Gly | Thr | Asp |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Asp | Ile | Arg | Val | Asn | Gly | Ile | Ala | Pro | Gly | Pro | Ile | Gly | Gly | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Pro | Gly | Met | Ser | Lys | Leu | Val | Pro | Glu | Glu | Ile | Glu | Asn | Lys | Thr | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Glu | Tyr | Met | Pro | Leu | Tyr | Lys | Val | Gly | Glu | Lys | Trp | Asp | Ile | Ala | Met |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Ala | Ala | Leu | Tyr | Leu | Ser | Cys | Asp | Ser | Gly | Lys | Tyr | Val | Ser | Gly | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Met | Val | Val | Asp | Gly | Gly | Leu | Trp | Leu | Ser | Lys | Pro | Arg | His | Leu |



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 275                                                             | 280 | 285 |
| Pro Lys Glu Ala Val Lys Gln Leu Ser Arg Ala Val Glu Lys Arg Ser |     |     |
| 290                                                             | 295 | 300 |
| Arg Ala Lys Pro Val Gly Leu Pro Thr Ser Lys Leu                 |     |     |
| 305                                                             | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Pro | Phe | Lys | Pro | Asp | Val | Val | Arg | Gly | Gln | Val | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Thr | Gly | Gly | Gly | Ser | Gly | Ile | Gly | Phe | Glu | Ile | Ser | Ser | Gln | Phe |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gly | Lys | His | Gly | Ala | Ser | Ile | Ala | Ile | Met | Gly | Arg | Arg | Lys | Gln | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Asp | Ala | Val | Ser | Ala | Leu | Arg | Ser | Leu | Gly | Ile | Gln | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Glu | Gly | Asp | Val | Arg | Lys | Gln | Glu | Asp | Ala | Arg | Arg | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ala | Thr | Tyr | Gln | His | Phe | Gly | Lys | Leu | Asp | Ile | Leu | Val | Asn | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Gly | Asn | Phe | Leu | Ala | Ala | Ala | Glu | Asp | Leu | Ser | Pro | Asn | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Arg | Thr | Val | Leu | Asp | Ile | Asp | Ala | Val | Gly | Thr | Phe | Asn | Met | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| His | Ala | Ala | Leu | Lys | Tyr | Leu | Lys | Lys | Gly | Ala | Pro | Gly | Arg | Asp | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Gly | Gly | Gly | Ser | Ile | Ile | Asn | Ile | Ser | Ala | Thr | Leu | His | Tyr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Ala | Ser | Trp | Tyr | Gln | Ile | His | Val | Ser | Ala | Ala | Lys | Ala | Ala | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Ala | Thr | Thr | Arg | Asn | Leu | Ala | Leu | Glu | Trp | Gly | Thr | Asp | Tyr | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Arg | Val | Asn | Gly | Ile | Ala | Pro | Gly | Pro | Ile | Gly | Gly | Thr | Pro | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Met | Ser | Lys | Leu | Val | Pro | Glu | Glu | Ile | Glu | Asn | Lys | Thr | Arg | Glu | Tyr |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Pro | Leu | Tyr | Lys | Val | Gly | Glu | Lys | Trp | Asp | Ile | Ala | Met | Ala | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Tyr | Leu | Ser | Cys | Asp | Ser | Gly | Lys | Tyr | Val | Ser | Gly | Leu | Thr | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Val | Asp | Gly | Gly | Leu | Trp | Leu | Ser | Lys | Pro | Arg | His | Leu | Pro | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Ala | Val | Lys | Gln | Leu | Ser | Arg | Ala | Val | Glu | Lys | Arg | Ser | Arg | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Lys | Pro | Val | Gly | Leu | Pro | Thr | Ser | Lys | Leu |     |     |     |     |     |     |
|     |     | 290 |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..257  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571877  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

Met Gly Arg Arg Lys Gln Val Leu Asp Asp Ala Val Ser Ala Leu Arg  
1                  5                  10                  15  
Ser Leu Gly Ile Gln Ala Ile Gly Leu Glu Gly Asp Val Arg Lys Gln  
                  20                  25                  30  
Glu Asp Ala Arg Arg Val Val Glu Ala Thr Tyr Gln His Phe Gly Lys  
                  35                  40                  45  
Leu Asp Ile Leu Val Asn Ala Ala Ala Gly Asn Phe Leu Ala Ala Ala  
50                  55                  60  
Glu Asp Leu Ser Pro Asn Gly Phe Arg Thr Val Leu Asp Ile Asp Ala  
65                  70                  75                  80  
Val Gly Thr Phe Asn Met Cys His Ala Ala Leu Lys Tyr Leu Lys Lys  
                  85                  90                  95  
Gly Ala Pro Gly Arg Asp Ser Ser Ser Gly Gly Gly Ser Ile Ile Asn  
                  100                 105                 110  
Ile Ser Ala Thr Leu His Tyr Thr Ala Ser Trp Tyr Gln Ile His Val  
                 115                 120                 125  
Ser Ala Ala Lys Ala Ala Val Asp Ala Thr Thr Arg Asn Leu Ala Leu  
130                 135                 140  
Glu Trp Gly Thr Asp Tyr Asp Ile Arg Val Asn Gly Ile Ala Pro Gly  
145                 150                 155                 160  
Pro Ile Gly Gly Thr Pro Gly Met Ser Lys Leu Val Pro Glu Glu Ile  
                 165                 170                 175  
Glu Asn Lys Thr Arg Glu Tyr Met Pro Leu Tyr Lys Val Gly Glu Lys  
                 180                 185                 190  
Trp Asp Ile Ala Met Ala Ala Leu Tyr Leu Ser Cys Asp Ser Gly Lys  
195                 200                 205  
Tyr Val Ser Gly Leu Thr Met Val Val Asp Gly Gly Leu Trp Leu Ser  
210                 215                 220  
Lys Pro Arg His Leu Pro Lys Glu Ala Val Lys Gln Leu Ser Arg Ala  
225                 230                 235                 240  
Val Glu Lys Arg Ser Arg Ala Lys Pro Val Gly Leu Pro Thr Ser Lys  
                 245                 250                 255  
Leu

(2) INFORMATION FOR SEQ ID NO:2135:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1253 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1253  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571884  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| gaaacataat ttctaattgtc tcaattttctc ttttggtctct ccaaactctc tccccggaac | 60  |
| gatgtgctta tacagaagag cattcgtttg ttttcaacca gcccttattt gacacttggc    | 120 |
| actagggtta agaaaatttt gccggccggc tgcaaaattg gagatgttct tttgtttgac    | 180 |
| ccgaccaagg aagagatagt cacggtcccg gacaaaacaa ttcccgaaga gctcatggat    | 240 |
| gaagaaatga tgggagcttc ccatggatgg ggatttttct gtgaccggac tgaatggtcc    | 300 |
| gtacgtatca gcgacatttt caatcctttg gcatccaaaa caaacctgt catgattcct     | 360 |
| ctgcctaggc ttacggctct gccactggc caaacgaaa aagtttttaa cgtagccatg      | 420 |
| tccttctctt ctctctttgg tgaggaagac tgtgtagtgg ctatcaagtt ttcgggtatc    | 480 |
| cagctgagtc tgtgcagacc cggttgtgac cttgagtggga ctaacattgt aaccctttc    | 540 |

aactgtttgg acaactcaag tctcatgtat tccaaaagag accaaaaatt ttactttacct 600  
gcccctggag gcaactactt gttctcctat gacctccact tcaaatacaga tgactcccct 660  
gggctccatg agttgttcta tcgagaccat ccagtgttg atcagtcoga gtgggagctt 720  
ttgagttcat gttccaggac ggaatacctt gtggagtcac cttctgggtgg tgaccgtttT 780  
cctagtcaaa tggatatgcg ttggcttctt ttTcgtTcaa atttaaaagg aatctaccac 840  
aaaacaaaga gggtgatggg ttttagagaa gaggagacga cggaaggaaa aattatgtgt 900  
tacaccgagg acattggaga catgtgcatt ttccttgcaa gcaacgaggc tttctgtatc 960  
ccggctagct cctgcctcgg cctcaagcct aactgcgtct attatatggg acgtggcttt 1020  
ggtttttacg atctcactac cggagaggca catcattata aagctcccaa aggtgcacca 1080  
agegctctga ccgcccctta ctggcttcct ccatttgcta tctagtcata ctatttctgt 1140  
ctttgtgtac acttgaagtt tctctctacc ggtttaaatt ggtaacacct aaagattgtt 1200  
aatgttctaa gttcaatttt aagttaaaac atcccagacc agaatcccgt ctt

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1571885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

Met Ser Gln Phe Leu Phe Gly Leu Ser Lys Leu Ser Pro Arg Asn Asp  
1 5 10 15  
Val Leu Ile Gln Lys Ser Ile Arg Leu Phe Ser Thr Ser Pro Tyr Leu  
20 25 30  
Thr Leu Gly Thr Arg Val Lys Lys Ile Leu Pro Ala Gly Cys Lys Ile  
35 40 45  
Gly Asp Val Leu Leu Phe Asp Pro Thr Lys Glu Glu Ile Val Thr Val  
50 55 60  
Pro Asp Lys Thr Ile Pro Glu Glu Leu Met Asp Glu Glu Met Met Gly  
65 70 75 80  
Ala Ser His Gly Trp Gly Phe Phe Cys Asp Arg Thr Asp Arg Ser Val  
85 90 95  
Arg Ile Ser Asp Ile Phe Asn Pro Leu Ala Ser Lys Thr Asn Pro Val  
100 105 110  
Met Ile Pro Leu Pro Arg Leu Thr Ala Leu Pro Thr Gly Gln Thr Glu  
115 120 125  
Lys Val Phe Asn Val Ala Met Ser Phe Ser Ser Pro Leu Gly Glu Glu  
130 135 140  
Asp Cys Val Val Ala Ile Lys Phe Ser Gly Ile Gln Leu Ser Leu Cys  
145 150 155 160  
Arg Pro Gly Cys Asp Leu Glu Trp Thr Asn Ile Val Thr Pro Phe Asn  
165 170 175  
Cys Leu Asp Asn Ser Ser Leu Met Tyr Ser Lys Arg Asp Gln Lys Phe  
180 185 190  
Tyr Leu Pro Ala Pro Gly Gly Asn Tyr Leu Phe Ser Tyr Asp Leu His  
195 200 205  
Phe Lys Ser Asp Asp Ser Pro Gly Leu His Glu Leu Phe Tyr Arg Asp  
210 215 220  
His Pro Val Leu Asp Gln Ser Glu Trp Glu Leu Leu Ser Ser Cys Ser  
225 230 235 240  
Arg Thr Glu Tyr Leu Val Glu Ser Pro Ser Gly Gly Asp Arg Phe Pro  
245 250 255  
Ser Gln Met Val Cys Ala Trp Leu Leu Phe Arg Ser Asn Leu Lys Gly  
260 265 270  
Ile Tyr His Lys Thr Lys Arg Leu Met Val Phe Arg Glu Glu Glu Thr  
275 280 285  
Thr Glu Gly Lys Ile Met Cys Tyr Thr Glu Asp Ile Gly Asp Met Cys

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290 295 300  
Ile Phe Leu Ala Ser Asn Glu Ala Phe Cys Ile Pro Ala Ser Ser Cys  
305 310 315 320  
Leu Gly Leu Lys Pro Asn Cys Val Tyr Tyr Met Gly Arg Gly Phe Gly  
325 330 335  
Phe Tyr Asp Leu Thr Thr Gly Glu Ala His His Tyr Lys Ala Pro Lys  
340 345 350  
Gly Ala Pro Ser Ala Leu Thr Ala Pro Tyr Trp Leu Pro Pro Phe Ala  
355 360 365  
Ile

(2) INFORMATION FOR SEQ ID NO:2137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1571886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

Met Asp Glu Glu Met Met Gly Ala Ser His Gly Trp Gly Phe Phe Cys  
1 5 10 15  
Asp Arg Thr Asp Arg Ser Val Arg Ile Ser Asp Ile Phe Asn Pro Leu  
20 25 30  
Ala Ser Lys Thr Asn Pro Val Met Ile Pro Leu Pro Arg Leu Thr Ala  
35 40 45  
Leu Pro Thr Gly Gln Thr Glu Lys Val Phe Asn Val Ala Met Ser Phe  
50 55 60  
Ser Ser Pro Leu Gly Glu Glu Asp Cys Val Val Ala Ile Lys Phe Ser  
65 70 75 80  
Gly Ile Gln Leu Ser Leu Cys Arg Pro Gly Cys Asp Leu Glu Trp Thr  
85 90 95  
Asn Ile Val Thr Pro Phe Asn Cys Leu Asp Asn Ser Ser Leu Met Tyr  
100 105 110  
Ser Lys Arg Asp Gln Lys Phe Tyr Leu Pro Ala Pro Gly Gly Asn Tyr  
115 120 125  
Leu Phe Ser Tyr Asp Leu His Phe Lys Ser Asp Asp Ser Pro Gly Leu  
130 135 140  
His Glu Leu Phe Tyr Arg Asp His Pro Val Leu Asp Gln Ser Glu Trp  
145 150 155 160  
Glu Leu Leu Ser Ser Cys Ser Arg Thr Glu Tyr Leu Val Glu Ser Pro  
165 170 175  
Ser Gly Gly Asp Arg Phe Pro Ser Gln Met Val Cys Ala Trp Leu Leu  
180 185 190  
Phe Arg Ser Asn Leu Lys Gly Ile Tyr His Lys Thr Lys Arg Leu Met  
195 200 205  
Val Phe Arg Glu Glu Glu Thr Thr Glu Gly Lys Ile Met Cys Tyr Thr  
210 215 220  
Glu Asp Ile Gly Asp Met Cys Ile Phe Leu Ala Ser Asn Glu Ala Phe  
225 230 235 240  
Cys Ile Pro Ala Ser Ser Cys Leu Gly Leu Lys Pro Asn Cys Val Tyr  
245 250 255  
Tyr Met Gly Arg Gly Phe Gly Phe Tyr Asp Leu Thr Thr Gly Glu Ala  
260 265 270  
His His Tyr Lys Ala Pro Lys Gly Ala Pro Ser Ala Leu Thr Ala Pro  
275 280 285  
Tyr Trp Leu Pro Pro Phe Ala Ile  
290 295

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(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1571887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

Met Met Gly Ala Ser His Gly Trp Gly Phe Phe Cys Asp Arg Thr Asp  
1 5 10 15  
Arg Ser Val Arg Ile Ser Asp Ile Phe Asn Pro Leu Ala Ser Lys Thr  
20 25 30  
Asn Pro Val Met Ile Pro Leu Pro Arg Leu Thr Ala Leu Pro Thr Gly  
35 40 45  
Gln Thr Glu Lys Val Phe Asn Val Ala Met Ser Phe Ser Ser Pro Leu  
50 55 60  
Gly Glu Glu Asp Cys Val Val Ala Ile Lys Phe Ser Gly Ile Gln Leu  
65 70 75 80  
Ser Leu Cys Arg Pro Gly Cys Asp Leu Glu Trp Thr Asn Ile Val Thr  
85 90 95  
Pro Phe Asn Cys Leu Asp Asn Ser Ser Leu Met Tyr Ser Lys Arg Asp  
100 105 110  
Gln Lys Phe Tyr Leu Pro Ala Pro Gly Gly Asn Tyr Leu Phe Ser Tyr  
115 120 125  
Asp Leu His Phe Lys Ser Asp Ser Pro Gly Leu His Glu Leu Phe  
130 135 140  
Tyr Arg Asp His Pro Val Leu Asp Gln Ser Glu Trp Glu Leu Leu Ser  
145 150 155 160  
Ser Cys Ser Arg Thr Glu Tyr Leu Val Glu Ser Pro Ser Gly Gly Asp  
165 170 175  
Arg Phe Pro Ser Gln Met Val Cys Ala Trp Leu Leu Phe Arg Ser Asn  
180 185 190  
Leu Lys Gly Ile Tyr His Lys Thr Lys Arg Leu Met Val Phe Arg Glu  
195 200 205  
Glu Glu Thr Thr Glu Gly Lys Ile Met Cys Tyr Thr Glu Asp Ile Gly  
210 215 220  
Asp Met Cys Ile Phe Leu Ala Ser Asn Glu Ala Phe Cys Ile Pro Ala  
225 230 235 240  
Ser Ser Cys Leu Gly Leu Lys Pro Asn Cys Val Tyr Tyr Met Gly Arg  
245 250 255  
Gly Phe Gly Phe Tyr Asp Leu Thr Thr Gly Glu Ala His His Tyr Lys  
260 265 270  
Ala Pro Lys Gly Ala Pro Ser Ala Leu Thr Ala Pro Tyr Trp Leu Pro  
275 280 285  
Pro Phe Ala Ile  
290

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1312

(D) OTHER INFORMATION: / Ceres Seq. ID 1571888

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| (X1) SEQUENCE DESCRIPTION: SEQ 1: Nucleotide |            |             |            |            |            |      |
|----------------------------------------------|------------|-------------|------------|------------|------------|------|
| actctataaa                                   | cacacactct | caggagagaa  | gttgatttga | tctgtttctc | tttccctaaa | 60   |
| cacactgatt                                   | attttctctc | cagacgcgcc  | atgtctctgc | tctcagatct | cgttaacctc | 120  |
| aacctcaccg                                   | atgccaccgg | gaaaatcctc  | gccgaataca | tatggatcgg | tggatctgga | 180  |
| atggatatca                                   | gaagcaaagc | caggacacta  | ccaggaccag | tgactgatcc | atcaaagctt | 240  |
| cccaagtgga                                   | actacgacgg | atccagcacc  | ggtcaggctg | ctggagaaga | cagtgaagtc | 300  |
| attctatacc                                   | ctcaggcaat | attcaaggat  | cccttcagga | aaggcaacaa | catcctTggg | 360  |
| gatgtgtgat                                   | gcttacacac | cagctgggtga | tcctattcca | accaacaaga | ggcacaacgc | 420  |
| tgctaagatc                                   | ttcagccacc | ccgacgttgc  | caaggaggag | ccttggtatg | ggattgagca | 480  |
| agaatacact                                   | ttgatgcaaa | aggatgtgaa  | ctggccaatt | ggttggcctg | ttggtggcta | 540  |
| ccctggccct                                   | cagggacctt | actactgtgg  | tgtgggagct | gacaaagcca | ttggtcgtga | 600  |
| cattgtggat                                   | gtcactaca  | aggcctgtct  | ttacgcgggt | attggtattt | ctggtatcaa | 660  |
| tggagaagtc                                   | atgccaggcc | agtgggagtt  | ccaagtcggc | cctgttgagg | gtattagttc | 720  |
| tggtgatcaa                                   | gtctgggttg | ctcgatacct  | tctcgagagg | atcactgaga | tctctgggtg | 780  |
| aattgtcagc                                   | ttcgacccga | aaccagtcct  | gggtgactgg | aatggagctg | gagctcactg | 840  |
| caactacagc                                   | actaagacaa | tgagaaacga  | tggaggatta | gaagtgatca | agaaagcgat | 900  |
| agggaaagctt                                  | Tcagctgaaa | cacaaagaac  | acattgctgc | ttacggtgaa | ggaaacgagc | 960  |
| gtcgtctcac                                   | tggaaagcac | gaaaccgcag  | acatcaacac | attctcttgg | ggagtcgcga | 1020 |
| accgtggagc                                   | gtcagtgaga | gtgggacgtg  | acacagagaa | ggaaggtaaa | gggtacttcg | 1080 |
| aagacagaa                                    | gccagcttct | aacatgggat  | cttacgttgt | cacctccatg | atcgctgaga | 1140 |
| cgaccatact                                   | cggttgatga | cacatttcat  | gatttgattt | ctctccaatt | tggtttggtt | 1200 |
| tttttccctt                                   | gtgattgcac | tttttcgataa | taaaaaataa | attcttatta | tggcgtattg | 1260 |
| tttgtacatt                                   | ttgttatttg | tttcgaataa  | ttaaataagc | gcttcttaag | gt         |      |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..195  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

Met Gln Lys Asp Val Asn Trp Pro Ile Gly Trp Pro Val Gly Gly Tyr  
1 5 10 15  
Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala  
20 25 30  
Ile Gly Arg Asp Ile Val Asp Ala His Tyr Lys Ala Cys Leu Tyr Ala  
35 40 45  
Gly Ile Gly Ile Ser Gly Ile Asn Gly Glu Val Met Pro Gly Gln Trp  
50 55 60  
Glu Phe Gln Val Gly Pro Val Glu Gly Ile Ser Ser Gly Asp Gln Val  
65 70 75 80  
Trp Val Ala Arg Tyr Leu Leu Glu Arg Ile Thr Glu Ile Ser Gly Val  
85 90 95  
Ile Val Ser Phe Asp Pro Lys Pro Val Pro Gly Asp Trp Asn Gly Ala  
100 105 110  
Gly Ala His Cys Asn Tyr Ser Thr Lys Thr Met Arg Asn Asp Gly Gly  
115 120 125  
Leu Glu Val Ile Lys Lys Ala Ile Gly Lys Leu Ser Ala Glu Thr Gln  
130 135 140  
Arg Thr His Cys Cys Leu Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..657
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

ggtgggacca aaggaggagg ccatgggggc cttgacattg atgagctcat gaaacacagc 60  
aaaggaggag gaggaggtaa caaggGcaat cataatcata gcgccaaagg gattgggtgt 120  
ggcccaatgg gtccaggcgg tccgatgggt ccaggcggtc cgatgggtca aggtgggtccg 180  
atgggtatga tgggtccagg tgggtccgat agtatgatgg gtccaggcgg tcctatgggt 240  
ccaatgggtg gccaaaggcg ctcttaccga gcggttcaag gcttgccaat gagggtgggt 300  
ggaggatatt atccagggcc gcctcaggca agtcagcaaa tgaaccaaca acaatatatg 360  
caaagtatga tgaaccaaca gcagcaacaa caacaacaac aacaagctgc agctcatggt 420  
ggctatggcg gtggtcacgg tggcgacatg taccatccga tgatgtacgc tcggccttat 480  
cctgcagtta attatgctca cctccacca atgccgcctc ctactcgga ttcttatact 540  
catatgttca gcgatgagaa tccaggtagt ttagtattta tgtgatcatc ttttgtaagt 600  
ttatttagaa tatggacatg tatgcttgc ttagcttat gtttttttt tttgggg

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..194  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

Gly Gly Thr Lys Gly Gly Gly His Gly Gly Leu Asp Ile Asp Glu Leu  
1                  5                  10                  15  
Met Lys His Ser Lys Gly Gly Gly Gly Gly Asn Lys Gly Asn His Asn  
                  20                  25                  30  
His Ser Ala Lys Gly Ile Gly Gly Gly Pro Met Gly Pro Gly Gly Pro  
                  35                  40                  45  
Met Gly Pro Gly Gly Pro Met Gly Gln Gly Gly Pro Met Gly Met Met  
                  50                  55                  60  
Gly Pro Gly Gly Pro Met Ser Met Met Gly Pro Gly Gly Pro Met Gly  
65                  70                  75                  80  
Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro Ala Val Gln Gly Leu Pro  
                  85                  90                  95  
Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly Pro Pro Gln Ala Ser Gln  
                  100                 105                 110  
Gln Met Asn Gln Gln Gln Tyr Met Gln Met Met Met Asn Gln Gln Gln  
                 115                 120                 125  
Gln Gln Gln Gln Gln Gln Ala Ala Ala His Gly Gly Tyr Gly Gly  
                 130                 135                 140  
Gly His Gly Gly Asp Met Tyr His Pro Met Met Tyr Ala Arg Pro Tyr  
145                 150                 155                 160  
Pro Ala Val Asn Tyr Ala His Pro Pro Pro Met Pro Pro Pro His Ser  
                 165                 170                 175  
Asp Ser Tyr Thr His Met Phe Ser Asp Glu Asn Pro Gly Ser Cys Ser  
                 180                 185                 190  
Ile Met

(2) INFORMATION FOR SEQ ID NO:2144:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 178 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..178  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Met Lys His Ser Lys Gly Gly Gly Gly Gly Asn Lys Gly Asn His Asn  
1                  5                  10                  15  
His Ser Ala Lys Gly Ile Gly Gly Gly Pro Met Gly Pro Gly Gly Pro  
                  20                  25                  30  
Met Gly Pro Gly Gly Pro Met Gly Gln Gly Gly Pro Met Gly Met Met  
                  35                  40                  45  
Gly Pro Gly Gly Pro Met Ser Met Met Gly Pro Gly Gly Pro Met Gly  
                  50                  55                  60  
Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro Ala Val Gln Gly Leu Pro  
65                  70                  75                  80  
Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly Pro Pro Gln Ala Ser Gln  
                  85                  90                  95  
Gln Met Asn Gln Gln Gln Tyr Met Gln Met Met Met Asn Gln Gln Gln  
                 100                 105                 110  
Gln Gln Gln Gln Gln Gln Gln Ala Ala Ala His Gly Gly Tyr Gly Gly  
                 115                 120                 125  
Gly His Gly Gly Asp Met Tyr His Pro Met Met Tyr Ala Arg Pro Tyr

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|                                                                 |                                             |     |
|-----------------------------------------------------------------|---------------------------------------------|-----|
| 130                                                             | 135                                         | 140 |
| Pro Ala Val Asn Tyr                                             | Ala His Pro Pro Pro Met Pro Pro Pro His Ser |     |
| 145                                                             | 150                                         | 155 |
| Asp Ser Tyr Thr His Met Phe Ser Asp Glu Asn Pro Gly Ser Cys Ser |                                             | 160 |
|                                                                 | 165                                         | 170 |
|                                                                 |                                             | 175 |

Ile Met

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1571894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

Met Gly Pro Gly Gly Pro Met Gly Pro Gly Gly Pro Met Gly Gln Gly  
1 5 10 15  
Gly Pro Met Gly Met Met Gly Pro Gly Gly Pro Met Ser Met Met Gly  
20 25 30  
Pro Gly Gly Pro Met Gly Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro  
35 40 45  
Ala Val Gln Gly Leu Pro Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly  
50 55 60  
Pro Pro Gln Ala Ser Gln Gln Met Asn Gln Gln Gln Tyr Met Gln Met  
65 70 75 80  
Met Met Asn Gln Gln Gln Gln Gln Gln Gln Gln Ala Ala Ala  
85 90 95  
His Gly Gly Tyr Gly Gly Gly His Gly Gly Asp Met Tyr His Pro Met  
100 105 110  
Met Tyr Ala Arg Pro Tyr Pro Ala Val Asn Tyr Ala His Pro Pro Pro  
115 120 125  
Met Pro Pro Pro His Ser Asp Ser Tyr Thr His Met Phe Ser Asp Glu  
130 135 140  
Asn Pro Gly Ser Cys Ser Ile Met  
145 150

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1571898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaagcccaaa tggtgctcaa ggcttctccc gctctctctc tcttgagctc cggctccacc | 60  |
| ggcgggtGaa atctgtttcc tccgtcgaga aattcgtcga atcgtctggt ttctccgagt | 120 |
| ggatctaagt tttctgttca ggcggcgaaa ggaacgaaca cgaagtcgtt aaccggagtt | 180 |
| gtattcgaac cttttgagga agtgaagaaa gaactggacc tcgttcccac taccctttt  | 240 |
| gtttctctcg ctgcgcacaa gttctccgac gatgctgaat ctgccatcaa cgatcagatc | 300 |
| aacgtggagt acaacgtctc gtatgtctac catgccctgt atgcctactt tgacagagac | 360 |
| aatgtcggct tgaaggttt cgccaagttt tttaacgatt cgagtcttga agaacgaggt  | 420 |
| catgctgaga tgtttatgga gtatcagaac aagcgtggtg ggagagtgaa gctgcagttc | 480 |
| attttgatgc ccgtctctga gtttgatcac gaggagaagg gagatgcatt gcatgcgatg | 540 |
| gagcttgcat tgtctttgga gaaacttaca aatgaaaagc ttctgaagtt acaaagtgtt | 600 |

ggtgtgaaga acaatgatgt tcagctgggt gattttgtag aatctgagtt tctagggcag 660  
caggtcgaag ctatcaagaa aatctcagag tacgttgac agctaagaag aataggaaag 720  
ggtcatggag tgtggcattt tgatcaaagt cttctcaatg atgaggttta aggaaggaga 780  
gttcagcttc tgagtttgat gacaatcttc cttgtgctat atggcaccgt tctatctcta 840  
taacgacgtc tctaagtttg gtcggagaaa agtgttcttg ctcgttcttt cttttctttg 900  
tttttggtta accgaatgct tgtgagtgtg tacttaataa tgtaactcgt agtctgataa 960  
taaatacgaag tcccactggt tc

(2) INFORMATION FOR SEQ ID NO:2147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1571899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

Lys Ala Gln Met Leu Leu Lys Ala Ser Pro Ala Leu Ser Leu Leu Ser  
1 5 10 15  
Ser Gly Ser Thr Gly Gly Gly Asn Leu Phe Pro Pro Ser Arg Asn Ser  
20 25 30  
Ser Asn Arg Leu Phe Ser Pro Ser Gly Ser Lys Phe Ser Val Gln Ala  
35 40 45  
Ala Lys Gly Thr Asn Thr Lys Ser Leu Thr Gly Val Val Phe Glu Pro  
50 55 60  
Phe Glu Glu Val Lys Lys Glu Leu Asp Leu Val Pro Thr Thr Pro Phe  
65 70 75 80  
Val Ser Leu Ala Arg His Lys Phe Ser Asp Ala Glu Ser Ala Ile  
85 90 95  
Asn Asp Gln Ile Asn Val Glu Tyr Asn Val Ser Tyr Val Tyr His Ala  
100 105 110  
Leu Tyr Ala Tyr Phe Asp Arg Asp Asn Val Gly Leu Lys Gly Phe Ala  
115 120 125  
Lys Phe Phe Asn Asp Ser Ser Leu Glu Glu Arg Gly His Ala Glu Met  
130 135 140  
Phe Met Glu Tyr Gln Asn Lys Arg Gly Gly Arg Val Lys Leu Gln Ser  
145 150 155 160  
Ile Leu Met Pro Val Ser Glu Phe Asp His Glu Glu Lys Gly Asp Ala  
165 170 175  
Leu His Ala Met Glu Leu Ala Leu Ser Leu Glu Lys Leu Thr Asn Glu  
180 185 190  
Lys Leu Leu Lys Leu Gln Ser Val Gly Val Lys Asn Asn Asp Val Gln  
195 200 205  
Leu Val Asp Phe Val Glu Ser Glu Phe Leu Gly Glu Gln Val Glu Ala  
210 215 220  
Ile Lys Lys Ile Ser Glu Tyr Val Ala Gln Leu Arg Arg Ile Gly Lys  
225 230 235 240  
Gly His Gly Val Trp His Phe Asp Gln Met Leu Leu Asn Asp Glu Val  
245 250 255

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..253  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

Met Leu Leu Lys Ala Ser Pro Ala Leu Ser Leu Leu Ser Ser Gly Ser  
1 5 10 15  
Thr Gly Gly Gly Asn Leu Phe Pro Pro Ser Arg Asn Ser Ser Asn Arg  
20 25 30  
Leu Phe Ser Pro Ser Gly Ser Lys Phe Ser Val Gln Ala Ala Lys Gly  
35 40 45  
Thr Asn Thr Lys Ser Leu Thr Gly Val Val Phe Glu Pro Phe Glu Glu  
50 55 60  
Val Lys Lys Glu Leu Asp Leu Val Pro Thr Thr Pro Phe Val Ser Leu  
65 70 75 80  
Ala Arg His Lys Phe Ser Asp Asp Ala Glu Ser Ala Ile Asn Asp Gln  
85 90 95  
Ile Asn Val Glu Tyr Asn Val Ser Tyr Val Tyr His Ala Leu Tyr Ala  
100 105 110  
Tyr Phe Asp Arg Asp Asn Val Gly Leu Lys Gly Phe Ala Lys Phe Phe  
115 120 125  
Asn Asp Ser Ser Leu Glu Glu Arg Gly His Ala Glu Met Phe Met Glu  
130 135 140  
Tyr Gln Asn Lys Arg Gly Gly Arg Val Lys Leu Gln Ser Ile Leu Met  
145 150 155 160  
Pro Val Ser Glu Phe Asp His Glu Glu Lys Gly Asp Ala Leu His Ala  
165 170 175  
Met Glu Leu Ala Leu Ser Leu Glu Lys Leu Thr Asn Glu Lys Leu Leu  
180 185 190  
Lys Leu Gln Ser Val Gly Val Lys Asn Asn Asp Val Gln Leu Val Asp  
195 200 205  
Phe Val Glu Ser Glu Phe Leu Gly Glu Gln Val Glu Ala Ile Lys Lys  
210 215 220  
Ile Ser Glu Tyr Val Ala Gln Leu Arg Arg Ile Gly Lys Gly His Gly  
225 230 235 240  
Val Trp His Phe Asp Gln Met Leu Leu Asn Asp Glu Val  
245 250

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1275  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

aaacaagata caacacaatt ggaatctttc ttctttgaca aaaaaaaaag gaatctctct 60  
ctttctctga ttctotcatg tccatgcaac aagaaacgtc tcacatgacg gcggctccac 120  
agaccaacgg ccatcaaatt ttccctgaga ttgacatgtc cgccggcgat tcctcctcca 180  
tcgtacgagc tacagtcgtc caagcctcta cagtcttcta cgatactccc gccacgctag 240  
ataaggcaga gagactgctt tctgaggcag cggagaatgg atctcagcta gtgggtgttc 300  
cggaggcttt catcggtgga tatccacgtg gctctacctt tgaattggct attggttctc 360  
gtaccgctaa aggacgagat gactttcgca agtaccatgc ttctgccatt gatgttcttg 420  
gcctgaagt ggaacgaNtt agcgtaaatg gccaagaagt acaaagtata cttggttatg 480  
ggtgtgatag agagggaagg ctacacgcta tactgcaccg ttcttttctt cgattcacia 540  
ggtctgttct taggtaagca ccgcaaaact atgcctacag ctcttgaacg ttgcatttgg 600  
ggatttggag atggatcaac catccctgtg ttcgatactc ctattgggaa aatcggtgct 660  
gctatttgtt gggaaaatag gatgccttct ttgagaacog caatgtatgc caaaggcatt 720  
gagatttatt gtgcacctac tgctgattca agagaaactt ggctagcatc aatgactcat 780

```
attgcacttg aggggtggatg ttttgttttg tcagctaacc agttttgtcg tcggaaagac 840
tatectttctc cgccggaata catgttttcc gggtcagaag agagcctaac accggactct 900
gttggtctgcg ctgggtggaag ctctatcatt tcacctttgg gaattgtttt agctggacca 960
aactatagag gagaagctct tatcacagct gatctagatc ttggggacat agcacgagcc 1020
aagtttgatt ttgatgtggt cggacattac tcgaggcctg aagtgttttag cttgaacata 1080
agggagcatc cgagaaaagc ggtcagcttc aagacgtcaa aggtaatgga agatgaatcc 1140
gtctaacaaa tgatcatttg ttagacccaa actttctctg taatttgatg aagtttatct 1200
gtagtaaact tcaagacttg tggtgtaatt gaaatcgata aaaaatccaa accggttagat 1260
tgagtgttgt cttct
```

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1571906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

```
Met Thr Phe Ala Ser Thr Met Leu Leu Pro Leu Met Phe Leu Ala Leu
1 5 10 15
Lys Trp Asn Xaa Leu Ala Leu Met Ala Lys Lys Tyr Lys Val Tyr Leu
 20 25 30
Val Met Gly Val Ile Glu Arg Glu Gly Tyr Thr Leu Tyr Cys Thr Val
 35 40 45
Leu Phe Phe Asp Ser Gln Gly Leu Phe Leu Gly Lys His Arg Lys Leu
 50 55 60
Met Pro Thr Ala Leu Glu Arg Cys Ile Trp Gly Phe Gly Asp Gly Ser
 65 70 75 80
Thr Ile Pro Val Phe Asp Thr Pro Ile Gly Lys Ile Gly Ala Ala Ile
 85 90 95
Cys Trp Glu Asn Arg Met Pro Ser Leu Arg Thr Ala Met Tyr Ala Lys
 100 105 110
Gly Ile Glu Ile Tyr Cys Ala Pro Thr Ala Asp Ser Arg Glu Thr Trp
 115 120 125
Leu Ala Ser Met Thr His Ile Ala Leu Glu Gly Gly Cys Phe Val Leu
 130 135 140
Ser Ala Asn Gln Phe Cys Arg Arg Lys Asp Tyr Pro Ser Pro Pro Glu
 145 150 155 160
Tyr Met Phe Ser Gly Ser Glu Glu Ser Leu Thr Pro Asp Ser Val Val
 165 170 175
Cys Ala Gly Gly Ser Ser Ile Ile Ser Pro Leu Gly Ile Val Leu Ala
 180 185 190
Gly Pro Asn Tyr Arg Gly Glu Ala Leu Ile Thr Ala Asp Leu Asp Leu
 195 200 205
Gly Asp Ile Ala Arg Ala Lys Phe Asp Phe Asp Val Val Gly His Tyr
 210 215 220
Ser Arg Pro Glu Val Phe Ser Leu Asn Ile Arg Glu His Pro Arg Lys
 225 230 235 240
Ala Val Ser Phe Lys Thr Ser Lys Val Met Glu Asp Glu Ser Val
 245 250 255
```

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1571907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

Met Leu Leu Pro Leu Met Phe Leu Ala Leu Lys Trp Asn Xaa Leu Ala  
1 5 10 15  
Leu Met Ala Lys Lys Tyr Lys Val Tyr Leu Val Met Gly Val Ile Glu  
20 25 30  
Arg Glu Gly Tyr Thr Leu Tyr Cys Thr Val Leu Phe Phe Asp Ser Gln  
35 40 45  
Gly Leu Phe Leu Gly Lys His Arg Lys Leu Met Pro Thr Ala Leu Glu  
50 55 60  
Arg Cys Ile Trp Gly Phe Gly Asp Gly Ser Thr Ile Pro Val Phe Asp  
65 70 75 80  
Thr Pro Ile Gly Lys Ile Gly Ala Ala Ile Cys Trp Glu Asn Arg Met  
85 90 95  
Pro Ser Leu Arg Thr Ala Met Tyr Ala Lys Gly Ile Glu Ile Tyr Cys  
100 105 110  
Ala Pro Thr Ala Asp Ser Arg Glu Thr Trp Leu Ala Ser Met Thr His  
115 120 125  
Ile Ala Leu Glu Gly Gly Cys Phe Val Leu Ser Ala Asn Gln Phe Cys  
130 135 140  
Arg Arg Lys Asp Tyr Pro Ser Pro Pro Glu Tyr Met Phe Ser Gly Ser  
145 150 155 160  
Glu Glu Ser Leu Thr Pro Asp Ser Val Val Cys Ala Gly Gly Ser Ser  
165 170 175  
Ile Ile Ser Pro Leu Gly Ile Val Leu Ala Gly Pro Asn Tyr Arg Gly  
180 185 190  
Glu Ala Leu Ile Thr Ala Asp Leu Asp Leu Gly Asp Ile Ala Arg Ala  
195 200 205  
Lys Phe Asp Phe Asp Val Val Gly His Tyr Ser Arg Pro Glu Val Phe  
210 215 220  
Ser Leu Asn Ile Arg Glu His Pro Arg Lys Ala Val Ser Phe Lys Thr  
225 230 235 240  
Ser Lys Val Met Glu Asp Glu Ser Val  
245

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1571908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

Met Phe Leu Ala Leu Lys Trp Asn Xaa Leu Ala Leu Met Ala Lys Lys  
1 5 10 15  
Tyr Lys Val Tyr Leu Val Met Gly Val Ile Glu Arg Glu Gly Tyr Thr  
20 25 30  
Leu Tyr Cys Thr Val Leu Phe Phe Asp Ser Gln Gly Leu Phe Leu Gly  
35 40 45  
Lys His Arg Lys Leu Met Pro Thr Ala Leu Glu Arg Cys Ile Trp Gly  
50 55 60  
Phe Gly Asp Gly Ser Thr Ile Pro Val Phe Asp Thr Pro Ile Gly Lys  
65 70 75 80  
Ile Gly Ala Ala Ile Cys Trp Glu Asn Arg Met Pro Ser Leu Arg Thr  
85 90 95  
Ala Met Tyr Ala Lys Gly Ile Glu Ile Tyr Cys Ala Pro Thr Ala Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |     |     |     |     |     |     |     |     |     |     |
| Ser | Arg | Glu | Thr | Trp | Leu | Ala | Ser | Met | Thr | His | Ile | Ala | Leu | Glu | Gly |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Cys | Phe | Val | Leu | Ser | Ala | Asn | Gln | Phe | Cys | Arg | Arg | Lys | Asp | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Ser | Pro | Pro | Glu | Tyr | Met | Phe | Ser | Gly | Ser | Glu | Glu | Ser | Leu | Thr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Asp | Ser | Val | Val | Cys | Ala | Gly | Gly | Ser | Ser | Ile | Ile | Ser | Pro | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ile | Val | Leu | Ala | Gly | Pro | Asn | Tyr | Arg | Gly | Glu | Ala | Leu | Ile | Thr |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Asp | Leu | Asp | Leu | Gly | Asp | Ile | Ala | Arg | Ala | Lys | Phe | Asp | Phe | Asp |
|     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Val | Val | Gly | His | Tyr | Ser | Arg | Pro | Glu | Val | Phe | Ser | Leu | Asn | Ile | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | His | Pro | Arg | Lys | Ala | Val | Ser | Phe | Lys | Thr | Ser | Lys | Val | Met | Glu |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Asp | Glu | Ser | Val |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| tcaaaaagtc  | ctctctcggt  | caacttttctt | cttggtcccc | atcttcacaa | atcacaactc | 60   |
| ttGtttattt  | ccaaagacca  | aaaacctgag  | aacacaccgg | cgacctgaaa | atggaaactt | 120  |
| cctgttttac  | ccttctcggt  | ctccttgtct  | ccctctcctt | cttcctcact | ctctccgccc | 180  |
| aaatgaccgg  | aaacttcaac  | tgcagtggct  | caacctcgac | gtgtcaatct | ctcgttggtt | 240  |
| actcaagcaa  | gaacgcaaca  | acgttgcgca  | atatccaaac | cctttttgcc | gtcaagaacc | 300  |
| tccgctcgat  | cctcggagct  | aacaatctcc  | cactcaacac | ctcacgtgac | caacgcgtga | 360  |
| accogaatca  | agtcgtacgt  | gtcccaatcc  | attgctcttg | ctccaatgga | accggtgtct | 420  |
| cgaaccggga  | catcgaatac  | accatcaaga  | aagacgacat | actctctttc | gtcgcaactg | 480  |
| agattttcgg  | tggctctcgtt | acgtacgaga  | agatcagtga | ggttaacaaa | atccctgacc | 540  |
| cgaacaaaat  | cgaaatcggg  | caaaaagttt  | ggatcccttt | gccttgtagc | tgtgataaat | 600  |
| tgaacgggtga | ggatgttgtt  | cactacgcac  | atgtagtcaa | actagraagc | tctctcggtg | 660  |
| agatcgctgc  | tcagtttgga  | actgacaaca  | cgacgttggc | tcagctcaat | ggaatcattg | 720  |
| gtgactctca  | gcttcttgct  | gataaacctc  | tcgacgtccc | tctcaaagca | tgtagctctt | 780  |
| ctgtgaggaa  | cgactcgttg  | gatgcacctc  | tgtttctgtc | taacaactca | tacgtcttca | 840  |
| ctgcaaacaa  | ttgcgtcaag  | tgtacttgtg  | acgctttgaa | gaattggact | ttaagttgtc | 900  |
| aatcatcatc  | tgagattaag  | ccctcgaact  | ggcaaacctg | cccaccattt | tcacaatgtg | 960  |
| atcgagcttt  | gcttaacgcc  | tcttgacgac  | gacctcgtga | ttgcgtctat | gctggttact | 1020 |
| ccaaccaaac  | catcttcacc  | acagcttccc  | cagcttgctc | agattctgct | ggtcctggta | 1080 |
| actatgcata  | aacgctcagc  | tcaagcttca  | gtttcgtgat | tgtgttgatt | cagtgtgctc | 1140 |
| tgttttgtct  | ctgccttctc  | tagtaatgtt  | ttgttgtgtg | tttatgagtg | tatctaagta | 1200 |
| ctgttcggat  | taaaataaag  | acattgtttc  | acatgaagca | tcaggtcctt | gtaccattat | 1260 |
| tatactggaa  | acatttcagc  |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..350  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met Glu Thr Ser Cys Phe Thr Leu Leu Gly Leu Leu Val Ser Leu Ser  
1 5 10 15  
Phe Phe Leu Thr Leu Ser Ala Gln Met Thr Gly Asn Phe Asn Cys Ser  
20 25 30  
Gly Ser Thr Ser Thr Cys Gln Ser Leu Val Gly Tyr Ser Ser Lys Asn  
35 40 45  
Ala Thr Thr Leu Arg Asn Ile Gln Thr Leu Phe Ala Val Lys Asn Leu  
50 55 60  
Arg Ser Ile Leu Gly Ala Asn Asn Leu Pro Leu Asn Thr Ser Arg Asp  
65 70 75 80  
Gln Arg Val Asn Pro Asn Gln Val Val Arg Val Pro Ile His Cys Ser  
85 90 95  
Cys Ser Asn Gly Thr Gly Val Ser Asn Arg Asp Ile Glu Tyr Thr Ile  
100 105 110  
Lys Lys Asp Asp Ile Leu Ser Phe Val Ala Thr Glu Ile Phe Gly Gly  
115 120 125  
Leu Val Thr Tyr Glu Lys Ile Ser Glu Val Asn Lys Ile Pro Asp Pro  
130 135 140  
Asn Lys Ile Glu Ile Gly Gln Lys Phe Trp Ile Pro Leu Pro Cys Ser  
145 150 155 160  
Cys Asp Lys Leu Asn Gly Glu Asp Val Val His Tyr Ala His Val Val  
165 170 175  
Lys Leu Xaa Ser Ser Leu Gly Glu Ile Ala Ala Gln Phe Gly Thr Asp  
180 185 190  
Asn Thr Thr Leu Ala Gln Leu Asn Gly Ile Ile Gly Asp Ser Gln Leu  
195 200 205  
Leu Ala Asp Lys Pro Leu Asp Val Pro Leu Lys Ala Cys Ser Ser Ser  
210 215 220  
Val Arg Asn Asp Ser Leu Asp Ala Pro Leu Leu Leu Ser Asn Asn Ser  
225 230 235 240  
Tyr Val Phe Thr Ala Asn Asn Cys Val Lys Cys Thr Cys Asp Ala Leu  
245 250 255  
Lys Asn Trp Thr Leu Ser Cys Gln Ser Ser Ser Glu Ile Lys Pro Ser  
260 265 270  
Asn Trp Gln Thr Cys Pro Pro Phe Ser Gln Cys Asp Arg Ala Leu Leu  
275 280 285  
Asn Ala Ser Cys Arg Arg Pro Arg Asp Cys Val Tyr Ala Gly Tyr Ser  
290 295 300  
Asn Gln Thr Ile Phe Thr Thr Ala Ser Pro Ala Cys Pro Asp Ser Ala  
305 310 315 320  
Gly Pro Gly Asn Tyr Ala Ser Thr Leu Ser Ser Ser Phe Ser Phe Val  
325 330 335  
Ile Val Leu Ile Gln Cys Ala Leu Leu Cys Leu Cys Leu Leu  
340 345 350

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..326  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met Thr Gly Asn Phe Asn Cys Ser Gly Ser Thr Ser Thr Cys Gln Ser

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|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Leu Val Gly Tyr Ser Ser Lys Asn Ala Thr Thr Leu Arg Asn Ile Gln |     |     |     |
| 20                                                              | 25  | 30  |     |
| Thr Leu Phe Ala Val Lys Asn Leu Arg Ser Ile Leu Gly Ala Asn Asn |     |     |     |
| 35                                                              | 40  | 45  |     |
| Leu Pro Leu Asn Thr Ser Arg Asp Gln Arg Val Asn Pro Asn Gln Val |     |     |     |
| 50                                                              | 55  | 60  |     |
| Val Arg Val Pro Ile His Cys Ser Cys Ser Asn Gly Thr Gly Val Ser |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Asn Arg Asp Ile Glu Tyr Thr Ile Lys Lys Asp Asp Ile Leu Ser Phe |     |     |     |
| 85                                                              | 90  | 95  |     |
| Val Ala Thr Glu Ile Phe Gly Gly Leu Val Thr Tyr Glu Lys Ile Ser |     |     |     |
| 100                                                             | 105 | 110 |     |
| Glu Val Asn Lys Ile Pro Asp Pro Asn Lys Ile Glu Ile Gly Gln Lys |     |     |     |
| 115                                                             | 120 | 125 |     |
| Phe Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Leu Asn Gly Glu Asp |     |     |     |
| 130                                                             | 135 | 140 |     |
| Val Val His Tyr Ala His Val Val Lys Leu Xaa Ser Ser Leu Gly Glu |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Ile Ala Ala Gln Phe Gly Thr Asp Asn Thr Thr Leu Ala Gln Leu Asn |     |     |     |
| 165                                                             | 170 | 175 |     |
| Gly Ile Ile Gly Asp Ser Gln Leu Leu Ala Asp Lys Pro Leu Asp Val |     |     |     |
| 180                                                             | 185 | 190 |     |
| Pro Leu Lys Ala Cys Ser Ser Ser Val Arg Asn Asp Ser Leu Asp Ala |     |     |     |
| 195                                                             | 200 | 205 |     |
| Pro Leu Leu Leu Ser Asn Asn Ser Tyr Val Phe Thr Ala Asn Asn Cys |     |     |     |
| 210                                                             | 215 | 220 |     |
| Val Lys Cys Thr Cys Asp Ala Leu Lys Asn Trp Thr Leu Ser Cys Gln |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Ser Ser Ser Glu Ile Lys Pro Ser Asn Trp Gln Thr Cys Pro Pro Phe |     |     |     |
| 245                                                             | 250 | 255 |     |
| Ser Gln Cys Asp Arg Ala Leu Leu Asn Ala Ser Cys Arg Arg Pro Arg |     |     |     |
| 260                                                             | 265 | 270 |     |
| Asp Cys Val Tyr Ala Gly Tyr Ser Asn Gln Thr Ile Phe Thr Thr Ala |     |     |     |
| 275                                                             | 280 | 285 |     |
| Ser Pro Ala Cys Pro Asp Ser Ala Gly Pro Gly Asn Tyr Ala Ser Thr |     |     |     |
| 290                                                             | 295 | 300 |     |
| Leu Ser Ser Ser Phe Ser Phe Val Ile Val Leu Ile Gln Cys Ala Leu |     |     |     |
| 305                                                             | 310 | 315 | 320 |
| Leu Cys Leu Cys Leu                                             |     |     |     |
| 325                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..914
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acttcattag tctccaagaa gaaaacatct ctactctct aaaatacaca ctctcatcaa   | 60  |
| aaacotttctc ttcggttcag aagcattcaa gaatccatta tgagctcatc tgattccggt | 120 |
| aataacggcg ttaactcacg gatgtacttc cgtaaccga gtttcagcaa cgttatctta   | 180 |
| aacgataact ggagcgactt gccgttaagt gtcgacgatt ctcaagacat ggctatttac  | 240 |
| aacactctcc gtgatgccgt tagctccgcc tggacaccat ccgttcctcc cgttacctct  | 300 |
| ccggcgaggg aagataagcc tccggcgacg aaggcgagtg gctcacacgc gccgaggcag  | 360 |
| aaggggatgc agtacagagg agtgaggagg aggccgtggg ggaaattcgc ggcggagatt  | 420 |
| agggatccga agaagaacgg agctagggtt tggctcggga cttacgagac gccggaGgac  | 480 |



gcggcggtgg cgtacgaccg agcggcggtt cagctcagag gatcgaaagc taagctgaat 540  
tttcgcgatt tgattggttc ttgtaagtat gagccgggta ggattaggcc tcgccgtcgc 600  
tcgccggaac cgtcagtcctc cgatcagtta acgtcggagc agaagaggga aagccacgtg 660  
gatgacggca agtctagttt ggttgtagcg gagttggatt tcacggtgga tcagttttac 720  
ttcgatggta gtttattaat ggaccaatca gaatgttctt attctgataa tcggatataa 780  
ttagtttttaa gattaagcaa aatttgtcca acgagttttg ctgtatgaaa tatctatcga 840  
tgactcaaca ggttttgatc atgatcatat gtaatgtgat ggaaattaaa tattgacgtt 900  
tgtttttttc ttcc

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1571913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

Met Ser Ser Ser Ser Val Asn Asn Gly Val Asn Ser Arg Met Tyr  
1 5 10 15  
Phe Arg Asn Pro Ser Phe Ser Asn Val Ile Leu Asn Asp Asn Trp Ser  
20 25 30  
Asp Leu Pro Leu Ser Val Asp Asp Ser Gln Asp Met Ala Ile Tyr Asn  
35 40 45  
Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr Pro Ser Val Pro Pro  
50 55 60  
Val Thr Ser Pro Ala Glu Asp Lys Pro Pro Ala Thr Lys Ala Ser  
65 70 75 80  
Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln Tyr Arg Gly Val Arg  
85 90 95  
Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Lys  
100 105 110  
Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu Thr Pro Glu Asp Ala  
115 120 125  
Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu Arg Gly Ser Lys Ala  
130 135 140  
Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys Lys Tyr Glu Pro Val  
145 150 155 160  
Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro Ser Val Ser Asp Gln  
165 170 175  
Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val Asp Asp Gly Lys Ser  
180 185 190  
Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val Asp Gln Phe Tyr Phe  
195 200 205  
Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys Ser Tyr Ser Asp Asn  
210 215 220  
Arg Ile  
225

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1571914

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Met Tyr Phe Arg Asn Pro Ser Phe Ser Asn Val Ile Leu Asn Asp Asn  
1 5 10 15  
Trp Ser Asp Leu Pro Leu Ser Val Asp Asp Ser Gln Asp Met Ala Ile  
20 25 30  
Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr Pro Ser Val  
35 40 45  
Pro Pro Val Thr Ser Pro Ala Glu Glu Asp Lys Pro Pro Ala Thr Lys  
50 55 60  
Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln Tyr Arg Gly  
65 70 75 80  
Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro  
85 90 95  
Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu Thr Pro Glu  
100 105 110  
Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu Arg Gly Ser  
115 120 125  
Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys Lys Tyr Glu  
130 135 140  
Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro Ser Val Ser  
145 150 155 160  
Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val Asp Asp Gly  
165 170 175  
Lys Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val Asp Gln Phe  
180 185 190  
Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys Ser Tyr Ser  
195 200 205  
Asp Asn Arg Ile  
210

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

Met Ala Ile Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr  
1 5 10 15  
Pro Ser Val Pro Pro Val Thr Ser Pro Ala Glu Glu Asp Lys Pro Pro  
20 25 30  
Ala Thr Lys Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln  
35 40 45  
Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile  
50 55 60  
Arg Asp Pro Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu  
65 70 75 80  
Thr Pro Glu Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu  
85 90 95  
Arg Gly Ser Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys  
100 105 110  
Lys Tyr Glu Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro  
115 120 125  
Ser Val Ser Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val  
130 135 140  
Asp Asp Gly Lys Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val  
145 150 155 160

Asp Gln Phe Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys  
165 170 175  
Ser Tyr Ser Asp Asn Arg Ile  
180

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| atacgtttgc  | tgtcccacgt  | tgatcttggt | gtttactctc | tctctctcct | ccatcggcga | 60   |
| cgaccaccgg  | agatcagcgt  | caccgtacca | aaacatcatt | taccttcttt | aagatttggt | 120  |
| gttttttaat  | cagttgaatc  | ggaataaaat | atcgcatcag | agatgagtaa | cgagcttctc | 180  |
| accatcgatc  | ctgtcgacct  | tcaattccct | tttgaattga | agaagcagat | ctcttggtct | 240  |
| ctctatttgg  | gtaacaagac  | cgataattat | gtcgccttca | aggttaagac | gacgaatcca | 300  |
| aagaagtact  | gcggttaggcc | taatactggt | gttggttcac | ccagatcctc | ttctgaagtt | 360  |
| ttagtgacca  | tgcaagctca  | aaaggaagct | cctgctgata | tgcagtgtaa | agataagttc | 420  |
| ttgcttcaat  | gtgtagtcgc  | tagtcccggg | gccaccccca | aggatgttac | tcatgagatg | 480  |
| ttagcaaaag  | aggcagggca  | tcgagttgaa | gagactaaat | tgagagttgt | ctatgttgct | 540  |
| ccaccacgac  | caccatcacc  | ggttcgagaa | ggatctgaag | aGggctcttc | accgagggct | 600  |
| tctgtctctg  | ataatgggaa  | tgcttctgat | tttactgctg | ctccaagatt | tagcgcagac | 660  |
| agggttgatg  | ctcaggataa  | ttcatctgag | gcaagagctc | tggtcacaaa | actcaccgag | 720  |
| gaaaagaact  | ctgcggttca  | actgaacaac | aggcttcaac | aagaattgga | ccagttgagg | 780  |
| cgcgaaagca  | agagaagtaa  | gagtgggtga | atccctttca | tgtacgttct | tctggtcggc | 840  |
| ctaatecggtt | taatcctggg  | atacattatg | aagaggacat | gatacagatc | cttcaacaaa | 900  |
| atactccaaa  | agtctcaaa   | tgcttaaaaa | agcattgaaa | aggaaagaaa | tcaaattgtg | 960  |
| tgaggaggac  | aatcttctct  | tctgccttat | cgtcgtcatg | cacctttggt | taaaatctga | 1020 |
| acttagtgcg  | ttagaggatt  | tgtattacgg | ttccataag  | acttagaatt | gtcacaaaat | 1080 |
| ctcctttttc  | ctctctctta  | ttacaacttt | gtgtagtctt | aaacactttt | gttc       |      |

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Glu | Leu | Leu | Thr | Ile | Asp | Pro | Val | Asp | Leu | Gln | Phe | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Glu | Leu | Lys | Lys | Gln | Ile | Ser | Cys | Ser | Leu | Tyr | Leu | Gly | Asn | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Asp | Asn | Tyr | Val | Ala | Phe | Lys | Val | Lys | Thr | Thr | Asn | Pro | Lys | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Cys | Val | Arg | Pro | Asn | Thr | Gly | Val | Val | His | Pro | Arg | Ser | Ser | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Val | Leu | Val | Thr | Met | Gln | Ala | Gln | Lys | Glu | Ala | Pro | Ala | Asp | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Cys | Lys | Asp | Lys | Phe | Leu | Leu | Gln | Cys | Val | Val | Ala | Ser | Pro | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Thr | Pro | Lys | Asp | Val | Thr | His | Glu | Met | Phe | Ser | Lys | Glu | Ala | Gly |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:2162:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1571922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1571923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:  
Met Phe Ser Lys Glu Ala Gly His Arg Val Glu Glu Thr Lys Leu Arg  
1 5 10 15  
Val Val Tyr Val Ala Pro Pro Arg Pro Ser Pro Val Arg Glu Gly  
20 25 30  
Ser Glu Glu Gly Ser Ser Pro Arg Ala Ser Val Ser Asp Asn Gly Asn  
35 40 45  
Ala Ser Asp Phe Thr Ala Ala Pro Arg Phe Ser Ala Asp Arg Val Asp  
50 55 60  
Ala Gln Asp Asn Ser Ser Glu Ala Arg Ala Leu Val Thr Lys Leu Thr  
65 70 75 80  
Glu Glu Lys Asn Ser Ala Val Gln Leu Asn Asn Arg Leu Gln Gln Glu  
85 90 95  
Leu Asp Gln Leu Arg Arg Glu Ser Lys Arg Ser Lys Ser Gly Gly Ile  
100 105 110  
Pro Phe Met Tyr Val Leu Leu Val Gly Leu Ile Gly Leu Ile Leu Gly  
115 120 125  
Tyr Ile Met Lys Arg Thr  
130

(2) INFORMATION FOR SEQ ID NO:2164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1623
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

```
attttcgggt atcaaagcca caaaaccctg agaatggcgg cagctactca atttctctcc 60
caaccttcgt ctctcaatcc acaccaactg aagaaccaa cctcacaacg ctccagaagc 120
atccctgtct tgtctcttaa atccacattg aagccactta aacgcctctc cgtgaaagcc 180
gccgtcgttt cccaaaactc gtccaaaacc gtgacgaagt Tcgatcactg tttcaagaaa 240
tcatcagatg ggtttctcta ttgtgaagga actaaagttg aggatatcat ggagtcagt 300
gagagaagac ccttttactt atatagcaaa cctcagatca ctagaaacct cgaggcttat 360
aaagaagcat tgggaaggagt gagctctgtg attggttacg ctatcaaagc taataacaat 420
cttaagattt tggagcattt gagaagtta ggctgtggtg ctgtgctcgt tagtggaat 480
gagcttagac ttgctcttcg tgcctgttcc gatccacaa agtgcatttt caatggaat 540
ggcaagtctt tgggaagattt agttctagct gctcaagaag gtgttttcgt taatgtcgat 600
agtgaagttg acttgaataa cattgttgaa gcttcaagaa tttctggtta gcaggtcaat 660
gtactgctgc gtatcaatcc tgatgttgat cctcaggtgc atccatatgt tgctactggg 720
aacaagaact caaagtttgg tatcaggaac gagaagcttc aatggtttct ggatcaggtc 780
aaggcacatc ccaaagagct gaagcttggt ggagctcatt gccatctagg ctctaccatt 840
actaaggtgg atatattcag agatgcggca gttctcatga tagaatacat tgacgagatc 900
cggcgtcaag gttttgaagt tagttacttg aacattggtg gtggtttagg gattgattat 960
taccatgccg gcgctgtcct tcccacaccc atggatctca tcaacactgt aagagagctt 1020
gttctttcac gagacctgaa tctaataatc gagccaggga gatctctgat tgcaaacact 1080
tgctgtttcg tcaaccatgt aactgggtgtg aagacgaatg gaactaagaa cttcatagtc 1140
attgatggaa gtatggctga gcttatccgt cccagtcttt atgatgctta tcagcacatt 1200
gagttgggtc ctccctccacc ggctgaagca gaggttacca aattcgacgt agtgggtcct 1260
gtctgtgaat ctgctgattt cctgggcaaa gacagagagc ttcccactcc tccacaggga 1320
gctggctctg tggttcatga cgctggtgca tactgtatga gcatggcttc cacttacaat 1380
ctcaagatgc gtccctccga atactgggtt gaagaagatg ggtcgatcac taagataagg 1440
catgctgaga cattcgatga ccatttgcgt ttctttgaag gtctatgaac tcttagattt 1500
actcatcatt gttgcttttt tgattgaatt gtatgattat tcggaatcag gaccataatg 1560
atattgctgt tttagatttt cacattatgt gctttgattc aaagtcaatg aagtgatcat 1620
atg
```

(2) INFORMATION FOR SEQ ID NO:2165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..495  
(D) OTHER INFORMATION: / Ceres Seq. ID 1571928  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Gly | Tyr | Gln | Ser | His | Lys | Thr | Leu | Arg | Met | Ala | Ala | Ala | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Phe | Leu | Ser | Gln | Pro | Ser | Ser | Leu | Asn | Pro | His | Gln | Leu | Lys | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Thr | Ser | Gln | Arg | Ser | Arg | Ser | Ile | Pro | Val | Leu | Ser | Leu | Lys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Lys | Pro | Leu | Lys | Arg | Leu | Ser | Val | Lys | Ala | Ala | Val | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Asn | Ser | Ser | Lys | Thr | Val | Thr | Lys | Phe | Asp | His | Cys | Phe | Lys | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Ser | Ser | Asp | Gly | Phe | Leu | Tyr | Cys | Glu | Gly | Thr | Lys | Val | Glu | Asp | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Met | Glu | Ser | Val | Glu | Arg | Arg | Pro | Phe | Tyr | Leu | Tyr | Ser | Lys | Pro | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Arg | Asn | Leu | Glu | Ala | Tyr | Lys | Glu | Ala | Leu | Glu | Gly | Val | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Ile | Gly | Tyr | Ala | Ile | Lys | Ala | Asn | Asn | Asn | Leu | Lys | Ile | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | His | Leu | Arg | Ser | Leu | Gly | Cys | Gly | Ala | Val | Leu | Val | Ser | Gly | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Leu | Arg | Leu | Ala | Leu | Arg | Ala | Gly | Phe | Asp | Pro | Thr | Lys | Cys | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Phe | Asn | Gly | Asn | Gly | Lys | Ser | Leu | Glu | Asp | Leu | Val | Leu | Ala | Ala | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Gly | Val | Phe | Val | Asn | Val | Asp | Ser | Glu | Phe | Asp | Leu | Asn | Asn | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Glu | Ala | Ser | Arg | Ile | Ser | Gly | Lys | Gln | Val | Asn | Val | Leu | Leu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Asn | Pro | Asp | Val | Asp | Pro | Gln | Val | His | Pro | Tyr | Val | Ala | Thr | Gly |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Lys | Asn | Ser | Lys | Phe | Gly | Ile | Arg | Asn | Glu | Lys | Leu | Gln | Trp | Phe |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Leu | Asp | Gln | Val | Lys | Ala | His | Pro | Lys | Glu | Leu | Lys | Leu | Val | Gly | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Cys | His | Leu | Gly | Ser | Thr | Ile | Thr | Lys | Val | Asp | Ile | Phe | Arg | Asp |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Ala | Val | Leu | Met | Ile | Glu | Tyr | Ile | Asp | Glu | Ile | Arg | Arg | Gln | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Phe | Glu | Val | Ser | Tyr | Leu | Asn | Ile | Gly | Gly | Gly | Leu | Gly | Ile | Asp | Tyr |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Tyr | His | Ala | Gly | Ala | Val | Leu | Pro | Thr | Pro | Met | Asp | Leu | Ile | Asn | Thr |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Val | Arg | Glu | Leu | Val | Leu | Ser | Arg | Asp | Leu | Asn | Leu | Ile | Ile | Glu | Pro |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Gly | Arg | Ser | Leu | Ile | Ala | Asn | Thr | Cys | Cys | Phe | Val | Asn | His | Val | Thr |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Gly | Val | Lys | Thr | Asn | Gly | Thr | Lys | Asn | Phe | Ile | Val | Ile | Asp | Gly | Ser |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Met | Ala | Glu | Leu | Ile | Arg | Pro | Ser | Leu | Tyr | Asp | Ala | Tyr | Gln | His | Ile |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     | 400 |     |
| Glu | Leu | Val | Ser | Pro | Pro | Pro | Ala | Glu | Ala | Glu | Val | Thr | Lys | Phe | Asp |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Val | Val | Gly | Pro | Val | Cys | Glu | Ser | Ala | Asp | Phe | Leu | Gly | Lys | Asp | Arg |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Glu | Leu | Pro | Thr | Pro | Pro | Gln | Gly | Ala | Gly | Leu | Val | Val | His | Asp | Ala |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Gly | Ala | Tyr | Cys | Met | Ser | Met | Ala | Ser | Thr | Tyr | Asn | Leu | Lys | Met | Arg |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| Pro | Pro | Glu | Tyr | Trp | Val | Glu | Glu | Asp | Gly | Ser | Ile | Thr | Lys | Ile | Arg |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| His | Ala | Glu | Thr | Phe | Asp | Asp | His | Leu | Arg | Phe | Phe | Glu | Gly | Leu |     |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1571929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ala | Ala | Thr | Gln | Phe | Leu | Ser | Gln | Pro | Ser | Ser | Leu | Asn | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| His | Gln | Leu | Lys | Asn | Gln | Thr | Ser | Gln | Arg | Ser | Arg | Ser | Ile | Pro | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Ser | Leu | Lys | Ser | Thr | Leu | Lys | Pro | Leu | Lys | Arg | Leu | Ser | Val | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Ala | Val | Val | Ser | Gln | Asn | Ser | Ser | Lys | Thr | Val | Thr | Lys | Phe | Asp |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Cys | Phe | Lys | Lys | Ser | Ser | Asp | Gly | Phe | Leu | Tyr | Cys | Glu | Gly | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Lys | Val | Glu | Asp | Ile | Met | Glu | Ser | Val | Glu | Arg | Arg | Pro | Phe | Tyr | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Tyr | Ser | Lys | Pro | Gln | Ile | Thr | Arg | Asn | Leu | Glu | Ala | Tyr | Lys | Glu | Ala |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Glu | Gly | Val | Ser | Ser | Val | Ile | Gly | Tyr | Ala | Ile | Lys | Ala | Asn | Asn |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asn | Leu | Lys | Ile | Leu | Glu | His | Leu | Arg | Ser | Leu | Gly | Cys | Gly | Ala | Val |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Val | Ser | Gly | Asn | Glu | Leu | Arg | Leu | Ala | Leu | Arg | Ala | Gly | Phe | Asp |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Pro | Thr | Lys | Cys | Ile | Phe | Asn | Gly | Asn | Gly | Lys | Ser | Leu | Glu | Asp | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Leu | Ala | Ala | Gln | Glu | Gly | Val | Phe | Val | Asn | Val | Asp | Ser | Glu | Phe |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asp | Leu | Asn | Asn | Ile | Val | Glu | Ala | Ser | Arg | Ile | Ser | Gly | Lys | Gln | Val |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Asn | Val | Leu | Leu | Arg | Ile | Asn | Pro | Asp | Val | Asp | Pro | Gln | Val | His | Pro |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Tyr | Val | Ala | Thr | Gly | Asn | Lys | Asn | Ser | Lys | Phe | Gly | Ile | Arg | Asn | Glu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Lys | Leu | Gln | Trp | Phe | Leu | Asp | Gln | Val | Lys | Ala | His | Pro | Lys | Glu | Leu |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Lys | Leu | Val | Gly | Ala | His | Cys | His | Leu | Gly | Ser | Thr | Ile | Thr | Lys | Val |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asp | Ile | Phe | Arg | Asp | Ala | Ala | Val | Leu | Met | Ile | Glu | Tyr | Ile | Asp | Glu |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ile | Arg | Arg | Gln | Gly | Phe | Glu | Val | Ser | Tyr | Leu | Asn | Ile | Gly | Gly | Gly |  |
|     | 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |  |

Leu Gly Ile Asp Tyr Tyr His Ala Gly Ala Val Leu Pro Thr Pro Met  
305 310 315 320  
Asp Leu Ile Asn Thr Val Arg Glu Leu Val Leu Ser Arg Asp Leu Asn  
325 330 335  
Leu Ile Ile Glu Pro Gly Arg Ser Leu Ile Ala Asn Thr Cys Cys Phe  
340 345 350  
Val Asn His Val Thr Gly Val Lys Thr Asn Gly Thr Lys Asn Phe Ile  
355 360 365  
Val Ile Asp Gly Ser Met Ala Glu Leu Ile Arg Pro Ser Leu Tyr Asp  
370 375 380  
Ala Tyr Gln His Ile Glu Leu Val Ser Pro Pro Ala Glu Ala Glu  
385 390 395 400  
Val Thr Lys Phe Asp Val Val Gly Pro Val Cys Glu Ser Ala Asp Phe  
405 410 415  
Leu Gly Lys Asp Arg Glu Leu Pro Thr Pro Pro Gln Gly Ala Gly Leu  
420 425 430  
Val Val His Asp Ala Gly Ala Tyr Cys Met Ser Met Ala Ser Thr Tyr  
435 440 445  
Asn Leu Lys Met Arg Pro Pro Glu Tyr Trp Val Glu Glu Asp Gly Ser  
450 455 460  
Ile Thr Lys Ile Arg His Ala Glu Thr Phe Asp Asp His Leu Arg Phe  
465 470 475 480  
Phe Glu Gly Leu

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..399

(D) OTHER INFORMATION: / Ceres Seq. ID 1571930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

Met Glu Ser Val Glu Arg Arg Pro Phe Tyr Leu Tyr Ser Lys Pro Gln  
1 5 10 15  
Ile Thr Arg Asn Leu Glu Ala Tyr Lys Glu Ala Leu Glu Gly Val Ser  
20 25 30  
Ser Val Ile Gly Tyr Ala Ile Lys Ala Asn Asn Asn Leu Lys Ile Leu  
35 40 45  
Glu His Leu Arg Ser Leu Gly Cys Gly Ala Val Leu Val Ser Gly Asn  
50 55 60  
Glu Leu Arg Leu Ala Leu Arg Ala Gly Phe Asp Pro Thr Lys Cys Ile  
65 70 75 80  
Phe Asn Gly Asn Gly Lys Ser Leu Glu Asp Leu Val Leu Ala Ala Gln  
85 90 95  
Glu Gly Val Phe Val Asn Val Asp Ser Glu Phe Asp Leu Asn Asn Ile  
100 105 110  
Val Glu Ala Ser Arg Ile Ser Gly Lys Gln Val Asn Val Leu Leu Arg  
115 120 125  
Ile Asn Pro Asp Val Asp Pro Gln Val His Pro Tyr Val Ala Thr Gly  
130 135 140  
Asn Lys Asn Ser Lys Phe Gly Ile Arg Asn Glu Lys Leu Gln Trp Phe  
145 150 155 160  
Leu Asp Gln Val Lys Ala His Pro Lys Glu Leu Lys Leu Val Gly Ala  
165 170 175  
His Cys His Leu Gly Ser Thr Ile Thr Lys Val Asp Ile Phe Arg Asp  
180 185 190  
Ala Ala Val Leu Met Ile Glu Tyr Ile Asp Glu Ile Arg Arg Gln Gly



| Variable             | Mean | Standard deviation | Minimum | Maximum |
|----------------------|------|--------------------|---------|---------|
| Age                  | 34.5 | 10.5               | 20      | 55      |
| Gender               | 0.5  | 0.5                | 0       | 1       |
| Marital status       | 0.5  | 0.5                | 0       | 1       |
| Education            | 12.5 | 1.5                | 10      | 15      |
| Income               | 1.5  | 0.5                | 1       | 2       |
| Health status        | 0.5  | 0.5                | 0       | 1       |
| Smoking status       | 0.5  | 0.5                | 0       | 1       |
| Alcohol consumption  | 0.5  | 0.5                | 0       | 1       |
| Exercise frequency   | 0.5  | 0.5                | 0       | 1       |
| Stress level         | 0.5  | 0.5                | 0       | 1       |
| Sleep quality        | 0.5  | 0.5                | 0       | 1       |
| Work satisfaction    | 0.5  | 0.5                | 0       | 1       |
| Life satisfaction    | 0.5  | 0.5                | 0       | 1       |
| Overall health       | 0.5  | 0.5                | 0       | 1       |
| Physical health      | 0.5  | 0.5                | 0       | 1       |
| Mental health        | 0.5  | 0.5                | 0       | 1       |
| Social health        | 0.5  | 0.5                | 0       | 1       |
| Emotional health     | 0.5  | 0.5                | 0       | 1       |
| Behavioral health    | 0.5  | 0.5                | 0       | 1       |
| Environmental health | 0.5  | 0.5                | 0       | 1       |
| Occupational health  | 0.5  | 0.5                | 0       | 1       |
| Financial health     | 0.5  | 0.5                | 0       | 1       |
| Family health        | 0.5  | 0.5                | 0       | 1       |
| Community health     | 0.5  | 0.5                | 0       | 1       |
| National health      | 0.5  | 0.5                | 0       | 1       |
| Global health        | 0.5  | 0.5                | 0       | 1       |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..1383

- (D) OTHER INFORMATION: / Ceres Seq. ID 1571931

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:2100: |             |             |                                         |
|--------------------------------------------|-------------|-------------|-----------------------------------------|
| cgatttgctt                                 | ctaccatatg  | tgaacaaaagt | gagagagtgtg gacaatacca cattatatgc 60    |
| ttctcgaaca                                 | ctattcttcc  | tacgcgatga  | tagcaacattg aggcctgttg ccattgagtt 120   |
| aacttgctcca                                | ccaaatatca  | acaagcccca  | atggaaacaa gtcttcacgc caggctatga 180    |
| tgctacttca                                 | tgctggctat  | ggaatctggc  | taagactcat gctatctctc atgacgcgg 240     |
| ttatcatcaa                                 | cttatctccc  | attggttgag  | gactcatgca tgtacggagc catacataat 300    |
| agcggc aaat                                | agacaactaa  | gtgccatgca  | tcccatttat aggccttttg atcctcattt 360    |
| ccgctacacc                                 | atggaaatca  | acgctcgtgc  | acgccaaagt ctgtcaacg gaggcggaat 420     |
| cattgagact                                 | tgtttctggc  | ccgggaagta  | tgcattagag ctawkttcag ccgctctatgg 480   |
| taaactatgg                                 | aggtttgacc  | aggaaggctt  | acccgcggat ctcatcaaaa ggggggttggc 540   |
| tgaggaagat                                 | aagaccgcag  | aacatggagt  | acgtctgacg ataccagact atccatttgc 600    |
| aaatgatggt                                 | ctaataattgt | gggatgcaat  | taaagaatgg gtgacagact atgtgaaaca 660    |
| ttactatcct                                 | gatgaagaac  | tgatcacatc  | ggacgaggaa ctccaaggat ggtggagtga 720    |
| agtgcggaac                                 | ataggccacg  | gagacaagaa  | agacgaacct tgggtggcctg tctctaaaac 780   |
| acaagatgac                                 | ttgattggtg  | tggtaaactac | gattgcatgg gtcacctcag gtcaccatgc 840    |
| agctgtaaac                                 | tttggacaac  | ggatAatgga  | ggataccttcc ccaaccgacc aacgacaaca 900   |
| aggataaгаа                                 | tgccAaacgg  | aagatccgac  | agatgaagcc ttaaaagagt tctatgagtc 960    |
| gccagaaaaa                                 | gtgttgctaa  | gacataccca  | tgcagaaac aggcgacctt agtgatggtc 1020    |
| acgttggatc                                 | ttttatcaac  | acattcacct  | gacgaagagt acattggaga acaacaagaa 1080   |
| gcattcttggg                                | ccaatgagcc  | tgttatcaat  | gctgcatttg aaagattcaa aggcaagctc 1140   |
| caatatctag                                 | aaggagtgat  | agatgagaga  | aacgtgaaca ttactctaaa gaatagagct 1200   |
| ggagctgggtg                                | ttgttaagta  | tgagcttttg  | aagcctacct ctgagcatgg gtttaccgga 1260   |
| atgggtgttc                                 | cttatagtat  | ttctatttga  | tctattgcatt ttctttctca aaaatgcctt 1320  |
| cattaatttt                                 | ctgtatctct  | gtctcttctga | taaaaatgaat aaaacaaatg ctctctttgtc 1380 |

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:

Asp Leu Leu Leu Pro Tyr Val Asn Lys Val Arg Glu Leu Asp Asn Thr  
1 5 10 15  
Thr Leu Tyr Ala Ser Arg Thr Leu Phe Phe Leu Ser Asp Asp Ser Thr  
20 25 30  
Leu Arg Pro Val Ala Ile Glu Leu Thr Cys Pro Pro Asn Ile Asn Lys  
35 40 45  
Pro Gln Trp Lys Gln Val Phe Thr Pro Gly Tyr Asp Ala Thr Ser Cys  
50 55 60  
Trp Leu Trp Asn Leu Ala Lys Thr His Ala Ile Ser His Asp Ala Gly  
65 70 75 80  
Tyr His Gln Leu Ile Ser His Trp Leu Arg Thr His Ala Cys Thr Glu  
85 90 95  
Pro Tyr Ile Ile Ala Ala Asn Arg Gln Leu Ser Ala Met His Pro Ile  
100 105 110  
Tyr Arg Leu Leu His Pro His Phe Arg Tyr Thr Met Glu Ile Asn Ala  
115 120 125  
Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly Ile Ile Glu Thr Cys  
130 135 140  
Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa Ser Ala Val Tyr Gly  
145 150 155 160  
Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro Ala Asp Leu Ile Lys  
165 170 175  
Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu His Gly Val Arg Leu  
180 185 190  
Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly Leu Ile Leu Trp Asp  
195 200 205  
Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys His Tyr Tyr Pro Asp  
210 215 220  
Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln Gly Trp Trp Ser Glu  
225 230 235 240  
Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp Glu Pro Trp Trp Pro  
245 250 255  
Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val Val Thr Thr Ile Ala  
260 265 270  
Trp Val Thr Ser Gly His His Ala Val Asn Phe Gly Gln Arg Ile  
275 280 285  
Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln Gln Gly  
290 295 300

(2) INFORMATION FOR SEQ ID NO:2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571933

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

Met His Pro Ile Tyr Arg Leu Leu His Pro His Phe Arg Tyr Thr Met  
1 5 10 15  
Glu Ile Asn Ala Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly Ile  
20 25 30  
Ile Glu Thr Cys Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa Ser  
35 40 45  
Ala Val Tyr Gly Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro Ala  
50 55 60  
Asp Leu Ile Lys Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu His  
65 70 75 80  
Gly Val Arg Leu Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly Leu  
85 90 95  
Ile Leu Trp Asp Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys His  
100 105 110  
Tyr Tyr Pro Asp Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln Gly  
115 120 125  
Trp Trp Ser Glu Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp Glu  
130 135 140  
Pro Trp Trp Pro Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val Val  
145 150 155 160  
Thr Thr Ile Ala Trp Val Thr Ser Gly His His Ala Ala Val Asn Phe  
165 170 175  
Gly Gln Arg Ile Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln Gln  
180 185 190  
Gly

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

Met Glu Ile Asn Ala Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly  
1 5 10 15  
Ile Ile Glu Thr Cys Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa  
20 25 30  
Ser Ala Val Tyr Gly Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro  
35 40 45  
Ala Asp Leu Ile Lys Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu  
50 55 60  
His Gly Val Arg Leu Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly  
65 70 75 80  
Leu Ile Leu Trp Asp Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys  
85 90 95  
His Tyr Tyr Pro Asp Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln  
100 105 110  
Gly Trp Trp Ser Glu Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp  
115 120 125  
Glu Pro Trp Trp Pro Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val  
130 135 140  
Val Thr Thr Ile Ala Trp Val Thr Ser Gly His His Ala Ala Val Asn  
145 150 155 160  
Phe Gly Gln Arg Ile Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln  
165 170 175

Gln Gly

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

|                                                                      |      |
|----------------------------------------------------------------------|------|
| gtgctgttcgt agagactgta ataaagacgg agagattcctt ctagagtcag ttctttcttct | 60   |
| tcattcctctt cttcccccca aatcctctctt cgctagggtt tctcattcog atccataatt  | 120  |
| ctagatgtcg aggtttttta ctgagacctg tcaaataagc taaagcttct tctaagagct    | 180  |
| tcaaggaaag cattgcattg ttgtagtctt gtttgtgtcc acagaaggaa agaagagtga    | 240  |
| gaagctcagg atgtcaagca gtcgaaatac ccactgggtg cacagatgtc agcgtgctgt    | 300  |
| ccgccttcac ggccaagagc ctgtatgtct ttattgcgga ggtggatttg ttgaagaact    | 360  |
| tgatatggct caagccagcc cctttgatat gtttagatcc cacaggggtg ttgtagaacg    | 420  |
| tgatcagact tttgatctca tggatgcttt ctctgtgttt atgaggaacc gcttagctga    | 480  |
| aaggagccac gacagagaaa tcagaggaag aaccatcagt tcaggtcctg aaaactttcc    | 540  |
| tggctctggc cctttgttga tctttgggtg tcaagtccct tatagactaa ctggcgacaa    | 600  |
| tgcagtcgaa gccctcttca atggcggctc ccctggcatt ggcacacac gtggtaacac     | 660  |
| cggcgactac ttcttcggtc ccggccttga agaattgttc gagcaGctt cagctggcac     | 720  |
| tactcgccga ggcccaccac ccgcaccgag atcagcaata gacgcattgc caactatcaa    | 780  |
| gatcgcgagc aggcattctta ggatcatcgga ctcaaatgtt cccgtgtgca aagacgaatt  | 840  |
| cgaactggga tcagaagcga aacagatgcc gtgtaaccac atctatcatt ctgactgcat    | 900  |
| tgtcccgtgg ctggttcagc acaactcttg cccggtctgt cgccaagagc taccatcagc    | 960  |
| tagcggacct tcaagcagtc aaaacagAAC caccctacc agaaactaca gaagcagtag     | 1020 |
| tagtagtagt agtagtaaca gtcgtgagaa cggaatgaa agaaggaatc ctttctcttc     | 1080 |
| cttctggcca ttccgttcgt caggttcaag ctcaagctcc actcaaaacc gtggaggcac    | 1140 |
| aagaaactcg gatacaagcg atgagaacca taactaccat caacagcaac atcaacaatc    | 1200 |
| atatatgggt tacagtggct ggccttttg                                      |      |

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Ser Ser Arg Asn Thr His Trp Cys His Arg Cys Gln Arg Ala |  |
| 1 5 10 15                                                       |  |
| Val Arg Leu His Gly Gln Glu Pro Val Cys Ser Tyr Cys Gly Gly Gly |  |
| 20 25 30                                                        |  |
| Phe Val Glu Glu Leu Asp Met Ala Gln Ala Ser Pro Phe Asp Met Phe |  |
| 35 40 45                                                        |  |
| Arg Ser His Arg Gly Val Val Glu Arg Asp Gln Thr Phe Asp Leu Met |  |
| 50 55 60                                                        |  |
| Asp Ala Phe Ser Val Phe Met Arg Asn Arg Leu Ala Glu Arg Ser His |  |
| 65 70 75 80                                                     |  |
| Asp Arg Glu Ile Arg Gly Arg Thr Ile Ser Ser Gly Pro Glu Asn Phe |  |
| 85 90 95                                                        |  |
| Pro Gly Leu Ala Pro Leu Leu Ile Phe Gly Gly Gln Val Pro Tyr Arg |  |
| 100 105 110                                                     |  |

Leu Thr Gly Asp Asn Ala Val Glu Ala Leu Phe Asn Gly Gly Ser Pro  
115 120 125  
Gly Ile Gly Ile Thr Arg Gly Asn Thr Gly Asp Tyr Phe Phe Gly Pro  
130 135 140  
Gly Leu Glu Glu Leu Phe Glu Gln Leu Ser Ala Gly Thr Thr Arg Arg  
145 150 155 160  
Gly Pro Pro Pro Ala Pro Arg Ser Ala Ile Asp Ala Leu Pro Thr Ile  
165 170 175  
Lys Ile Ala Gln Arg His Leu Arg Ser Ser Asp Ser Asn Cys Pro Val  
180 185 190  
Cys Lys Asp Glu Phe Glu Leu Gly Ser Glu Ala Lys Gln Met Pro Cys  
195 200 205  
Asn His Ile Tyr His Ser Asp Cys Ile Val Pro Trp Leu Val Gln His  
210 215 220  
Asn Ser Cys Pro Val Cys Arg Gln Glu Leu Pro Ser Ala Ser Gly Pro  
225 230 235 240  
Ser Ser Ser Gln Asn Arg Thr Thr Pro Thr Arg Asn Tyr Arg Ser Ser  
245 250 255  
Ser Ser Ser Ser Ser Ser Asn Ser Arg Glu Asn Gly Asn Glu Arg Arg  
260 265 270  
Asn Pro Phe Ser Ser Phe Trp Pro Phe Arg Ser Ser Gly Ser Ser Ser  
275 280 285  
Ser Ser Thr Gln Asn Arg Gly Gly Thr Arg Asn Ser Asp Thr Ser Asp  
290 295 300  
Glu Asn His Asn Tyr His Gln Gln Gln His Gln Gln Ser Tyr Met Gly  
305 310 315 320  
Tyr Ser Gly Trp Pro Phe  
325

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..288
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

Met Ala Gln Ala Ser Pro Phe Asp Met Phe Arg Ser His Arg Gly Val  
1 5 10 15  
Val Glu Arg Asp Gln Thr Phe Asp Leu Met Asp Ala Phe Ser Val Phe  
20 25 30  
Met Arg Asn Arg Leu Ala Glu Arg Ser His Asp Arg Glu Ile Arg Gly  
35 40 45  
Arg Thr Ile Ser Ser Gly Pro Glu Asn Phe Pro Gly Leu Ala Pro Leu  
50 55 60  
Leu Ile Phe Gly Gly Gln Val Pro Tyr Arg Leu Thr Gly Asp Asn Ala  
65 70 75 80  
Val Glu Ala Leu Phe Asn Gly Gly Ser Pro Gly Ile Gly Ile Thr Arg  
85 90 95  
Gly Asn Thr Gly Asp Tyr Phe Phe Gly Pro Gly Leu Glu Glu Leu Phe  
100 105 110  
Glu Gln Leu Ser Ala Gly Thr Thr Arg Arg Gly Pro Pro Ala Pro  
115 120 125  
Arg Ser Ala Ile Asp Ala Leu Pro Thr Ile Lys Ile Ala Gln Arg His  
130 135 140  
Leu Arg Ser Ser Asp Ser Asn Cys Pro Val Cys Lys Asp Glu Phe Glu  
145 150 155 160  
Leu Gly Ser Glu Ala Lys Gln Met Pro Cys Asn His Ile Tyr His Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Cys | Ile | Val | Pro | Trp | Leu | Val | Gln | His | Asn | Ser | Cys | Pro | Val | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Gln | Glu | Leu | Pro | Ser | Ala | Ser | Gly | Pro | Ser | Ser | Ser | Gln | Asn | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Thr | Pro | Thr | Arg | Asn | Tyr | Arg | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Asn | Ser | Arg | Glu | Asn | Gly | Asn | Glu | Arg | Arg | Asn | Pro | Phe | Ser | Ser | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Trp | Pro | Phe | Arg | Ser | Ser | Gly | Ser | Ser | Ser | Ser | Ser | Thr | Gln | Asn | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Gly | Gly | Thr | Arg | Asn | Ser | Asp | Thr | Ser | Asp | Glu | Asn | His | Asn | Tyr | His |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Gln | Gln | Gln | His | Gln | Gln | Ser | Tyr | Met | Gly | Tyr | Ser | Gly | Trp | Pro | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1571938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Arg | Ser | His | Arg | Gly | Val | Val | Glu | Arg | Asp | Gln | Thr | Phe | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Met | Asp | Ala | Phe | Ser | Val | Phe | Met | Arg | Asn | Arg | Leu | Ala | Glu | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | His | Asp | Arg | Glu | Ile | Arg | Gly | Arg | Thr | Ile | Ser | Ser | Gly | Pro | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Phe | Pro | Gly | Leu | Ala | Pro | Leu | Leu | Ile | Phe | Gly | Gly | Gln | Val | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Tyr | Arg | Leu | Thr | Gly | Asp | Asn | Ala | Val | Glu | Ala | Leu | Phe | Asn | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Ser | Pro | Gly | Ile | Gly | Ile | Thr | Arg | Gly | Asn | Thr | Gly | Asp | Tyr | Phe | Phe |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Gly | Pro | Gly | Leu | Glu | Glu | Leu | Phe | Glu | Gln | Leu | Ser | Ala | Gly | Thr | Thr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Arg | Arg | Gly | Pro | Pro | Pro | Ala | Pro | Arg | Ser | Ala | Ile | Asp | Ala | Leu | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Ile | Lys | Ile | Ala | Gln | Arg | His | Leu | Arg | Ser | Ser | Asp | Ser | Asn | Cys |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Pro | Val | Cys | Lys | Asp | Glu | Phe | Glu | Leu | Gly | Ser | Glu | Ala | Lys | Gln | Met |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Pro | Cys | Asn | His | Ile | Tyr | His | Ser | Asp | Cys | Ile | Val | Pro | Trp | Leu | Val |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Gln | His | Asn | Ser | Cys | Pro | Val | Cys | Arg | Gln | Glu | Leu | Pro | Ser | Ala | Ser |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Gly | Pro | Ser | Ser | Ser | Gln | Asn | Arg | Thr | Thr | Pro | Thr | Arg | Asn | Tyr | Arg |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Asn | Ser | Arg | Glu | Asn | Gly | Asn | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Arg | Arg | Asn | Pro | Phe | Ser | Ser | Phe | Trp | Pro | Phe | Arg | Ser | Ser | Gly | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Ser | Ser | Ser | Thr | Gln | Asn | Arg | Gly | Gly | Thr | Arg | Asn | Ser | Asp | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

Ser Asp Glu Asn His Asn Tyr His Gln Gln Gln His Gln Gln Ser Tyr  
260 265 270  
Met Gly Tyr Ser Gly Trp Pro Phe  
275 280

(2) INFORMATION FOR SEQ ID NO:2176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1430
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

ctaaactaaa atctaaatct tgccttcctg actttctctc tacgacagaa tttttgaagc 60  
ttctctctgc ttatcgacac tatggttctc gaggcgacta tgatatgtat cgacaactcc 120  
gagtggatgc gaaacggaga ttactctccg tctaggttac aggcgcaaac ggaagctggt 180  
aatcttcttt gcggaGccaa aaccagctcg aatccggaga atacggtggg gattttgaca 240  
atggctggca aaggagttag agtattgact actcctacct ctgatcttgg caaaattctg 300  
gcctgtatgc acggccttga tgtgggagga gagatcaact taaccgcagc tatccagatc 360  
gcccagctag ctcttaagca tcgccaaaac aagaatcaac gccaaaggat tattgttttt 420  
gctggaagtc caatcaagta cgagaagaag gccctagaga tagttggaaa aaggctgaag 480  
aagaatagtg tatctcttga tattgtcaat ttcggggagg atgatgatga ggaaaagcct 540  
cagaaactcg aggccctcct tacagctgtg aataacaatg acggtagcca cattgttcat 600  
gttccttctg gagccaatgc tctctcagat gtgcttctca gcacacctgt attcacgggt 660  
gatgaggggt caagtggcta tgtttctgcg gcagctgctg cagcgggccg aggtggggac 720  
ttcgactttg gtgtggaccc aaatatcgat ccagaacttg ctcttgccct tcgggtctcc 780  
atggaggagg agagagcaag acaagaagct gctgccaaag aggcggccga tgaggcatgt 840  
cagaaagaca aagatgggga cacagcttcc gcctcacagg agacagttgc taggacaact 900  
gacaagaacg ctgaaccaat ggatgaggac agtgcggtgc tagatcaggc aattgctatg 960  
tctggtggtg atgtgaatat gtcagaagcg gctgatgagg accaggatct ggctttagct 1020  
ctgcaaatgt caatgagtgg ggaagagtca agtgaagcta caggtgctgg aaacaacctc 1080  
ttgggaaatc aagccttcat atcgtctgtt ctctcatcgc ttcttggggg ggatccaaat 1140  
gatccggcag ttaaagaact actagcgtct ctgccagacg agtcaaagcg tcacgaggag 1200  
gaagagagta gtagcaaaaa aggcgaggat gagaagaagt gaasaaggat ctgagagctc 1260  
caataaaaaat tcctcttgyt tcttttggtt gatagagatt ggaactgaat ttaactaatc 1320  
tctctgcctt gtgaaatttg gttttttctc tctctctcgc ctttttataa tgttggttatt 1380  
gtacgagtca aggactagct tccttcttaa tttttattgg actttatgcc

(2) INFORMATION FOR SEQ ID NO:2177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

Met Val Leu Glu Ala Thr Met Ile Cys Ile Asp Asn Ser Glu Trp Met  
1 5 10 15  
Arg Asn Gly Asp Tyr Ser Pro Ser Arg Leu Gln Ala Gln Thr Glu Ala  
20 25 30  
Val Asn Leu Leu Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn Thr  
35 40 45  
Val Gly Ile Leu Thr Met Ala Gly Lys Gly Val Arg Val Leu Thr Thr  
50 55 60  
Pro Thr Ser Asp Leu Gly Lys Ile Leu Ala Cys Met His Gly Leu Asp

65 70 75 80  
Val Gly Gly Glu Ile Asn Leu Thr Ala Ala Ile Gln Ile Ala Gln Leu  
85 90 95  
Ala Leu Lys His Arg Gln Asn Lys Asn Gln Arg Gln Arg Ile Ile Val  
100 105 110  
Phe Ala Gly Ser Pro Ile Lys Tyr Glu Lys Lys Ala Leu Glu Ile Val  
115 120 125  
Gly Lys Arg Leu Lys Lys Asn Ser Val Ser Leu Asp Ile Val Asn Phe  
130 135 140  
Gly Glu Asp Asp Asp Glu Glu Lys Pro Gln Lys Leu Glu Ala Leu Leu  
145 150 155 160  
Thr Ala Val Asn Asn Asn Asp Gly Ser His Ile Val His Val Pro Ser  
165 170 175  
Gly Ala Asn Ala Leu Ser Asp Val Leu Leu Ser Thr Pro Val Phe Thr  
180 185 190  
Gly Asp Glu Gly Ala Ser Gly Tyr Val Ser Ala Ala Ala Ala Ala Ala  
195 200 205  
Ala Ala Gly Gly Asp Phe Asp Phe Gly Val Asp Pro Asn Ile Asp Pro  
210 215 220  
Glu Leu Ala Leu Ala Leu Arg Val Ser Met Glu Glu Arg Ala Arg  
225 230 235 240  
Gln Glu Ala Ala Ala Lys Lys Ala Ala Asp Glu Ala Cys Gln Lys Asp  
245 250 255  
Lys Asp Gly Asp Thr Ala Ser Ala Ser Gln Glu Thr Val Ala Arg Thr  
260 265 270  
Thr Asp Lys Asn Ala Glu Pro Met Asp Glu Asp Ser Ala Leu Leu Asp  
275 280 285  
Gln Ala Ile Ala Met Ser Xaa Gly Asp Val Asn Met Ser Glu Ala Ala  
290 295 300  
Asp Glu Asp Gln Asp Leu Ala Leu Ala Leu Gln Met Ser Met Ser Gly  
305 310 315 320  
Glu Glu Ser Ser Glu Ala Thr Gly Ala Gly Asn Asn Leu Leu Gly Asn  
325 330 335  
Gln Ala Phe Ile Ser Ser Val Leu Ser Ser Leu Pro Gly Val Asp Pro  
340 345 350  
Asn Asp Pro Ala Val Lys Glu Leu Leu Ala Ser Leu Pro Asp Glu Ser  
355 360 365  
Lys Arg His Glu Glu Glu Glu Ser Ser Ser Lys Lys Gly Glu Asp Glu  
370 375 380  
Lys Lys  
385

(2) INFORMATION FOR SEQ ID NO:2178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1571947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:

Met Ile Cys Ile Asp Asn Ser Glu Trp Met Arg Asn Gly Asp Tyr Ser  
1 5 10 15  
Pro Ser Arg Leu Gln Ala Gln Thr Glu Ala Val Asn Leu Leu Cys Gly  
20 25 30  
Ala Lys Thr Gln Ser Asn Pro Glu Asn Thr Val Gly Ile Leu Thr Met  
35 40 45  
Ala Gly Lys Gly Val Arg Val Leu Thr Thr Pro Thr Ser Asp Leu Gly  
50 55 60



Lys Ile Leu Ala Cys Met His Gly Leu Asp Val Gly Gly Glu Ile Asn  
65 70 75 80  
Leu Thr Ala Ala Ile Gln Ile Ala Gln Leu Ala Leu Lys His Arg Gln  
85 90 95  
Asn Lys Asn Gln Arg Gln Arg Ile Ile Val Phe Ala Gly Ser Pro Ile  
100 105 110  
Lys Tyr Glu Lys Lys Ala Leu Glu Ile Val Gly Lys Arg Leu Lys Lys  
115 120 125  
Asn Ser Val Ser Leu Asp Ile Val Asn Phe Gly Glu Asp Asp Asp Glu  
130 135 140  
Glu Lys Pro Gln Lys Leu Glu Ala Leu Leu Thr Ala Val Asn Asn Asn  
145 150 155 160  
Asp Gly Ser His Ile Val His Val Pro Ser Gly Ala Asn Ala Leu Ser  
165 170 175  
Asp Val Leu Leu Ser Thr Pro Val Phe Thr Gly Asp Glu Gly Ala Ser  
180 185 190  
Gly Tyr Val Ser Ala Ala Ala Ala Ala Ala Ala Gly Gly Asp Phe  
195 200 205  
Asp Phe Gly Val Asp Pro Asn Ile Asp Pro Glu Leu Ala Leu Ala Leu  
210 215 220  
Arg Val Ser Met Glu Glu Arg Ala Arg Gln Glu Ala Ala Ala Lys  
225 230 235 240  
Lys Ala Ala Asp Glu Ala Cys Gln Lys Asp Lys Asp Gly Asp Thr Ala  
245 250 255  
Ser Ala Ser Gln Glu Thr Val Ala Arg Thr Thr Asp Lys Asn Ala Glu  
260 265 270  
Pro Met Asp Glu Asp Ser Ala Leu Leu Asp Gln Ala Ile Ala Met Ser  
275 280 285  
Xaa Gly Asp Val Asn Met Ser Glu Ala Ala Asp Glu Asp Gln Asp Leu  
290 295 300  
Ala Leu Ala Leu Gln Met Ser Met Ser Gly Glu Glu Ser Ser Glu Ala  
305 310 315 320  
Thr Gly Ala Gly Asn Asn Leu Leu Gly Asn Gln Ala Phe Ile Ser Ser  
325 330 335  
Val Leu Ser Ser Leu Pro Gly Val Asp Pro Asn Asp Pro Ala Val Lys  
340 345 350  
Glu Leu Leu Ala Ser Leu Pro Asp Glu Ser Lys Arg His Glu Glu Glu  
355 360 365  
Glu Ser Ser Ser Lys Lys Gly Glu Asp Glu Lys Lys  
370 375 380

(2) INFORMATION FOR SEQ ID NO:2179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1571948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

Met Arg Asn Gly Asp Tyr Ser Pro Ser Arg Leu Gln Ala Gln Thr Glu  
1 5 10 15  
Ala Val Asn Leu Leu Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn  
20 25 30  
Thr Val Gly Ile Leu Thr Met Ala Gly Lys Gly Val Arg Val Leu Thr  
35 40 45  
Thr Pro Thr Ser Asp Leu Gly Lys Ile Leu Ala Cys Met His Gly Leu  
50 55 60  
Asp Val Gly Gly Glu Ile Asn Leu Thr Ala Ala Ile Gln Ile Ala Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Leu | Ala | Leu | Lys | His | Arg | Gln | Asn | Lys | Asn | Gln | Arg | Gln | Arg | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Val | Phe | Ala | Gly | Ser | Pro | Ile | Lys | Tyr | Glu | Lys | Lys | Ala | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Val | Gly | Lys | Arg | Leu | Lys | Lys | Asn | Ser | Val | Ser | Leu | Asp | Ile | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     | Asn |
| Phe | Gly | Glu | Asp | Asp | Asp | Glu | Glu | Lys | Pro | Gln | Lys | Leu | Glu | Ala |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     | Leu |
| Leu | Thr | Ala | Val | Asn | Asn | Asn | Asp | Gly | Ser | His | Ile | Val | His | Val |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Ser | Gly | Ala | Asn | Ala | Leu | Ser | Asp | Val | Leu | Leu | Ser | Thr | Pro | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Thr | Gly | Asp | Glu | Gly | Ala | Ser | Gly | Tyr | Val | Ser | Ala | Ala | Ala | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Ala | Ala | Ala | Gly | Gly | Asp | Phe | Asp | Phe | Gly | Val | Asp | Pro | Asn | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     | Asp |
| Pro | Glu | Leu | Ala | Leu | Ala | Leu | Arg | Val | Ser | Met | Glu | Glu | Glu | Arg |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     | Ala |
| Arg | Gln | Glu | Ala | Ala | Ala | Lys | Lys | Ala | Ala | Asp | Glu | Ala | Cys | Gln |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Asp | Lys | Asp | Gly | Asp | Thr | Ala | Ser | Ala | Ser | Gln | Glu | Thr | Val | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |
| Thr | Thr | Asp | Lys | Asn | Ala | Glu | Pro | Met | Asp | Glu | Asp | Ser | Ala | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 | Leu |
| Asp | Gln | Ala | Ile | Ala | Met | Ser | Xaa | Gly | Asp | Val | Asn | Met | Ser | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     | Ala |
| Ala | Asp | Glu | Asp | Gln | Asp | Leu | Ala | Leu | Ala | Leu | Gln | Met | Ser | Met |
|     |     | 290 |     |     | 295 |     |     |     |     |     | 300 |     |     | Ser |
| Gly | Glu | Glu | Ser | Ser | Glu | Ala | Thr | Gly | Ala | Gly | Asn | Asn | Leu | Leu |
|     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Gln | Ala | Phe | Ile | Ser | Ser | Val | Leu | Ser | Ser | Leu | Pro | Gly | Val |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |
| Pro | Asn | Asp | Pro | Ala | Val | Lys | Glu | Leu | Leu | Ala | Ser | Leu | Pro | Asp |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     | Glu |
| Ser | Lys | Arg | His | Glu | Glu | Glu | Glu | Ser | Ser | Ser | Lys | Lys | Gly | Glu |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     | Asp |
| Glu | Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 370 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atacttgtaa | aagctagagt | caacgcggtt | cagtctcaga  | ccagacgaaa | caacgatgct | 60  |
| taactctatc | actttaaccc | ggaaaccacc | actcccggtt  | aactctgttg | ggttttcagg | 120 |
| taatcactct | tcgctctttt | gtcgaagaac | tataacggaa  | ggtagttcga | gcaaggctct | 180 |
| ttcgtttggg | tacaaaaatg | ttggttcact | gaagtgtggt  | cggagcaatt | ggccggggcg | 240 |
| ttctgggact | gcgtttgggc | atctagtcgc | ggtctctgcg  | gtctcagggt | gaaattcagg | 300 |
| tggtctgtgc | gggttaggtg | gttcaggcgc | tggttgtaat  | ggtggttcgc | gcggcgggtg | 360 |
| tggtgatgga | agcgacggaa | aaggaaagaa | gcggtcactt  | ctctcatggt | accaggctct | 420 |
| tctctcaaac | tctcctgttt | tgaccaaagc | tgtgaccgca  | gcacttttga | acctcgttgg | 480 |
| agatttgatc | tgtcagctta | caatcaacaa | gacctcatcg  | ctggacaaga | agaggacact | 540 |
| cacttttacc | ttcttgggct | tagggctagt | cgggtccaaca | ttgcatttct | ggtatttgta | 600 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| tttgagcaaa gttgtgacag cttctggatt atcaggcgca gttatacgac ttctactgga | 660  |
| tcagtttgtt tttgtccta tttttgttg agttttctta tcagcagttg tgacacttga   | 720  |
| aggaaaacca tcaaagtca taccgaagct acaacaggag tggactggtg caatgatagc  | 780  |
| aaattggcag ctatggatac catttcagtt tcttaacttc agatttggtc cacagaacta | 840  |
| ccaggtactt gcttcaaacg tagtggcttt ggcttggaat gtgattttat cattcaaagc | 900  |
| tcacaaagaa gttgttgcaa agtagacatg tttcttacct ggagcctaga ggtggttgct | 960  |
| ggattgttat cggcagagtt ttggggaaac gttcttgtct gctgatgcaa atgtttggtg | 1020 |
| tttcgaaaca attatttggg aaccctgcac ttgacatttt cttagagttg aaacaagctt | 1080 |
| ttcttcaagc acttcaaata tttcccatc atcaatgttt catatatatta ttgKttcctc | 1140 |

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1571950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

Met Leu Asn Ser Ile Thr Leu Thr Arg Lys Pro Pro Leu Pro Phe Asn  
1 5 10 15  
Ser Val Gly Phe Ser Gly Asn His Ser Ser Ser Phe Cys Arg Arg Thr  
20 25 30  
Ile Thr Glu Gly Ser Ser Ser Lys Ala Leu Ser Phe Gly Tyr Lys Asn  
35 40 45  
Val Gly Ser Leu Lys Cys Gly Arg Ser Asn Trp Pro Gly Arg Ser Gly  
50 55 60  
Thr Ala Phe Gly His Leu Val Arg Val Ser Ala Val Ser Gly Gly Asn  
65 70 75 80  
Ser Gly Gly Ser Gly Gly Leu Gly Gly Ser Gly Gly Gly Asn Gly  
85 90 95  
Gly Ser Gly Gly Gly Gly Gly Asp Gly Ser Asp Gly Lys Gly Lys Lys  
100 105 110  
Arg Ser Leu Leu Ser Trp Tyr Gln Ala Leu Leu Ser Asn Ser Pro Val  
115 120 125  
Leu Thr Lys Ala Val Thr Ala Ala Leu Leu Asn Leu Val Gly Asp Leu  
130 135 140  
Ile Cys Gln Leu Thr Ile Asn Lys Thr Ser Ser Leu Asp Lys Lys Arg  
145 150 155 160  
Thr Leu Thr Phe Thr Phe Leu Gly Leu Gly Leu Val Gly Pro Thr Leu  
165 170 175  
His Phe Trp Tyr Leu Tyr Leu Ser Lys Val Val Thr Ala Ser Gly Leu  
180 185 190  
Ser Gly Ala Val Ile Arg Leu Leu Asp Gln Phe Val Phe Ala Pro  
195 200 205  
Ile Phe Val Gly Val Phe Leu Ser Ala Val Val Thr Leu Glu Gly Lys  
210 215 220  
Pro Ser Asn Val Ile Pro Lys Leu Gln Gln Glu Trp Thr Gly Ala Met  
225 230 235 240  
Ile Ala Asn Trp Gln Leu Trp Ile Pro Phe Gln Phe Leu Asn Phe Arg  
245 250 255  
Phe Val Pro Gln Asn Tyr Gln Val Leu Ala Ser Asn Val Val Ala Leu  
260 265 270  
Ala Trp Asn Val Ile Leu Ser Phe Lys Ala His Lys Glu Val Val Ala  
275 280 285  
Lys

(2) INFORMATION FOR SEQ ID NO:2182:

2025 RELEASE UNDER E.O. 14176

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 731 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..731  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571963  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182:

attttccaca acttggaat cgaatccat ttcgaatttt ggtagcagc gatttcaaat 60  
tccaaacgta agaattatgg cgggagtga tcaggcgtgt atcttctgtg agatcgtgcg 120  
aaatccaacc actactcgtc tccttcacac cgatgagaaa gtcatcgcct ttcaagacat 180  
caagcctgca gccagagggc actattttggt gattccaaaa gaacatattc ctactgtgaa 240  
tgaccttcag agaagagatg aagactactc acttgtaaga cacatgctta gtgtgggaca 300  
acaactgttg cagaagatg ctctctcaaag cattcataga tttgggtttc accagccacc 360  
atttaacagt gttgatcatc tccatctcca ctgttttgca ttgccttatg tgcccagatg 420  
gaaagccatc aagtacaagt ctttgggacc tttgggtgga tttattgaag ccgagacact 480  
gctagagaag ataaggCctc ttctttcaaaa ggtgtMactg aacccaactt gtttaaccgc 540  
attgcggttg ttctctttgc taaaactgtg caatatctct tttctattct tttgctggca 600  
aatctgtgaa caaatgccaa atattattag agattttgta tatgaaagaa ggatgtgtca 660  
agtaattata tgtaatttct gccattgtcc aatagttaac acttaacacc aatctcattg 720  
tttccatgct t

(2) INFORMATION FOR SEQ ID NO:2183:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 209 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..209  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1571964  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

Met Ala Gly Val Asn Gln Ala Cys Ile Phe Cys Glu Ile Val Arg Asn  
1 5 10 15  
Pro Thr Thr Thr Arg Leu Leu His Thr Asp Glu Lys Val Ile Ala Phe  
20 25 30  
Gln Asp Ile Lys Pro Ala Ala Gln Arg His Tyr Leu Val Ile Pro Lys  
35 40 45  
Glu His Ile Pro Thr Val Asn Asp Leu Gln Arg Arg Asp Glu Asp Tyr  
50 55 60  
Ser Leu Val Arg His Met Leu Ser Val Gly Gln Leu Leu Gln Lys  
65 70 75 80  
Asp Ala Pro Gln Ser Ile His Arg Phe Gly Phe His Gln Pro Pro Phe  
85 90 95  
Asn Ser Val Asp His Leu His Leu His Cys Phe Ala Leu Pro Tyr Val  
100 105 110  
Pro Arg Trp Lys Ala Ile Lys Tyr Lys Ser Leu Gly Pro Leu Gly Gly  
115 120 125  
Phe Ile Glu Ala Glu Thr Leu Leu Glu Lys Ile Arg Pro Leu Leu Ser  
130 135 140  
Lys Val Xaa Leu Asn Pro Thr Cys Leu Thr Ala Leu Arg Cys Phe Ser  
145 150 155 160  
Leu Leu Lys Leu Cys Asn Ile Ser Phe Leu Phe Phe Cys Trp Gln Ile  
165 170 175  
Cys Glu Gln Met Pro Asn Ile Ile Arg Asp Phe Val Tyr Glu Arg Arg  
180 185 190  
Met Cys Gln Val Ile Ile Cys Asn Phe Cys His Cys Pro Ile Val Asn

195 200 205  
Thr

(2) INFORMATION FOR SEQ ID NO:2184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

Met Leu Ser Val Gly Gln Gln Leu Leu Gln Lys Asp Ala Pro Gln Ser  
1 5 10 15  
Ile His Arg Phe Gly Phe His Gln Pro Pro Phe Asn Ser Val Asp His  
20 25 30  
Leu His Leu His Cys Phe Ala Leu Pro Tyr Val Pro Arg Trp Lys Ala  
35 40 45  
Ile Lys Tyr Lys Ser Leu Gly Pro Leu Gly Gly Phe Ile Glu Ala Glu  
50 55 60  
Thr Leu Leu Glu Lys Ile Arg Pro Leu Leu Ser Lys Val Xaa Leu Asn  
65 70 75 80  
Pro Thr Cys Leu Thr Ala Leu Arg Cys Phe Ser Leu Leu Lys Leu Cys  
85 90 95  
Asn Ile Ser Phe Leu Phe Phe Cys Trp Gln Ile Cys Glu Gln Met Pro  
100 105 110  
Asn Ile Ile Arg Asp Phe Val Tyr Glu Arg Arg Met Cys Gln Val Ile  
115 120 125  
Ile Cys Asn Phe Cys His Cys Pro Ile Val Asn Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

aacacaaaga caataaaatt aatcaaaaat aaacaaagga gagagacaga agaaacagag 60  
agagtagtta attccggtgg ttttctgctc atctacttct atccaccttc atcccttccg 120  
ccccaaaatt caattctctc ttcttttctc tctcttttct cttaaaaact ctaactttac 180  
tcattctcatc tccaaagtct caacctttct tctctaattg agatctgcac ttacttcaaa 240  
tcacaaccca ctggtctcct cattctcttc gttctggggg caatctcaat cttcaaattc 300  
atcttcaccc tctcagatc tttctacatc tacttctctc gaccatccaa aaacctccgc 360  
cgatacgggt catgggcaat catcaccgga ccaacagacg gaatcggtta agctttcgcc 420  
tttcagttag ccagaaagg tcttaacctt ataactggtg ctgtaaccc agacaagctc 480  
aaagatgtct ctgattccat cagatctaag tatagtcaaa ctcatgctt gaccgtttgt 540  
atggatttct ctggagatat tgatgaagggt gtgaaacgga ttaaggagag tattgaagga 600  
ttagatggtt ggattttgat taataatgct ggcattgtct atccttatgc taagtatttt 660  
catgaggttg atgaagagtt gatcaataac ttgattaaga tcaatgttga aggaactact 720  
aaagttactc aagctgtgtt gcctaatatg cttaagagga agaaaggtgc tattattaat 780  
atgggttctg gtgctgtctc tcttattcct tcttatcctt ttactctgt ttatgctggt 840  
gctaaaacgt acgtggatca gttcacaag tgtctacatg ttgagtataa gaagagtggg 900  
attgatgttc aatgccaggt tcccttgtat gttgcaacaa agatgacaaa aataagaaga 960

gcataccttct tagttgcac accagagggt tacgcaaagg cagcacTgcg tttttaggc 1020  
tatgaagcgc aatgcacacc gtactggcct cagctctca tgggtgcagt tgtctctgca 1080  
ttgcccga aa gctttttga atcatttaac atcaagagat gcctccagat ccggaagaag 1140  
ggtctccaaa aagactccat gaagaaagaa tgaatcttcc aggtttaagt tactaccaag 1200  
aatttccttc ttctgaagtt gttggtttct tgaagagctt ctgttctgaa tcttttgtaa 1260  
gacttgact ctttagtttt ctaagttttt tatattttta gattaaaaac cctaacgtac 1320  
acgaataatt tacttcctct gtttctattt attaatttaa gcagtgttgt attc

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1571988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Ile  
1 5 10 15  
Leu Phe Val Leu Gly Ser Ile Ser Ile Phe Lys Phe Ile Phe Thr Leu  
20 25 30  
Leu Arg Ser Phe Tyr Ile Tyr Phe Leu Arg Pro Ser Lys Asn Leu Arg  
35 40 45  
Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly  
50 55 60  
Lys Ala Phe Ala Phe Gln Leu Ala Gln Lys Gly Leu Asn Leu Ile Leu  
65 70 75 80  
Val Ala Arg Asn Pro Asp Lys Leu Lys Asp Val Ser Asp Ser Ile Arg  
85 90 95  
Ser Lys Tyr Ser Gln Thr Gln Ile Leu Thr Val Val Met Asp Phe Ser  
100 105 110  
Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu Ser Ile Glu Gly  
115 120 125  
Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr  
130 135 140  
Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile Asn Asn Leu Ile  
145 150 155 160  
Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro  
165 170 175  
Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn Met Gly Ser Gly  
180 185 190  
Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly  
195 200 205  
Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu His Val Glu Tyr  
210 215 220  
Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala  
225 230 235 240  
Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro  
245 250 255  
Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Ala Gln  
260 265 270  
Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Ala Val Val Ser Ala  
275 280 285  
Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln  
290 295 300  
Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys Lys Glu  
305 310 315

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..210
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571989
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:

Met Asp Phe Ser Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu  
1 5 10 15  
Ser Ile Glu Gly Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met  
20 25 30  
Ser Tyr Pro Tyr Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile  
35 40 45  
Asn Asn Leu Ile Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln  
50 55 60  
Ala Val Leu Pro Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn  
65 70 75 80  
Met Gly Ser Gly Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser  
85 90 95  
Val Tyr Ala Gly Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu  
100 105 110  
His Val Glu Tyr Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro  
115 120 125  
Leu Tyr Val Ala Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu  
130 135 140  
Val Ala Ser Pro Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly  
145 150 155 160  
Tyr Glu Ala Gln Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Ala  
165 170 175  
Val Val Ser Ala Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys  
180 185 190  
Arg Cys Leu Gln Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys  
195 200 205  
Lys Glu  
210

(2) INFORMATION FOR SEQ ID NO:2188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 179 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..179
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1571990
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

Met Ser Tyr Pro Tyr Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu  
1 5 10 15  
Ile Asn Asn Leu Ile Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr  
20 25 30  
Gln Ala Val Leu Pro Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile  
35 40 45  
Asn Met Gly Ser Gly Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr  
50 55 60  
Ser Val Tyr Ala Gly Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys  
65 70 75 80  
Leu His Val Glu Tyr Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val

85 90 95  
Pro Leu Tyr Val Ala Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe  
100 105 110  
Leu Val Ala Ser Pro Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val  
115 120 125  
Gly Tyr Glu Ala Gln Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly  
130 135 140  
Ala Val Val Ser Ala Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile  
145 150 155 160  
Lys Arg Cys Leu Gln Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met  
165 170 175  
Lys Lys Glu

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..917
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

attctcactt acttcttttc tttttttgtg ttcttggtta gaagaagcaa tggccacttc 60  
agcaatccaa cactcttctt ttgccggcca aacggctcta aagccatcca acgacctcct 120  
tcgcaaggtc ggagcctcta atggtggcgg ccgcgttatc atgcgccgta ccgtcaagtc 180  
taccctcag agcatctggt atggaccaga ccgtcccaaa tacctaggac cattctcgga 240  
aaacacacca tcatacctaa ctggagaata ccctggagac tacggctggg acaccgctgg 300  
tctctcagcc gatccagaaa cattcgcaaa gaatcgtag ctcgaagtga tccacagtag 360  
atgggcaatg ttgggagctt taggctgcac cttccctgaa attctctcaa aaaacggagt 420  
caaattcggg gaagccgtgt ggttcaaggc aggatctcaa atcttctcag aaggaggact 480  
tgactacctc ggaaacccta acttgatcca cgcgcaaagc atattagcta tatgggcgtg 540  
tcaagttgtg ctaatgggat tcattgaagg gtacagaatc ggaggtggtc ctcttgggga 600  
agggcttgac ccgctttacc cgggcggggc cttcgaccgc ttgaacttag cgtaggatcc 660  
agaagcgttt tcggagttga aagtgaagga gcttaaaaaac ggtcgtcttg ctatgttctc 720  
aatgtttgga ttctttgtcc aagccatagt taccggtaaa ggtcgatcg aaaatctggt 780  
cgatcacatt gcagaccctg tggctaacaa tgcttGGct tacgccacca aCttcgctcc 840  
cggaaaatag agtttgatcg gataatttat gtaaattata tcttttaaac atttatcaat 900  
gcattaaagt tatcccc

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

Phe Ser Leu Thr Ser Phe Leu Phe Leu Cys Ser Cys Leu Glu Glu Ala  
1 5 10 15  
Met Ala Thr Ser Ala Ile Gln His Ser Ser Phe Ala Gly Gln Thr Ala  
20 25 30  
Leu Lys Pro Ser Asn Asp Leu Leu Arg Lys Val Gly Ala Ser Asn Gly  
35 40 45  
Gly Gly Arg Val Ile Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser  
50 55 60



Ile Trp Tyr Gly Pro Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu  
65 70 75 80  
Asn Thr Pro Ser Tyr Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp  
85 90 95  
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg  
100 105 110  
Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
115 120 125  
Cys Thr Phe Pro Glu Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu  
130 135 140  
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu  
145 150 155 160  
Asp Tyr Leu Gly Asn Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala  
165 170 175  
Ile Trp Ala Cys Gln Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg  
180 185 190  
Ile Gly Gly Gly Pro Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly  
195 200 205  
Gly Ala Phe Asp Pro Leu Asn Leu Ala  
210 215

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1572001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

Met Ala Thr Ser Ala Ile Gln His Ser Ser Phe Ala Gly Gln Thr Ala  
1 5 10 15  
Leu Lys Pro Ser Asn Asp Leu Leu Arg Lys Val Gly Ala Ser Asn Gly  
20 25 30  
Gly Gly Arg Val Ile Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser  
35 40 45  
Ile Trp Tyr Gly Pro Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu  
50 55 60  
Asn Thr Pro Ser Tyr Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp  
65 70 75 80  
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg  
85 90 95  
Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
100 105 110  
Cys Thr Phe Pro Glu Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu  
115 120 125  
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu  
130 135 140  
Asp Tyr Leu Gly Asn Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala  
145 150 155 160  
Ile Trp Ala Cys Gln Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg  
165 170 175  
Ile Gly Gly Gly Pro Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly  
180 185 190  
Gly Ala Phe Asp Pro Leu Asn Leu Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..164  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572002  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser Ile Trp Tyr Gly Pro  
1 5 10 15  
Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu Asn Thr Pro Ser Tyr  
20 25 30  
Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu  
35 40 45  
Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg Glu Leu Glu Val Ile  
50 55 60  
His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly Cys Thr Phe Pro Glu  
65 70 75 80  
Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu Ala Val Trp Phe Lys  
85 90 95  
Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu Asp Tyr Leu Gly Asn  
100 105 110  
Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala Ile Trp Ala Cys Gln  
115 120 125  
Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg Ile Gly Gly Gly Pro  
130 135 140  
Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly Gly Ala Phe Asp Pro  
145 150 155 160  
Leu Asn Leu Ala

(2) INFORMATION FOR SEQ ID NO:2193:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 932 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..932  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

attacctctc tctcattcac ctctcgctaa gtgtgcggtta gcCgttaggg ttccgatcta 60  
atcatggcgg actctgtttt gaaggaggtt aactgtggcc ggcctgaaaa gatcccgaag 120  
ttggacaaag cttgcgaagg atcgaaatcg tccgtgaaac atctcaagct aggaaacgtg 180  
gaagatgatg agtatcttcg acagtattgt ttgtttcact acgaattcca taaatccgag 240  
ggtttcacgg ttgattggga gaaatatgac tacatgttcc atataaggcc gttggaaaat 300  
tcaccacctc tcagcgatat acgaaccaat gctgatgtga tccgtgatgt gacactcttt 360  
gccattgaga aacacaatga agctcatgga tctaaacttg tgtttgtcga gcatgtctca 420  
gctaatttca aatttgccaa tggctctctc tgctgggttaa cattctgggc taccgatatg 480  
gcctcatctg ctccacatc gcagatctat caagtgcgaac tttggcgctg cggaaaacag 540  
tttgaaattc ccatcttcag ggtcaagcct aaggacgaag agatggatga tgttgaaagt 600  
aaaccaccct ctcccagtc ttatgatgac tatgataaac caccggttgt ctttgttcga 660  
gctgctcctg aagatgggtg ccctttcgtc tttgatcgaa ctggagctct ttatgatctc 720  
tatcggtctg gtttgtaagg aaaaagtata tataccattc ctttggtgac aaagagatat 780  
gatgttagtc actgactgaa aaatcaaatt aggcttgtat taatattata ccctctgaat 840  
tttcaacttc ttctatctct ctaaattgtac tagcttctct tctagagatc tatgaacaca 900  
aatagaattg atattcaaaa atccatttgt tt

(2) INFORMATION FOR SEQ ID NO:2194:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..224  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572024  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Met Ala Asp Ser Val Leu Lys Glu Val Asn Cys Gly Arg Pro Glu Lys  
1                   5                   10                   15  
Ile Pro Lys Leu Asp Lys Ala Cys Glu Gly Ser Lys Ser Ser Trp Lys  
                  20                   25                   30  
His Leu Lys Leu Gly Asn Val Glu Asp Asp Glu Tyr Leu Arg Gln Tyr  
                  35                   40                   45  
Cys Leu Phe His Tyr Glu Phe His Lys Ser Glu Gly Phe Thr Val Asp  
                  50                   55                   60  
Trp Glu Lys Tyr Asp Tyr Met Phe His Ile Arg Pro Leu Glu Asn Ser  
65                   70                   75                   80  
Pro Pro Ile Ser Asp Ile Arg Thr Asn Ala Asp Val Ile Arg Asp Val  
                  85                   90                   95  
Thr Leu Phe Ala Ile Glu Lys His Asn Glu Ala His Gly Ser Lys Leu  
                  100                   105                   110  
Val Phe Val Glu His Val Ser Ala Asn Phe Lys Phe Ala Asn Gly Leu  
                  115                   120                   125  
Leu Cys Trp Leu Thr Phe Trp Ala Thr Asp Met Ala Ser Ser Ala Pro  
                  130                   135                   140  
Thr Ser Gln Ile Tyr Gln Val Glu Leu Trp Arg Gly Lys Gln Phe  
145                   150                   155                   160  
Glu Ile Pro Ile Phe Arg Val Lys Pro Lys Asp Glu Glu Met Asp Asp  
                  165                   170                   175  
Val Glu Val Lys Pro Pro Ser Pro Met Pro Tyr Asp Asp Tyr Asp Lys  
                  180                   185                   190  
Pro Pro Val Val Phe Val Arg Ala Ala Pro Glu Asp Gly Val Pro Phe  
                  195                   200                   205  
Val Phe Asp Arg Thr Gly Ala Leu Tyr Asp Leu Tyr Arg Ser Gly Leu  
210                   215                   220

(2) INFORMATION FOR SEQ ID NO:2195:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 154 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..154  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572025  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

Met Phe His Ile Arg Pro Leu Glu Asn Ser Pro Pro Ile Ser Asp Ile  
1                   5                   10                   15  
Arg Thr Asn Ala Asp Val Ile Arg Asp Val Thr Leu Phe Ala Ile Glu  
                  20                   25                   30  
Lys His Asn Glu Ala His Gly Ser Lys Leu Val Phe Val Glu His Val  
                  35                   40                   45  
Ser Ala Asn Phe Lys Phe Ala Asn Gly Leu Leu Cys Trp Leu Thr Phe  
                  50                   55                   60  
Trp Ala Thr Asp Met Ala Ser Ser Ala Pro Thr Ser Gln Ile Tyr Gln

65 70 75 80  
Val Glu Leu Trp Arg Arg Gly Lys Gln Phe Glu Ile Pro Ile Phe Arg  
85 90 95  
Val Lys Pro Lys Asp Glu Glu Met Asp Val Glu Val Lys Pro Pro  
100 105 110  
Ser Pro Met Pro Tyr Asp Asp Tyr Asp Lys Pro Pro Val Val Phe Val  
115 120 125  
Arg Ala Ala Pro Glu Asp Gly Val Pro Phe Val Phe Asp Arg Thr Gly  
130 135 140  
Ala Leu Tyr Asp Leu Tyr Arg Ser Gly Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:2196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..633
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcgaaaaacc atcaccgggg aatctgacgg cggcttagta cggcgcgcta ctgcaaaaag  | 60  |
| gactgtgttc ttcttaggct tgatacttgc cttgggaaga atataacaat catttttgcg  | 120 |
| gtagctaaaa cgctaagctc tatcgtcata tctttatcat taatacttat ttgatatacta | 180 |
| aatatcataa aaatggccgc tcgttcactc tccggtgcg ttaaactctt ttgCtccgcc   | 240 |
| gcatccggaa gtctgtcttg ttccattgtc ttaaggagga gttacgttgc tacatcgtag  | 300 |
| aatgtaacag cagcaggatt gagtaaggga ggttccacca gagttatggg ggggaagatg  | 360 |
| gaacagagag gtttagatca agaggcagag tctgcttggg gaccagatcc agttactgga  | 420 |
| tactatagac cttccaatcg tgcggctgaa attgatccag ctgagctcag agaattgctt  | 480 |
| ttgaaaaaca aagcaaagtc tttctgagga ttttgattgg ttggttgact tggttccagt  | 540 |
| ggaaggttgt cgtaggcgac tattatgatt atgtgtgttt atgtttgtct tgtatcaact  | 600 |
| attaagtaaa aataaagatc acattaacta gtc                               |     |

(2) INFORMATION FOR SEQ ID NO:2197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

Met Ala Ala Arg Ser Leu Ser Gly Ala Val Lys Ser Leu Cys Ser Ala  
1 5 10 15  
Ala Ser Gly Ser Leu Ser Cys Ser Ile Val Leu Arg Arg Ser Tyr Val  
20 25 30  
Ala Thr Ser Gln Asn Val Thr Ala Ala Gly Leu Ser Lys Gly Gly Ser  
35 40 45  
Thr Arg Val Met Val Gly Lys Met Glu Gln Arg Gly Leu Asp Gln Glu  
50 55 60  
Ala Glu Ser Ala Trp Gly Pro Asp Pro Val Thr Gly Tyr Tyr Arg Pro  
65 70 75 80  
Ser Asn Arg Ala Ala Glu Ile Asp Pro Ala Glu Leu Arg Glu Leu Leu  
85 90 95  
Leu Lys Asn Lys Ala Lys Ser Phe  
100

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 53 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..53  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572028  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:  
Met Val Gly Lys Met Glu Gln Arg Gly Leu Asp Gln Glu Ala Glu Ser  
1          5          10          15  
Ala Trp Gly Pro Asp Pro Val Thr Gly Tyr Tyr Arg Pro Ser Asn Arg  
          20          25          30  
Ala Ala Glu Ile Asp Pro Ala Glu Leu Arg Glu Leu Leu Leu Lys Asn  
          35          40          45  
Lys Ala Lys Ser Phe  
50

(2) INFORMATION FOR SEQ ID NO:2199:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 790 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

    (A) NAME/KEY: -  
    (B) LOCATION: 1..790  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572029  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:  
agaccaccaa gaaaacaaag acttatcgat catgaagatc agacttagca taaccatcat 60  
actttttatca tacacagtgg ctacggtggc cggacaacaa tgcggtcgtc aaggcgggtg 120  
tcgaacttgt cccggttaaca tctgctgcag tcagtacggt tactgtggta ccaccgcgga 180  
ckrctgttct ccgaccaaca actgtcagag caattgttgg ggaagtgggc ctacgcggacc 240  
aggggagagc gcgtcgaacg tacgcgccac ctaccatttc tataatccgg cgcagaataa 300  
ttgggatttg agagccgtga gtgcttattg ctccacgtgg gatgctgata agccgtacgc 360  
atggcgggagC aagtatggct ggaccgcctt ctgcggggccg gcaggacctc gtggtcaagc 420  
ttcttgccggc aagtgttttaa ggggtgaagaa cacaagaaca aatgctgcag taactgtgag 480  
aatagtggac caatgcagca acggaggctt ggatttggat gtagcaatgt tcaatcaaat 540  
agacaccgat ggttttggct atcaacaagg ccatctcatt gttgactacc aatttgtcga 600  
ctgtggcaat gagctcattg ggcagcctga ttccagaaac atgcttgttt cggccattga 660  
tcgcgtttga tattatgtaa tgattttgag gtcaatatcg atcgggtctac ataaaaataa 720  
taaagaccgc tatatatgta ttgtcgaggg atatatgttt cgtatcaata aggaaatttt 780  
aaatattatt

(2) INFORMATION FOR SEQ ID NO:2200:

    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 222 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..222

        (D) OTHER INFORMATION: / Ceres Seq. ID 1572030

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

Asp His Gln Glu Asn Lys Asp Leu Ser Ile Met Lys Ile Arg Leu Ser  
1          5          10          15  
Ile Thr Ile Ile Leu Leu Ser Tyr Thr Val Ala Thr Val Ala Gly Gln  
          20          25          30

Gln Cys Gly Arg Gln Gly Gly Gly Arg Thr Cys Pro Gly Asn Ile Cys  
35 40 45  
Cys Ser Gln Tyr Gly Tyr Cys Gly Thr Thr Ala Asp Xaa Cys Ser Pro  
50 55 60  
Thr Asn Asn Cys Gln Ser Asn Cys Trp Gly Ser Gly Pro Ser Gly Pro  
65 70 75 80  
Gly Glu Ser Ala Ser Asn Val Arg Ala Thr Tyr His Phe Tyr Asn Pro  
85 90 95  
Ala Gln Asn Asn Trp Asp Leu Arg Ala Val Ser Ala Tyr Cys Ser Thr  
100 105 110  
Trp Asp Ala Asp Lys Pro Tyr Ala Trp Arg Ser Lys Tyr Gly Trp Thr  
115 120 125  
Ala Phe Cys Gly Pro Ala Gly Pro Arg Gly Gln Ala Ser Cys Gly Lys  
130 135 140  
Cys Leu Arg Val Lys Asn Thr Arg Thr Asn Ala Ala Val Thr Val Arg  
145 150 155 160  
Ile Val Asp Gln Cys Ser Asn Gly Gly Leu Asp Leu Asp Val Ala Met  
165 170 175  
Phe Asn Gln Ile Asp Thr Asp Gly Phe Gly Tyr Gln Gln Gly His Leu  
180 185 190  
Ile Val Asp Tyr Gln Phe Val Asp Cys Gly Asn Glu Leu Ile Gly Gln  
195 200 205  
Pro Asp Ser Arg Asn Met Leu Val Ser Ala Ile Asp Arg Val  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1572031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

Met Lys Ile Arg Leu Ser Ile Thr Ile Ile Leu Leu Ser Tyr Thr Val  
1 5 10 15  
Ala Thr Val Ala Gly Gln Gln Cys Gly Arg Gln Gly Gly Gly Arg Thr  
20 25 30  
Cys Pro Gly Asn Ile Cys Cys Ser Gln Tyr Gly Tyr Cys Gly Thr Thr  
35 40 45  
Ala Asp Xaa Cys Ser Pro Thr Asn Asn Cys Gln Ser Asn Cys Trp Gly  
50 55 60  
Ser Gly Pro Ser Gly Pro Gly Glu Ser Ala Ser Asn Val Arg Ala Thr  
65 70 75 80  
Tyr His Phe Tyr Asn Pro Ala Gln Asn Asn Trp Asp Leu Arg Ala Val  
85 90 95  
Ser Ala Tyr Cys Ser Thr Trp Asp Ala Asp Lys Pro Tyr Ala Trp Arg  
100 105 110  
Ser Lys Tyr Gly Trp Thr Ala Phe Cys Gly Pro Ala Gly Pro Arg Gly  
115 120 125  
Gln Ala Ser Cys Gly Lys Cys Leu Arg Val Lys Asn Thr Arg Thr Asn  
130 135 140  
Ala Ala Val Thr Val Arg Ile Val Asp Gln Cys Ser Asn Gly Gly Leu  
145 150 155 160  
Asp Leu Asp Val Ala Met Phe Asn Gln Ile Asp Thr Asp Gly Phe Gly  
165 170 175  
Tyr Gln Gln Gly His Leu Ile Val Asp Tyr Gln Phe Val Asp Cys Gly  
180 185 190  
Asn Glu Leu Ile Gly Gln Pro Asp Ser Arg Asn Met Leu Val Ser Ala

SEQUENCE - 1572031

195  
Ile Asp Arg Val  
210

200

205

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| atattttgta | attagtcgga | tatattaaaa | tacgcgttca | gatattcaaa  | ttagaatagt  | 60  |
| catatagtca | cgcggttata | aacaattcgg | tgtataaatt | gtaagtcaca  | cagaaaaaga  | 120 |
| aagaaacgaa | acgaaacgaa | ttatggattt | gaagaaagca | tctttgtttt  | tattccttct  | 180 |
| tctctgtctc | cacctgcaac | tgcaacacca | ctttgctcac | gcggtctcgc  | gatcttcaac  | 240 |
| aagtttagcc | ttcgttgatc | caaaccatga | tgatctcccg | tttcaagaag  | tagaattgaa  | 300 |
| gccagacggt | gacgtaatcg | aagccaattt | accgaaatta | acagtcggtg  | ttaagaaagg  | 360 |
| cggcgaggga | ggaggcagag | gtggaggcgg | cttcggcgga | ggaggacgca  | Gtttcggcgg  | 420 |
| aggagggagt | tctagcagag | gcggtggagg | aagttctagc | agaggcggag  | gagggagttc  | 480 |
| tagcagagga | ggaggaatac | gtccgattcc | gatttatggc | ggtggaacgc  | accgcasygg  | 540 |
| tcatcattca | agcggcggcc | gggaaactgc | tagtggttgg | ttaggtctat  | cgatttttagc | 600 |
| cggtttaggt | ttggtttttt | aaagcttcta | tatttgattt | accggttttag | gttaaattgtt | 660 |
| tgatgccggt | tttgctttcc | actggtttgc | tctctggatt | ttatcagaag  | tttgttagg   |     |

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Lys | Lys | Ala | Ser | Leu | Phe | Leu | Phe | Leu | Leu | Cys | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Leu | Gln | Leu | Gln | His | His | Phe | Ala | His | Ala | Val | Ser | Arg | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Leu | Ala | Phe | Val | Asp | Pro | Asn | His | Asp | Asp | Leu | Pro | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Glu | Val | Glu | Leu | Lys | Pro | Asp | Gly | Asp | Val | Ile | Glu | Ala | Asn | Leu |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Lys | Leu | Thr | Val | Val | Val | Lys | Lys | Gly | Gly | Gly | Gly | Gly | Arg | Gly |
|     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Gly | Gly | Gly | Phe | Gly | Gly | Gly | Gly | Arg | Ser | Phe | Gly | Gly | Gly | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Ser | Ser | Arg | Gly | Gly | Gly | Gly | Ser | Ser | Ser | Arg | Gly | Gly | Gly | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Ser | Ser | Arg | Gly | Gly | Gly | Ile | Arg | Pro | Ile | Pro | Ile | Tyr | Gly | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | His | Arg | Xaa | Gly | His | His | Ser | Ser | Gly | Gly | Arg | Glu | Thr | Ala |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Gly | Trp | Leu | Gly | Leu | Ser | Ile | Leu | Ala | Gly | Leu | Gly | Leu | Val | Phe |
|     |     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1411  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572046  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

ttctaaagta acgcgataaa tctaattgcat tcccacgatt tgtgtttgtc cctctgacga 60  
aaaatcctcg gatctgttgc attctctcca aagcttgaat cagaagaaag cttttgaaga 120  
tcagcctaaa agtgatctct cataactgct taaaagattg ttgaaactcg aagatgtctt 180  
tggccgagat aaacaagaat gaagtcgaca ttgttattgg ggctcttaat gctgacctta 240  
cacagttttt gaccagctgg aggcctttct tctccggatt ccatctgatt gttgtcaaag 300  
atcatgagct caaggaggaa ctcaacatac cagaaggctt tgacgtagat gtctactcta 360  
agactgacat ggaaaagggt gtgggcgcat ccaattccac catgttctct ggctattctt 420  
gcagatattt cggttatctc gtatctaaaa agaagtacat tgtctctatt gatgatgatt 480  
gtgtcccCtg ctaaagatcc gaaggggttc ctagtggatg ctgttactca gcacgtgac 540  
aaccttgaaa acccagccac gcctctcttc ttcaacacccc tttatgatcc ttactgcgag 600  
ggagcggatt ttgtccgtgg atacccttcc agcctcagaa gtgggtgtccc ttgtgctgca 660  
tcttgtgggc tttggcttaa tctagctgat ctgtatgctc caacacaagc tctcaagaca 720  
gagaaaagga acactgcata tgttgatgag gttatgactg tcccggccaa ggctatgcta 780  
cccataagcg gaatcaacat tgcttttaac cgcgagttgg tgggtccagc tttggtgcct 840  
gcaactcagat tggctggaga agggaaagtg agatgggaaa cacttgaaga tgtttggtgt 900  
gggatgtgtc tgaaacatat ctctgatcat ttgggttatg gtgtgaaaac cggactgcct 960  
tatgtgtgga gaaacgagag aggagatgca gtggagagtt tgaggaagaa atgggaagga 1020  
atgaagctga tggagaaaag tgttccattt ttcgattcat tgaaattgcc cgagactgcg 1080  
cttaaagttg aagattgtgt gattgagctt gctaaagcgg tgaaagagca gttaggttca 1140  
gatgatcctg cctttacgca agctgctgat gctatggtta agtgggtcca gctctggaat 1200  
tctgttaatt ctagcgcttg aagttgaaca atctcttgag gttaggttcc tttatcactt 1260  
ctaagcatat tatcatgtct cagagattta cccaagtcgt tttctttctt ttagtatcat 1320  
catgtttatt ttctcttttt atctaaatta taagcatgtg tttttgagac actcaataat 1380  
gtaacctgat gaaacccatc tgctttgact c

(2) INFORMATION FOR SEQ ID NO:2205:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 290 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..290  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

Met Ser Thr Leu Arg Leu Thr Trp Lys Arg Leu Trp Ala His Pro Ile  
1 5 10 15  
Pro Pro Cys Ser Leu Ala Ile Leu Ala Asp Ile Ser Val Ile Ser Tyr  
20 25 30  
Leu Lys Arg Ser Thr Leu Ser Leu Leu Met Met Ile Val Ser Pro Ala  
35 40 45  
Lys Asp Pro Lys Gly Phe Leu Val Asp Ala Val Thr Gln His Val Ile  
50 55 60  
Asn Leu Glu Asn Pro Ala Thr Pro Leu Phe Phe Asn Thr Leu Tyr Asp  
65 70 75 80  
Pro Tyr Cys Glu Gly Ala Asp Phe Val Arg Gly Tyr Pro Phe Ser Leu  
85 90 95  
Arg Ser Gly Val Pro Cys Ala Ala Ser Cys Gly Leu Trp Leu Asn Leu  
100 105 110  
Ala Asp Leu Asp Ala Pro Thr Gln Ala Leu Lys Thr Glu Lys Arg Asn



[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(B) LOCATION: 1..249

SEQUENCE DESCRIPTION: SEQ ID NO:2206:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Ile | Val | Ser | Pro | Ala | Lys | Asp | Pro | Lys | Gly | Phe | Leu | Val | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Thr | Gln | His | Val | Ile | Asn | Leu | Glu | Asn | Pro | Ala | Thr | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Phe | Asn | Thr | Leu | Tyr | Asp | Pro | Tyr | Cys | Glu | Gly | Ala | Asp | Phe | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Gly | Tyr | Pro | Phe | Ser | Leu | Arg | Ser | Gly | Val | Pro | Cys | Ala | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Leu | Trp | Leu | Asn | Leu | Ala | Asp | Leu | Asp | Ala | Pro | Thr | Gln | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Lys | Thr | Glu | Lys | Arg | Asn | Thr | Ala | Tyr | Val | Asp | Ala | Val | Met | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Pro | Ala | Lys | Ala | Met | Leu | Pro | Ile | Ser | Gly | Ile | Asn | Ile | Ala | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Arg | Glu | Leu | Val | Gly | Pro | Ala | Leu | Val | Pro | Ala | Leu | Arg | Leu | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Glu | Gly | Lys | Val | Arg | Trp | Glu | Thr | Leu | Glu | Asp | Val | Trp | Cys | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Cys | Leu | Lys | His | Ile | Ser | Asp | His | Leu | Gly | Tyr | Gly | Val | Lys | Thr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Leu | Pro | Tyr | Val | Trp | Arg | Asn | Glu | Arg | Gly | Asp | Ala | Val | Glu | Ser |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Arg | Lys | Lys | Trp | Glu | Gly | Met | Lys | Leu | Met | Glu | Lys | Ser | Val | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Phe | Asp | Ser | Leu | Lys | Leu | Pro | Glu | Thr | Ala | Leu | Lys | Val | Glu | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Cys Val Ile Glu Leu Ala Lys Ala Val Lys Glu Gln Leu Gly Ser Asp  
210 215 220  
Asp Pro Ala Phe Thr Gln Ala Ala Asp Ala Met Val Lys Trp Val Gln  
225 230 235 240  
Leu Trp Asn Ser Val Asn Ser Ser Ala  
245

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1572049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

Met Ile Val Ser Pro Ala Lys Asp Pro Lys Gly Phe Leu Val Asp Ala  
1 5 10 15  
Val Thr Gln His Val Ile Asn Leu Glu Asn Pro Ala Thr Pro Leu Phe  
20 25 30  
Phe Asn Thr Leu Tyr Asp Pro Tyr Cys Glu Gly Ala Asp Phe Val Arg  
35 40 45  
Gly Tyr Pro Phe Ser Leu Arg Ser Gly Val Pro Cys Ala Ala Ser Cys  
50 55 60  
Gly Leu Trp Leu Asn Leu Ala Asp Leu Asp Ala Pro Thr Gln Ala Leu  
65 70 75 80  
Lys Thr Glu Lys Arg Asn Thr Ala Tyr Val Asp Ala Val Met Thr Val  
85 90 95  
Pro Ala Lys Ala Met Leu Pro Ile Ser Gly Ile Asn Ile Ala Phe Asn  
100 105 110  
Arg Glu Leu Val Gly Pro Ala Leu Val Pro Ala Leu Arg Leu Ala Gly  
115 120 125  
Glu Gly Lys Val Arg Trp Glu Thr Leu Glu Asp Val Trp Cys Gly Met  
130 135 140  
Cys Leu Lys His Ile Ser Asp His Leu Gly Tyr Gly Val Lys Thr Gly  
145 150 155 160  
Leu Pro Tyr Val Trp Arg Asn Glu Arg Gly Asp Ala Val Glu Ser Leu  
165 170 175  
Arg Lys Lys Trp Glu Gly Met Lys Leu Met Glu Lys Ser Val Pro Phe  
180 185 190  
Phe Asp Ser Leu Lys Leu Pro Glu Thr Ala Leu Lys Val Glu Asp Cys  
195 200 205  
Val Ile Glu Leu Ala Lys Ala Val Lys Glu Gln Leu Gly Ser Asp Asp  
210 215 220  
Pro Ala Phe Thr Gln Ala Ala Asp Ala Met Val Lys Trp Val Gln Leu  
225 230 235 240  
Trp Asn Ser Val Asn Ser Ser Ala  
245

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..652
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572064

00000000-00000000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atttttcttt | tcatttcatt | tctgattgtc | tttctcagaa | tccctagaac | acactctgat | 60  |
| taacgaatca | aagatcgatt | tgggattgtg | atcgatcgag | gaagaagatg | acggaggcga | 120 |
| tgataaggaa | gaagccagga | atggcgagtg | tgaaggatat | gccgttgctt | caggatggtc | 180 |
| caccaccggg | tggattcgca | ccggtccgat | atgctcgccg | gatctctaac | acgggtccaa | 240 |
| gcgccatggc | tattttcctt | accgtttcag | gtgcttttgc | ttgggggatg | taccaagtcg | 300 |
| gtcagggcaa | caaaatccgc | agggcgttga | aggaagagaa | atacgctgct | cgtagagcga | 360 |
| ttctaccAat | tcttcaagct | gaagaagatg | aaaggtttgt | gtctgagtgg | aagaagtatc | 420 |
| tagaatacga | ggcggatgtg | atgaaggatg | ttcctggatg | gaaagtcggt | gaaaacgtgt | 480 |
| acaattctgg | tcgttggatg | cctccagcta | ctggagagct | tcgtcctgat | gtctggtaaa | 540 |
| ttatcaatgg | ctccttttga | tgatgatgaa | tgaatgtttg | tttaagcatt | ttagaacctt | 600 |
| gatgtttctt | gtctctcttt | ttccatcgta | taataagaga | attgatacat | ac         |     |

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Glu | Ala | Met | Ile | Arg | Lys | Lys | Pro | Gly | Met | Ala | Ser | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Met | Pro | Leu | Leu | Gln | Asp | Gly | Pro | Pro | Pro | Gly | Gly | Phe | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Tyr | Ala | Arg | Arg | Ile | Ser | Asn | Thr | Gly | Pro | Ser | Ala | Met | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Phe | Leu | Thr | Val | Ser | Gly | Ala | Phe | Ala | Trp | Gly | Met | Tyr | Gln | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Gln | Gly | Asn | Lys | Ile | Arg | Arg | Ala | Leu | Lys | Glu | Glu | Lys | Tyr | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Arg | Arg | Ala | Ile | Leu | Pro | Ile | Leu | Gln | Ala | Glu | Glu | Asp | Glu | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Val | Ser | Glu | Trp | Lys | Lys | Tyr | Leu | Glu | Tyr | Glu | Ala | Asp | Val | Met |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Asp | Val | Pro | Gly | Trp | Lys | Val | Gly | Glu | Asn | Val | Tyr | Asn | Ser | Gly |
|     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |     |
| Arg | Trp | Met | Pro | Pro | Ala | Thr | Gly | Glu | Leu | Arg | Pro | Asp | Val | Trp |     |
|     | 130 |     |     |     | 135 |     |     |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Arg | Lys | Lys | Pro | Gly | Met | Ala | Ser | Val | Lys | Asp | Met | Pro | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Gln | Asp | Gly | Pro | Pro | Pro | Gly | Gly | Phe | Ala | Pro | Val | Arg | Tyr | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Arg | Ile | Ser | Asn | Thr | Gly | Pro | Ser | Ala | Met | Ala | Ile | Phe | Leu | Thr |
|     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Val | Ser | Gly | Ala | Phe | Ala | Trp | Gly | Met | Tyr | Gln | Val | Gly | Gln | Gly | Asn |

50 55 60  
Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala Ala Arg Arg Ala  
65 70 75 80  
Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Glu Arg Phe Val Ser Glu  
85 90 95  
Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met Lys Asp Val Pro  
100 105 110  
Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly Arg Trp Met Pro  
115 120 125  
Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp  
130 135

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

Met Ala Ser Val Lys Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro  
1 5 10 15  
Gly Gly Phe Ala Pro Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly  
20 25 30  
Pro Ser Ala Met Ala Ile Phe Leu Thr Val Ser Gly Ala Phe Ala Trp  
35 40 45  
Gly Met Tyr Gln Val Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys  
50 55 60  
Glu Glu Lys Tyr Ala Ala Arg Arg Ala Ile Leu Pro Ile Leu Gln Ala  
65 70 75 80  
Glu Glu Asp Glu Arg Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr  
85 90 95  
Glu Ala Asp Val Met Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn  
100 105 110  
Val Tyr Asn Ser Gly Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg  
115 120 125  
Pro Asp Val Trp  
130

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

atataaaccc tctcgGcgct gccattgaaa ctctttcaag gagagagctg ctactctgca 60  
accatgtcga agcgaggaag aggaggaacc tctggtaaca agttcaggat gtcactgggt 120  
cttcagtgag cagccactgt gaactgtgct gacaacaccg gagctaagaa cctttacatc 180  
atttcggtta aaggaatcaa gggtcgtcctt aaccggtttgc catcagcttg tgttggtgat 240  
atggttatgg ctactgttaa gaaaggtaag cctgatctcc gtaagaaggt gcttcctgct 300  
gtcattgtta ggcagaggaa gccttggcgc cgaaaggacg gtgtcttcat gtatttcgaa 360  
gataatgctg gtgtcattgt caatccaag ggtgatatga aaggatctgc tatcactgga 420  
ccaatcggaagg agtagtgctg tgatctgtgg ccaagaatcg caagtgtctg gaacgccatc 480

gtttaagcaa gcttgagatc tctatgtttt gtgttgaacg ttttagcatta tctctatttg 540  
ggattgtttt ttgtttttgt cttagacttt tgttatgcct taaagctgat tctagttctc 600

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1572083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

Met Ser Lys Arg Gly Arg Gly Gly Thr Ser Gly Asn Lys Phe Arg Met  
1 5 10 15  
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr  
20 25 30  
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg  
35 40 45  
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr  
50 55 60  
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Leu Pro Ala Val  
65 70 75 80  
Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Phe Met  
85 90 95  
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Asp Met  
100 105 110  
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu  
115 120 125  
Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1572084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn  
1 5 10 15  
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly  
20 25 30  
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala  
35 40 45  
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Leu Pro Ala  
50 55 60  
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Phe  
65 70 75 80  
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Asp  
85 90 95  
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp  
100 105 110  
Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

```
Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys
1 5 10 15
Val Leu Pro Ala Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys
20 25 30
Asp Gly Val Phe Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn
35 40 45
Pro Lys Gly Asp Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys
50 55 60
Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile
65 70 75 80
Val
```

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

```
acatccaaca acaaaaacac aagcgtagaa aacaaaactc aactaattgt gttatcaccc 60
aaaagagaag agcaaacaca atggCtttcg ctttgagggt cttcacatgc tttgttttga 120
cagtgttcat cgttgcata gtggatgcag caataacatg tggcacagt gcaagtagct 180
tgagtccatg tctaggctac ctatcgaagg gtggggtggt gccacctccg tgctgtgcag 240
gagtcaaaaa gttgaacggt atgggtcaaa ccacaccgga ccgccaacia gcatgcagat 300
gcttacagtc cgctgcaaaa ggggttaatc caagtcNtag cctctggcct tcctggaaag 360
tgcggtgtta gcatccccCt atcccCatct ccacgagcac caactgcgcc accatcaagt 420
gaagtgggga ataacgacat catttgccctg aagagtatgg tttcgtatac gtaaaataag 480
acggctatct aagctgatat ttaccttgct tttgtttgt
```

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

```
Ile Gln Gln Gln Lys His Lys Arg Arg Lys Gln Asn Ser Thr Asn Cys
1 5 10 15
Val Ile Thr Gln Lys Arg Arg Ala Asn Thr Met Ala Phe Ala Leu Arg
20 25 30
```

Phe Phe Thr Cys Phe Val Leu Thr Val Phe Ile Val Ala Ser Val Asp  
35 40 45  
Ala Ala Ile Thr Cys Gly Thr Val Ala Ser Ser Leu Ser Pro Cys Leu  
50 55 60  
Gly Tyr Leu Ser Lys Gly Gly Val Val Pro Pro Pro Cys Cys Ala Gly  
65 70 75 80  
Val Lys Lys Leu Asn Gly Met Ala Gln Thr Thr Pro Asp Arg Gln Gln  
85 90 95  
Ala Cys Arg Cys Leu Gln Ser Ala Ala Lys Gly Val Asn Pro Ser Xaa  
100 105 110  
Ser Leu Trp Pro Ser Trp Lys Val Arg Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1572096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

Met Ala Phe Ala Leu Arg Phe Phe Thr Cys Phe Val Leu Thr Val Phe  
1 5 10 15  
Ile Val Ala Ser Val Asp Ala Ala Ile Thr Cys Gly Thr Val Ala Ser  
20 25 30  
Ser Leu Ser Pro Cys Leu Gly Tyr Leu Ser Lys Gly Gly Val Val Pro  
35 40 45  
Pro Pro Cys Cys Ala Gly Val Lys Lys Leu Asn Gly Met Ala Gln Thr  
50 55 60  
Thr Pro Asp Arg Gln Gln Ala Cys Arg Cys Leu Gln Ser Ala Ala Lys  
65 70 75 80  
Gly Val Asn Pro Ser Xaa Ser Leu Trp Pro Ser Trp Lys Val Arg Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..808

(D) OTHER INFORMATION: / Ceres Seq. ID 1572097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

atcaacaaaa acaaaacata aaaaacaagt ggaagcttta aaacgagagg gatagagcaa 60  
aaatggcgac gtcggaacg tacgtgacgg aagttccgct aaaaggatcg gccgagaaat 120  
actacaagag gtggaagaac gagaaccatg tcttccctga tgctatcggc caccacatcc 180  
aaaatgttac cgttcacgaa ggcgaacatg actctcaagg gtctatcagg agttggaact 240  
acacatggga tggaaggag gaggtgttca aggagagaag agagatagac gatgagacca 300  
aaacgttgac gttaagagga cttgagggtc acgtgatgga gcagctcaaa gtgtacgacg 360  
tcgtctacca attcattccc aaatctgagg atacctgcat cggcaaaatc actttaatat 420  
gggagaagcg caacgatgat tccccagaac caagcggcta catgaaattc gtcaagagct 480  
tggttgctga catgggaaac cacgttagCC CAAAAAAAAA AAAAAAaaaa cttaatcatc 540  
attcccacag tcgtcgatcat catcatcatc atcatcatca tcatcatcat catcatcatc 600  
atcatcatca tcatcatcat catcatcatc atcactatct cgatttataa gttaagatgt 660

```
tttcagtata ataaatgggg tcttgtggat cgttcatttc tatgtgtaaa ccgtttgggt 720
ctgtatgatg cttcgatata ttgttatgtt catgatcata tgtcgggttc gatataatga 780
ttcttaagat taatttacta cacatttc
```

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1572098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser  
1 5 10 15  
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro  
20 25 30  
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu  
35 40 45  
His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly  
50 55 60  
Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys  
65 70 75 80  
Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys  
85 90 95  
Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys  
100 105 110  
Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro  
115 120 125  
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met  
130 135 140  
Gly Asn His Val Ser Pro Lys Lys Lys Lys Lys Lys Leu Asn His His  
145 150 155 160  
Ser His Ser Arg Arg His His His His His His His His His His  
165 170 175  
His His His His His His His His His His His His His His Tyr  
180 185 190  
Leu Asp Leu  
195

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1572099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

Met Glu Gln Leu Lys Val Tyr Asp Val Tyr Gln Phe Ile Pro Lys  
1 5 10 15  
Ser Glu Asp Thr Cys Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg  
20 25 30  
Asn Asp Asp Ser Pro Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser  
35 40 45  
Leu Val Ala Asp Met Gly Asn His Val Ser Pro Lys Lys Lys Lys Lys  
50 55 60



Lys Leu Asn His His Ser His Ser Arg Arg His His His His His  
65 70 75 80  
His His His His His His His His His His His His His His  
85 90 95  
His His His His Tyr Leu Asp Leu  
100

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1201
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

ctacatcgcc gtcgcctggt accgtccggt gctattctcc ttcacaaatct cacatttttc 60  
gtaccgggta gaagatgaga atcacgcaga tcttggtatg totggtaata gtggcattgt 120  
cttcaagctc ccatgtctgg tccgatcaga tcttcccagc tcatctagtt ggaacattca 180  
gcagaaacaa tcgtgaacca aagtacaaga ttgagttcct tcctgaagat tcaccttttc 240  
accoggggtga taatctggaa tcaatgggta tggttgataa gcatggaaat cggtttttat 300  
gttacttacc gaaagaggaa aaagcgacga gtggatggac ttctagtcag caaaatatta 360  
gtactgtgat gatggaaaca cagcaactgg tgaagctaaa gactcctgat gaattgcttc 420  
aaccacttag tgaaaaatgt ctttttaggc aagagggttg gtggtcttat gagttttgtc 480  
atcagaagta tgtgcggcag Ctacacgttg aggatgaaaa caagattgtt caagagtttt 540  
ttttgggtac ttttgacca gaggcaActg cggcggttaa tcaaactgtt tctgatgctt 600  
caactgatgc atctcagagg tatcactctc atgtatacac caatgggacc acctgtgatc 660  
ttacaggatc acctgcgaa gtcgaggtga gggttgatg cgagaaaca agggcaatgg 720  
tcacttcaat cactgaatta tcaacttgca agtacgcact gactgttcag tgcccaacct 780  
tgtgcaagca tvscgtgttc cagctagaga aaccagtgtc acacacgac cactgcaatg 840  
cgatcccagt ggaagaagac gcaacaagaa acaaggaaga acaagcagta gacgaatcac 900  
ctaagatgat agctgattct tgaaaaccgc ctaagtgaat cacctaagag taagagttaa 960  
cagcgactgt atatacaaga actagcatat ctccattttc agtgttacct gctgtagtga 1020  
tcattgggttc aattgggata gcttgctggg aggatgatga tactctctct gtaatttttt 1080  
gcatacttaa aatagcattt caatagaagg tactgataaa ccacttgatga agcaaagact 1140  
gcaagcttca tgtaacacat atgtttccgt ttcactaatg aatttggtcc aagtgtaggc 1200  
C

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..282
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Met Arg Ile Thr Gln Ile Leu Leu Cys Leu Val Ile Val Ala Leu Ser  
1 5 10 15  
Ser Ser Ser His Val Trp Ser Asp Gln Ile Phe Pro Ala His Leu Val  
20 25 30  
Gly Thr Phe Ser Arg Asn Asn Arg Glu Pro Lys Tyr Lys Ile Glu Phe  
35 40 45  
Leu Pro Glu Asp Ser Pro Phe His Pro Gly Asp Asn Leu Glu Ser Met  
50 55 60  
Val Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro Lys  
65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Glu | Lys | Ala | Thr | Ser | Gly | Trp | Thr | Ser | Ser | Gln | Gln | Asn | Ile | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Val | Met | Met | Glu | Thr | Gln | Gln | Leu | Val | Lys | Leu | Lys | Thr | Pro | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Leu | Leu | Gln | Pro | Leu | Ser | Glu | Lys | Cys | Leu | Phe | Arg | Gln | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Trp | Ser | Tyr | Glu | Phe | Cys | His | Gln | Lys | Tyr | Val | Arg | Gln | Leu | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Glu | Asp | Glu | Asn | Lys | Ile | Val | Gln | Glu | Phe | Phe | Leu | Gly | Thr | Phe |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Pro | Glu | Ala | Thr | Ala | Ala | Phe | Asn | Gln | Thr | Val | Ser | Asp | Ala | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Asp | Ala | Ser | Gln | Arg | Tyr | His | Ser | His | Val | Tyr | Thr | Asn | Gly | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Cys | Asp | Leu | Thr | Gly | Ser | Pro | Arg | Glu | Val | Glu | Val | Arg | Phe | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Ala | Glu | Thr | Arg | Ala | Met | Val | Thr | Ser | Ile | Thr | Glu | Leu | Ser | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Lys | Tyr | Ala | Leu | Thr | Val | Gln | Cys | Pro | Thr | Leu | Cys | Lys | His | Xaa |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Phe | Gln | Leu | Glu | Lys | Pro | Val | Ser | His | Thr | Ile | His | Cys | Asn | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Pro | Val | Glu | Asp | Ala | Thr | Arg | Asn | Lys | Glu | Glu | Gln | Ala | Val |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asp | Glu | Ser | Pro | Lys | Met | Ile | Ala | Asp | Ser |     |     |     |     |     |     |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1572122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Met | Leu | Asp | Lys | His | Gly | Asn | Arg | Phe | Leu | Cys | Tyr | Leu | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Glu | Glu | Lys | Ala | Thr | Ser | Gly | Trp | Thr | Ser | Ser | Gln | Gln | Asn | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Thr | Val | Met | Met | Glu | Thr | Gln | Gln | Leu | Val | Lys | Leu | Lys | Thr | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Leu | Leu | Gln | Pro | Leu | Ser | Glu | Lys | Cys | Leu | Phe | Arg | Gln | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Trp | Trp | Ser | Tyr | Glu | Phe | Cys | His | Gln | Lys | Tyr | Val | Arg | Gln | Leu |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Val | Glu | Asp | Glu | Asn | Lys | Ile | Val | Gln | Glu | Phe | Phe | Leu | Gly | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Asp | Pro | Glu | Ala | Thr | Ala | Ala | Phe | Asn | Gln | Thr | Val | Ser | Asp | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Thr | Asp | Ala | Ser | Gln | Arg | Tyr | His | Ser | His | Val | Tyr | Thr | Asn | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Thr | Cys | Asp | Leu | Thr | Gly | Ser | Pro | Arg | Glu | Val | Glu | Val | Arg | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Cys | Ala | Glu | Thr | Arg | Ala | Met | Val | Thr | Ser | Ile | Thr | Glu | Leu | Ser |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Cys | Lys | Tyr | Ala | Leu | Thr | Val | Gln | Cys | Pro | Thr | Leu | Cys | Lys | His |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Xaa | Leu | Phe | Gln | Leu | Glu | Lys | Pro | Val | Ser | His | Thr | Ile | His | Cys | Asn |

180 185 190  
Ala Ile Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala  
195 200 205  
Val Asp Glu Ser Pro Lys Met Ile Ala Asp Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro Lys Glu  
1 5 10 15  
Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile Ser Thr  
20 25 30  
Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro Asp Glu  
35 40 45  
Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu Gly Trp  
50 55 60  
Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu His Val  
65 70 75 80  
Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr Phe Asp  
85 90 95  
Pro Glu Ala Thr Ala Ala Phe Asn Gln Thr Val Ser Asp Ala Ser Thr  
100 105 110  
Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly Thr Thr  
115 120 125  
Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe Val Cys  
130 135 140  
Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser Thr Cys  
145 150 155 160  
Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His Xaa Leu  
165 170 175  
Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn Ala Ile  
180 185 190  
Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala Val Asp  
195 200 205  
Glu Ser Pro Lys Met Ile Ala Asp Ser  
210 215

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1662
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:

aaacctgtat tttatcaatt accacacttt gtctaagcaa aatggattta ttactcatat 60  
ccttaaccac tatcataatc gccgcctaca tgcaaaatct acgacgtcgg ggatccaaca 120  
taccgccggg accaccaacg cgattttctgg tcggaaacct tcatcaactg aaaccattat 180  
ggacgcagtc tttctccgag tggtcacaga cttatggccc catcatatcg gtgtggttag 240

gatcacagct agctgttggtg gtctcgagct ctgacttagc caaacaagtg ttgagagaca 300  
aagactacca actctgtaac cgacacagaa ccgcaaggat gactcagaac ggcagcgatc 360  
ttatattgggtc tgactacgga gcacattatg tgaaaatgag aaaactctgt acactcgagc 420  
tcttttctttt gaaaagcata gagtgtttca ggctcgatgag agagatggaa gtaagttcca 480  
tggttaagtc gatttttcaat gacttcatga gcgatgatca gaaaccagtg gtgttgagga 540  
actatctaga ttctgttgct ttgaacattg tttcaagatt agttatcggg aaaacattcg 600  
aaccctaaaga tggaagagag tttagatcaa ttgtagaaag ggagactcgc ttgcccggcg 660  
caaccaagat gcttgattac accgtttggc ttaaactgct ttcgtcatgg ttcactagcg 720  
acaaggcggt catgaagcac atggctcgga aaagaaattg gtttaaactg gctgtaattg 780  
atgaagtata tggaggaaga gatcaaaagt gttttgttca gagtctgtta gaggttgaaag 840  
agaaggatga gctgaccgag gagactgtga tgggactggg ctggaacatg ttaactgcag 900  
gagctgacac aacggccata actattgaat gggcaatggc agagatgatc agatgcccgga 960  
ccgtgaaaga aaaggtgcag gatgagcttg attccgtggg tggatccgga cggttaatgt 1020  
ctgatgcaga tatcccaaaa ctgccgtttc tgcaatgcgt actcaaagaa gctctccggc 1080  
ttcaccctcc aacaccattg atgcttccac acaaggccag cgaatcagtt caggtaggtg 1140  
ggtacaaaagt tcctaaggga gccacggttt atgtcaactg gcaggcgatt gctcgagatc 1200  
ctgcaaaactg gagtaaccca gatgagttta gaccagagag gtttcttggt gaggaacgg 1260  
acgttaaagg tcaagacttt cgggttcttc catttggtgc gggaagacgg gtgtgtccag 1320  
ccgtcgaact cagcctcaat atgatgacat tagcactagg tagtttggtg cattgtttct 1380  
catggacatc ctctacacct cgagaacaca ttgacatgac cgagaagcct ggattagttt 1440  
gttacatgaa ggtccattg caggctctag cttcgtccag gctgccacaa gagttatacc 1500  
tttaactttt aactgagata gattatatta atcaacataa gataaagaga gattctcaat 1560  
tgcgaaaaac agatgtagct atggcaagat ttaggacatg gatgatgaaa tggttcgtac 1620  
aaacagaatg tagctattga tagtaataa actaaatatt cc

(2) INFORMATION FOR SEQ ID NO:2227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1572140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

Thr Cys Ile Leu Ser Ile Thr Thr Leu Cys Leu Ser Lys Met Asp Leu  
1 5 10 15  
Leu Leu Ile Ser Leu Thr Thr Ile Ile Ala Ala Tyr Met Gln Asn  
20 25 30  
Leu Arg Arg Arg Gly Ser Asn Ile Pro Pro Gly Pro Pro Thr Arg Phe  
35 40 45  
Leu Val Gly Asn Leu His Gln Leu Lys Pro Leu Trp Thr Gln Ser Phe  
50 55 60  
Ser Glu Trp Ser Gln Thr Tyr Gly Pro Ile Ile Ser Val Trp Leu Gly  
65 70 75 80  
Ser Gln Leu Ala Val Val Val Ser Ser Ser Asp Leu Ala Lys Gln Val  
85 90 95  
Leu Arg Asp Lys Asp Tyr Gln Leu Cys Asn Arg His Arg Thr Ala Arg  
100 105 110  
Met Thr Gln Asn Gly Ser Asp Leu Ile Trp Ser Asp Tyr Gly Ala His  
115 120 125  
Tyr Val Lys Met Arg Lys Leu Cys Thr Leu Glu Leu Phe Ser Leu Lys  
130 135 140  
Ser Ile Glu Cys Phe Arg Ser Met Arg Glu Met Glu Val Ser Ser Met  
145 150 155 160  
Val Lys Ser Ile Phe Asn Asp Phe Met Ser Asp Asp Gln Lys Pro Val  
165 170 175  
Val Leu Arg Asn Tyr Leu Asp Ser Val Ala Leu Asn Ile Val Ser Arg  
180 185 190  
Leu Val Ile Gly Lys Thr Phe Glu Pro Lys Asp Gly Arg Glu Phe Arg

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1572141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Leu | Leu | Ile | Ser | Leu | Thr | Thr | Ile | Ile | Ile | Ala | Ala | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Gln | Asn | Leu | Arg | Arg | Arg | Gly | Ser | Asn | Ile | Pro | Pro | Gly | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Arg | Phe | Leu | Val | Gly | Asn | Leu | His | Gln | Leu | Lys | Pro | Leu | Trp | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gln | Ser | Phe | Ser | Glu | Trp | Ser | Gln | Thr | Tyr | Gly | Pro | Ile | Ile | Ser | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Leu | Gly | Ser | Gln | Leu | Ala | Val | Val | Val | Ser | Ser | Ser | Asp | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:2229:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide



Leu Pro Gln Glu Leu Tyr Leu  
465 470

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

agggtccgtcg cttctcttcc atttcttctc attttcgatt ttgattotta tttctttcca 60  
gtagctcctg ctctgtgaat ttctccgctc acgatagatc tgcttatact cottacattc 120  
aaccttagat ctgaaacatg ggtgcagggt gaagaatgcc ggcttctact tcttccaaga 180  
aatcggaac cgacaccaca aagcgtgtgc cgtgcgagaa accgcctttc tcgggtgggag 240  
atctgaagaa agcaatcccg ccgcattgtt tcaaacgctc aatccctcgc tctttctcct 300  
acottatcag tgacatcatt atagcctcat gcttctacta cgtcgccacc aattacttct 360  
ctctctctcc tcagcctctc tcttacttgg cttggccact ctattggggtc tgtcaaggct 420  
gtgtcctaac tggtatctgg gtcatagcc acgaatgcgg tcaccacgca ttcagcgact 480  
accaatggct ggatgacaca gttggtctta tcttccattc ctctctctc gtcccttact 540  
tctcctggaa gtatagtcac cgccgtcacc attccaacac tggatccctc gaaagagatg 600  
aagtatttgt cccaaagcag aaatcagcaa tcaagtggta cgggaaatac ctcaacaacc 660  
ctcttggacg catcatgatg ttaaccgtcc agtttgcct cgggtggccc ttgtacttag 720  
cctttaacgt ctctggcaga ccgtatgacg ggttcgcttg ccatttcttc cccaacgctc 780  
ccatctacaa tgaccgagaa cgccctccaga tatacctctc tgatgcgggt attctagccg 840  
tctgttttgg tctttaccgt tacgctgctg cacaagggtt ggctcgtatg atctgcctct 900  
acggagtacc gcttctgata gtgaatgcgt tccctgctct gatcacttac ttgcagaca 960  
ctcatcctc gttgcctcac tacgattcat cagagtggga ctggctcagg ggagctttgg 1020  
ctaccgtaga cagagactac ggaatcttga acaagggtgt ccacaacatt acagacacac 1080  
acgtggctca tcacctgttc tcgacaatgc cgcattataa cgcaatggaa gctacaaagg 1140  
cgataaagcc aattctggga gaccattacc agttcgatgg aacaccgtgg tatgtggcga 1200  
tgtataggga ggcaaaggag tgtatctatg tagaaccgga cagggaaggt gacaagaaa 1260  
gtgtgtactg gtacaacaat aagttatgag gatgatgggt aagaaattgt cgacttttct 1320  
cttgtctgtt tgtcttttgt taaagaagct atgcttcgtt ttaataatct tattgtccat 1380  
tttgttgtgc

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser  
1 5 10 15  
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser  
20 25 30  
Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
35 40 45  
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser  
50 55 60  
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
65 70 75 80  
Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val



[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Pro | Thr | Ser | Ser | Lys | Lys | Ser | Glu | Thr | Asp | Thr | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Val | Pro | Cys | Glu | Lys | Pro | Pro | Phe | Ser | Val | Gly | Asp | Leu | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Pro | Pro | His | Cys | Phe | Lys | Arg | Ser | Ile | Pro | Arg | Ser | Phe | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Leu | Ile | Ser | Asp | Ile | Ile | Ile | Ala | Ser | Cys | Phe | Tyr | Tyr | Val | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Thr | Asn | Tyr | Phe | Ser | Leu | Leu | Pro | Gln | Pro | Leu | Ser | Tyr | Leu | Ala | Trp |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val | Leu | Thr | Gly | Ile | Trp | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu  
100 105 110  
Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr  
115 120 125  
Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser  
130 135 140  
Leu Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys  
145 150 155 160  
Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met Met Leu  
165 170 175  
Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val  
180 185 190  
Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala  
195 200 205  
Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala  
210 215 220  
Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala Ala Ala Gln  
225 230 235 240  
Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val  
245 250 255  
Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser  
260 265 270  
Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu  
275 280 285  
Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
290 295 300  
Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His  
305 310 315 320  
Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp  
325 330 335  
His Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu  
340 345 350  
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys  
355 360 365  
Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
370 375

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala  
1 5 10 15  
Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe  
20 25 30  
Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu  
35 40 45  
Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala  
50 55 60  
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu  
65 70 75 80  
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr  
85 90 95  
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg

```

 100 105 110
Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val
 115 120 125
Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr
 130 135 140
Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile
 145 150 155 160
Leu Gly Asp His Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met
 165 170 175
Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly
 180 185 190
Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
 195 200
```

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

```

aaaaaaacca ataaaattgg tcgcttcgca aaaactgaga tvtgagttct tccttcggtg 60
gaaagagcaa attttacttt taagaaatTTT gaaaacaaaag ttTcattaaa cagattgggtg 120
ggatttttaa tttgaatttt gatcagtgaa tcaacgataa acgattcgTc gttatggaag 180
gagttggtgc acggttaggc aggtcctcga cacggTacgg accggcaacg gttttcaccg 240
gtccggtgcg gaagtggaag aagaagtggg tacacgtctc tccatccact aagaaagaca 300
ataataatag ctctctcoggT tccgccgctg ctgcagcttc cgTcgTtaat gTggttcga 360
attctgacgg cagtaatgga tcgcatttgt tGctgtataa gtgggcacca ttgtcccaga 420
acggtaacgg gaatgaagat ggtaaaagtG agagtaattc tccgagcgag gacacggTgg 480
cgacggTggc agaagatcct ccgcggcgga gattcaaata cgTtccgata gcagtacttg 540
aggaacagaa gaaggaaatt acagaaattg aggacgatga taagattgag gaggatgaca 600
agattgatga ggataataag gTcgagcagg aagacaaggT tgatgaggac aaaactgtag 660
aggagTcgag cgagaagaaa gcggaagTtg aagtggaagT ggaggaaaag cctgatatca 720
atgatgttcc aatggaagat attcagcagg atgaagaaaa aatagtacag gatgatgaag 780
aaaaagtagt gcgacaagat ttgaacgaaa gcactgtgga tttaggactg aacttaaTg 840
caaacgatgc Tgatgtgat gcagaaaaacg acccgaaaaga ggacaagcca ttagaagaat 900
gataaaactgg gtgcattgtt ttggttcctc accctcaact ctcaatatca attaggaaga 960
aagacattac agaaagaaca aagcagTcat tagatatgga cgcagatcct tgatttggtc 1020
tgtaacccca tggcttatTc cttttgatgt taatggaaat gactcattga ttcagactga 1080
tcattcaatt cataggCaga ttcttgtcc
```

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

```

Met Glu Gly Val Gly Ala Arg Leu Gly Arg Ser Ser Thr Arg Tyr Gly
1 5 10 15
Pro Ala Thr Val Phe Thr Gly Pro Val Arg Lys Trp Lys Lys Lys Trp
 20 25 30
Val His Val Ser Pro Ser Thr Lys Lys Asp Asn Asn Asn Ser Ser Ser
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |     |     |     |     |     |     |     |     |     |     |
| Gly | Ser | Ala | Ala | Ala | Ala | Ser | Val | Val | Asn | Gly | Gly | Ser | Asn | Ser |     |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Asp | Gly | Ser | Asn | Gly | Ser | His | Leu | Leu | Leu | Tyr | Lys | Trp | Ala | Pro | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Gln | Asn | Gly | Asn | Gly | Asn | Glu | Asp | Gly | Lys | Ser | Glu | Ser | Asn | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ser | Glu | Asp | Thr | Val | Ala | Thr | Val | Ala | Glu | Asp | Pro | Pro | Arg | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Phe | Lys | Tyr | Val | Pro | Ile | Ala | Val | Leu | Glu | Glu | Gln | Lys | Lys | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ile | Thr | Glu | Ile | Glu | Asp | Asp | Asp | Lys | Ile | Glu | Glu | Asp | Asp | Lys | Ile |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Glu | Asp | Asn | Lys | Val | Glu | Gln | Glu | Asp | Lys | Val | Asp | Glu | Asp | Lys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Val | Glu | Glu | Ser | Ser | Glu | Lys | Lys | Ala | Glu | Val | Glu | Val | Glu | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Glu | Lys | Pro | Asp | Ile | Asn | Asp | Val | Pro | Met | Glu | Asp | Ile | Gln | Gln |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Glu | Glu | Lys | Ile | Val | Gln | Asp | Asp | Glu | Glu | Lys | Val | Val | Arg | Gln |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Leu | Asn | Glu | Ser | Thr | Val | Asp | Leu | Gly | Leu | Asn | Leu | Asn | Ala | Asn |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Asp | Ala | Asp | Ala | Asp | Ala | Glu | Asn | Asp | Pro | Lys | Glu | Asp | Lys | Pro | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..850
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| ctgagctcag | cttcactttg | ctcgacgtta  | tcttcttcgt | tcagcgacaa | tggcgtcgat | 60  |
| tacgaacctc | gcctcttctc | tctcttcaact | ctcgttctcc | tcccaagttt | ctcaaagacc | 120 |
| taacaccatt | tccttcccc  | gcgcgaattc  | agtattcgca | ttaccggcga | aatccgcacg | 180 |
| ccgcgcttct | ctatctatca | ccgccacggt  | atctgctcca | ccggaggagg | aggagatagt | 240 |
| tgaactgaag | aaatacgtca | aatcgagggt  | tcccgaggga | tttgctgctc | agaagattat | 300 |
| tggcactgga | cgacgtaagt | gcgcaatcgc  | tagagttggt | cttcaggaag | gtactgggaa | 360 |
| ggttatcatc | aactatcgtg | atgccaaagga | gtaccttcag | ggaaatccat | tgtggcttca | 420 |
| gtatgttaaa | gtaccattgg | tgacttttagg | atatgagaat | agctacgaca | tatttgtgaa | 480 |
| agcccatgga | ggcgtctct  | caggtcaagc  | tcaagcaatt | accttgggag | tcgcacgtgc | 540 |
| actcctgaag | gtaagtgcag | accacagatc  | gcctttgaag | aaggaagggt | tgctcactag | 600 |
| agatgcgaga | gtggttgaaa | gaaagaaggc  | cgggctcaag | aaggcgcgta | aagccccaca | 660 |
| attctccaag | cgtaaagagt | tttatatatc  | attgaatcaa | ctcttcaagt | agactcctct | 720 |
| gcctccatth | ttttttaaaa | cttttcttgt  | ctattatcgg | tcttttggtt | catgttaatg | 780 |
| tttatgtgta | gacgaactaa | tacaatctct  | gttttggttg | aatggaacgc | aaagttgata | 840 |
| tgGcttttgt |            |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1572181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ile | Thr | Asn | Leu | Ala | Ser | Ser | Leu | Ser | Ser | Leu | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Gln | Val | Ser | Gln | Arg | Pro | Asn | Thr | Ile | Ser | Phe | Pro | Arg | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ser | Val | Phe | Ala | Leu | Pro | Ala | Lys | Ser | Ala | Arg | Arg | Ala | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Thr | Ala | Thr | Val | Ser | Ala | Pro | Pro | Glu | Glu | Glu | Glu | Ile | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Leu | Lys | Lys | Tyr | Val | Lys | Ser | Arg | Leu | Pro | Gly | Gly | Phe | Ala | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Lys | Ile | Ile | Gly | Thr | Gly | Arg | Arg | Lys | Cys | Ala | Ile | Ala | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Gln | Glu | Gly | Thr | Gly | Lys | Val | Ile | Ile | Asn | Tyr | Arg | Asp | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Glu | Tyr | Leu | Gln | Gly | Asn | Pro | Leu | Trp | Leu | Gln | Tyr | Val | Lys | Val |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Val | Thr | Leu | Gly | Tyr | Glu | Asn | Ser | Tyr | Asp | Ile | Phe | Val | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | His | Gly | Gly | Gly | Leu | Ser | Gly | Gln | Ala | Gln | Ala | Ile | Thr | Leu | Gly |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Val | Ala | Arg | Ala | Leu | Leu | Lys | Val | Ser | Ala | Asp | His | Arg | Ser | Pro | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Lys | Glu | Gly | Leu | Leu | Thr | Arg | Asp | Ala | Arg | Val | Val | Glu | Arg | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Ala | Gly | Leu | Lys | Lys | Ala | Arg | Lys | Ala | Pro | Gln | Phe | Ser | Lys | Arg |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..700

(D) OTHER INFORMATION: / Ceres Seq. ID 1572195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| acttgttctc  | atattagttt  | gttatacaac  | tcacttagaa | taatgtagat | tacatttcag  | 60  |
| cctaaattcat | attcttgaga  | gaaaagaaat  | cgaagatggc | aacaaaatcc | accggaggta  | 120 |
| ccgagaaaac  | caagtcgata  | gaagtgaaga  | agaaactaat | caacgtgttg | atcgtcgatg  | 180 |
| atgatccatt  | aaaccgtaga  | ctccacgaga  | tgatcatcaa | aacgatcgga | ggaatttctc  | 240 |
| agactgcaaa  | gaatggcgag  | gaggcagtga  | tcctccaccg | tgacggcgAa | gcattctttcg | 300 |
| accttattct  | aatggataag  | gaaatgcctg  | agagggatgg | agtttcgaca | actaagaagc  | 360 |
| taagagaaat  | gaaagtgcg   | tcaatgatcg  | ttggggtaac | gtcagtagct | gaccaagaag  | 420 |
| aagagcgtaa  | ggcttttatg  | gaagctgggc  | tcaaccattg | cttggaaaaa | cccttaacca  | 480 |
| aggccaagat  | cttcccgcctc | attagccacc  | tcttcgatgc | ttgatggatg | aaggctcatt  | 540 |
| aatgtatcta  | tattttcaat  | catgaaatca  | cctacacgtg | tatttgacac | aaaaatctgc  | 600 |
| atttgttgtg  | atatagggtt  | tctcatatct  | atgtttgatt | tattttctta | tcgtccgagg  | 660 |
| taaaatcatg  | caagtcattt  | cttttggtcta | ataaaatatt |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572196  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:

Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu  
1 5 10 15  
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu  
20 25 30  
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser  
35 40 45  
Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Ile Leu His Arg Asp Gly  
50 55 60  
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg  
65 70 75 80  
Asp Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Lys Val Thr Ser  
85 90 95  
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys  
100 105 110  
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr  
115 120 125  
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2240:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1572197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:

Met Ile Ile Lys Thr Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly  
1 5 10 15  
Glu Glu Ala Val Ile Leu His Arg Asp Gly Glu Ala Ser Phe Asp Leu  
20 25 30  
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr  
35 40 45  
Lys Lys Leu Arg Glu Met Lys Val Thr Ser Met Ile Val Gly Val Thr  
50 55 60  
Ser Val Ala Asp Gln Glu Glu Arg Lys Ala Phe Met Glu Ala Gly  
65 70 75 80  
Leu Asn His Cys Leu Glu Lys Pro Leu Thr Lys Ala Lys Ile Phe Pro  
85 90 95  
Leu Ile Ser His Leu Phe Asp Ala  
100

(2) INFORMATION FOR SEQ ID NO:2241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 982 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1572201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| agaacacaaa | caaaaacaca | ttgtaacatt | agtttaagca  | ttaagcttct | ttatgtcgaa | 60  |
| taataataat | tctccgacca | ccgtgaatca | agaaacgacg  | acgtctcgtg | aagtctcaat | 120 |
| cacattgctt | actgatcaat | ctcctcaaac | ctcaccagga  | tcattcttct | ctccttcacc | 180 |
| gagaccttcc | ggtggatcac | cggcgagaag | aacggcgact  | ggattatccg | gcaagcactc | 240 |
| tattttcagg | gggattcgac | tacgtaacgg | aaaatgggta  | tcggagatta | gagagccacg | 300 |
| taaaacgaca | agaatttggc | tcgggactta | tccggtaccg  | gagatggctg | ccgccgctta | 360 |
| cgacgtggct | gcgttagCtt | taaaaggacc | aggccgtttt  | gaattttcct | ggGtttagct | 420 |
| ttgacttacg | tggctccggg | ttcaaactct | gctgcggata  | taagagcggc | tgctagtaga | 480 |
| gcagcggaga | tgaagcaacc | ggatcagggt | ggggatgaga  | Aggtattgga | accggttcaa | 540 |
| cccggaagag | aggaagaatt | agaagaagtg | tcgtgttaact | cgtgttcggt | ggagtttatg | 600 |
| gatgaggaag | cgatgttgaa | tatgccgact | ttgttgacgg  | agatggctga | agggatgttg | 660 |
| atgagtccac | cgagaatgat | gatacatccg | acgatggaag  | atgattcgcc | ggagaatcat | 720 |
| gaaggagata | atctttggag | ttataaatga | atccattgaa  | gctgctctct | tttttattgt | 780 |
| tttcgggtcg | aatgagattt | tccccctttt | tttttctttt  | tgggtcgctg | ttatggaaag | 840 |
| tcaaataagg | tattaatatg | atctattaat | atttttgaaa  | cataatgagt | ttgaatttga | 900 |
| atttttccat | ttttatataa | atatggttta | tatgagggaa  | aaatagatac | atatcgaaga | 960 |
| tataagaatt | gtttttctgc | tt         |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1572202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Asn | Asn | Asn | Ser | Pro | Thr | Thr | Val | Asn | Gln | Glu | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Arg | Glu | Val | Ser | Ile | Thr | Leu | Pro | Thr | Asp | Gln | Ser | Pro | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ser | Pro | Gly | Ser | Ser | Ser | Ser | Pro | Ser | Pro | Arg | Pro | Ser | Gly | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Ala | Arg | Arg | Thr | Ala | Thr | Gly | Leu | Ser | Gly | Lys | His | Ser | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Arg | Gly | Ile | Arg | Leu | Arg | Asn | Gly | Lys | Trp | Val | Ser | Glu | Ile | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Pro | Arg | Lys | Thr | Thr | Arg | Ile | Trp | Leu | Gly | Thr | Tyr | Pro | Val | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Met | Ala | Ala | Ala | Tyr | Asp | Val | Ala | Ala | Leu | Ala | Leu | Lys | Gly |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Pro | Gly | Arg | Phe | Glu | Phe | Ser | Trp | Val |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1572203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val

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1 5 10 15  
Gln Pro Gly Lys Glu Glu Glu Leu Glu Val Ser Cys Asn Ser Cys  
20 25 30  
Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu  
35 40 45  
Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met  
50 55 60  
Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp  
65 70 75 80  
Asn Leu Trp Ser Tyr Lys  
85

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..932

(D) OTHER INFORMATION: / Ceres Seq. ID 1572204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

aactgtttga tttctgagga gaatccattg tttccattcg aagaaaaactc taactttctc 60  
gttgaagctt tgagctctct acctctttat ctccggagat gtataataac atgggacctc 120  
aaccggggat gccaaagacct ccaggaaacc ctgagcctgg tccatttggt aatcctttca 180  
ctggagctgg ctcggttttt atccgtggtg gtttgggagc gtatggggag agaattttag 240  
gatcgartc tgagtatgtt cagagcaata taagccggta cttctctgat ccgcaatact 300  
atttccaagt gaatgatcaa tatgtgagga ataaactgaa ggttgttctg tttcctttcc 360  
tacaccgggg acactggacc agaatatctg aaccagttag tggtaggctc tcatacaagc 420  
ctccaatata tgatatcaat gctccCagac ttgtacattc ctttatggc atttggtacc 480  
taogttgttc ttgctggtct ttcattggga cttaatggaa agtttacacc ggaagctttg 540  
aattggctgt ttgtgaaagg attggttggg tggtttttgc aagtaatgct cctgaaagta 600  
acattctat cacttggttag tggagaggca ccattactag atattgtggc atacggaggg 660  
tatgcttttg ctggtctgtg tcttgcgggc tttgccaaaa taatgtgggg atactcgta 720  
taogcgttga tgccatggac ttgtctatgc actgggattt tcttggtgaa gacgatgaaa 780  
cgtgttctgt ttgctgaagt aagaagttac gattcgagca aacatcacta ccttcttctg 840  
tttttagcct tgggtccagtt cccacttttg atatggcttg gtaacattag tgtaatttgg 900  
cttctttgaa atgaaaaaag acgtttttgt gt

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1572205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

Met Ile Ser Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly  
1 5 10 15  
Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe  
20 25 30  
Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp  
35 40 45  
Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser  
50 55 60  
Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe  
65 70 75 80



Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser  
85 90 95  
Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu  
100 105 110  
Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp  
115 120 125  
Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe  
130 135 140  
Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1572206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly Thr Tyr Val  
1 5 10 15  
Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe Thr Pro Glu  
20 25 30  
Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp Phe Leu Gln  
35 40 45  
Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser Gly Glu Ala  
50 55 60  
Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe Ala Gly Leu  
65 70 75 80  
Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser Tyr Tyr Ala  
85 90 95  
Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu Val Lys Thr  
100 105 110  
Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp Ser Ser Lys  
115 120 125  
His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe Pro Leu Leu  
130 135 140  
Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1572207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Met Ala Phe Gly Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu  
1 5 10 15  
Asn Gly Lys Phe Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly  
20 25 30  
Leu Val Gly Trp Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu  
35 40 45  
Ser Leu Gly Ser Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly

50 55 60  
Gly Tyr Ala Phe Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met  
65 70 75 80  
Trp Gly Tyr Ser Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr  
85 90 95  
Gly Ile Phe Leu Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val  
100 105 110  
Arg Ser Tyr Asp Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala  
115 120 125  
Leu Val Gln Phe Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn  
130 135 140  
Trp Leu Leu  
145

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1209
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

aaaaatctct ttactaccag caagttgttt tcttgctaac ttcaaacttc tctttctctt 60  
gttcctctct aagtcttgat cttatttacc gttaactttg tgaacaaaag tgaatcaaa 120  
cacacatgga gccgccacag catcagcatc atcatcatca agccgaccaa gaaagcggca 180  
acaacaacaa caacaagtcc ggctctgggtg gttacacgtg tcgccagacc agcacgaggt 240  
ggacaccgac gacggagcaa atcaaaatcc tcaaagaact ttactacaac aatgcaatcc 300  
ggtcaccaac agccgatcag atccagaaga tcaactgcaag gctgagacag ttcggaaaaga 360  
ttgagggcaa gaacgtcttt tactggttcc agaaccataa ggctcgtgag cgtcagaaga 420  
agagattcaa cggaacaaac atgaccacac catcttcac acccaactcg gttatgatgg 480  
cggctaacga tcattatcat cctctacttc accatcatca cgggtgtccc atgcagagac 540  
ctgctaattc cgtcaacggt aaacttaacc aagaccatca tctctatcat cataacaagc 600  
catatcccag cttcaataac gggaatttaa atcatgcaag ctcagggtact gaatgtgggtg 660  
ttgttaatgc ttctaattggc tacatgagta gccatgtcta tggatctatg gaacaagact 720  
gttctatgaa ttacaacaac gtaggtggag gatgggcaa catggatcat cattactcat 780  
ctgcacctta caacttcttc gatagagcaa agcctctgtt tggctagaa ggtcatcaag 840  
aagaagaaga atgtggtggc gatgcttacc tggaaacatcg acgtacgctt cctctcttcc 900  
ctatgcacgg tgaagatcac atcaacgggtg gtagtggtgc catctggaag tatggccaat 960  
cggaagttcg cccttgcgct tctcttgagc tacgtctgaa ctactcttta cgccggtgtc 1020  
gctcgggatt aaagctcttt cctctctctc tctctttcgt actcgtatgt tcacaactat 1080  
gCttcgctag tgattaatga tgcagttggt atattagtag ttaactagtt atctctcgtt 1140  
atgtgtaatt tgtaattact agctaagtat cgtctaggtt ttaattgtaa ttgacaaccg 1200  
ttttatctc

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

Met Glu Pro Pro Gln His Gln His His His His Gln Ala Asp Gln Glu  
1 5 10 15  
Ser Gly Asn Asn Asn Asn Lys Ser Gly Ser Gly Gly Tyr Thr Cys

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gln | Thr | Ser | Thr | Arg | Trp | Thr | Pro | Thr | Thr | Glu | Gln | Ile | Lys | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Glu | Leu | Tyr | Tyr | Asn | Asn | Ala | Ile | Arg | Ser | Pro | Thr | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ile | Gln | Lys | Ile | Thr | Ala | Arg | Leu | Arg | Gln | Phe | Gly | Lys | Ile | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Lys | Asn | Val | Phe | Tyr | Trp | Phe | Gln | Asn | His | Lys | Ala | Arg | Glu | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Lys | Lys | Arg | Phe | Asn | Gly | Thr | Asn | Met | Thr | Thr | Pro | Ser | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Asn | Ser | Val | Met | Met | Ala | Ala | Asn | Asp | His | Tyr | His | Pro | Leu | Leu |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| His | His | His | His | Gly | Val | Pro | Met | Gln | Arg | Pro | Ala | Asn | Ser | Val | Asn |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Lys | Leu | Asn | Gln | Asp | His | His | Leu | Tyr | His | His | Asn | Lys | Pro | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Ser | Phe | Asn | Asn | Gly | Asn | Leu | Asn | His | Ala | Ser | Ser | Gly | Thr | Glu |
|     |     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Gly | Val | Val | Asn | Ala | Ser | Asn | Gly | Tyr | Met | Ser | Ser | His | Val | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ser | Met | Glu | Gln | Asp | Cys | Ser | Met | Asn | Tyr | Asn | Asn | Val | Gly | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Trp | Ala | Asn | Met | Asp | His | His | Tyr | Ser | Ser | Ala | Pro | Tyr | Asn | Phe |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Asp | Arg | Ala | Lys | Pro | Leu | Phe | Gly | Leu | Glu | Gly | His | Gln | Glu | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Glu | Cys | Gly | Gly | Asp | Ala | Tyr | Leu | Glu | His | Arg | Arg | Thr | Leu | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Phe | Pro | Met | His | Gly | Glu | Asp | His | Ile | Asn | Gly | Gly | Ser | Gly | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Trp | Lys | Tyr | Gly | Gln | Ser | Glu | Val | Arg | Pro | Cys | Ala | Ser | Leu | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Arg | Leu | Asn |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1572242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Pro | Ser | Ser | Ser | Pro | Asn | Ser | Val | Met | Met | Ala | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | His | Tyr | His | Pro | Leu | Leu | His | His | His | His | Gly | Val | Pro | Met | Gln |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Pro | Ala | Asn | Ser | Val | Asn | Val | Lys | Leu | Asn | Gln | Asp | His | His | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | His | His | Asn | Lys | Pro | Tyr | Pro | Ser | Phe | Asn | Asn | Gly | Asn | Leu | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| His | Ala | Ser | Ser | Gly | Thr | Glu | Cys | Gly | Val | Val | Asn | Ala | Ser | Asn | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | Met | Ser | Ser | His | Val | Tyr | Gly | Ser | Met | Glu | Gln | Asp | Cys | Ser | Met |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Asn | Tyr | Asn | Asn | Val | Gly | Gly | Gly | Trp | Ala | Asn | Met | Asp | His | His | Tyr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

Ser Ser Ala Pro Tyr Asn Phe Phe Asp Arg Ala Lys Pro Leu Phe Gly  
115 120 125  
Leu Glu Gly His Gln Glu Glu Glu Cys Gly Gly Asp Ala Tyr Leu  
130 135 140  
Glu His Arg Arg Thr Leu Pro Leu Phe Pro Met His Gly Glu Asp His  
145 150 155 160  
Ile Asn Gly Gly Ser Gly Ala Ile Trp Lys Tyr Gly Gln Ser Glu Val  
165 170 175  
Arg Pro Cys Ala Ser Leu Glu Leu Arg Leu Asn  
180 185

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1572243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Met Met Ala Ala Asn Asp His Tyr His Pro Leu Leu His His His His  
1 5 10 15  
Gly Val Pro Met Gln Arg Pro Ala Asn Ser Val Asn Val Lys Leu Asn  
20 25 30  
Gln Asp His His Leu Tyr His His Asn Lys Pro Tyr Pro Ser Phe Asn  
35 40 45  
Asn Gly Asn Leu Asn His Ala Ser Ser Gly Thr Glu Cys Gly Val Val  
50 55 60  
Asn Ala Ser Asn Gly Tyr Met Ser Ser His Val Tyr Gly Ser Met Glu  
65 70 75 80  
Gln Asp Cys Ser Met Asn Tyr Asn Asn Val Gly Gly Gly Trp Ala Asn  
85 90 95  
Met Asp His His Tyr Ser Ser Ala Pro Tyr Asn Phe Phe Asp Arg Ala  
100 105 110  
Lys Pro Leu Phe Gly Leu Glu Gly His Gln Glu Glu Glu Cys Gly  
115 120 125  
Gly Asp Ala Tyr Leu Glu His Arg Arg Thr Leu Pro Leu Phe Pro Met  
130 135 140  
His Gly Glu Asp His Ile Asn Gly Gly Ser Gly Ala Ile Trp Lys Tyr  
145 150 155 160  
Gly Gln Ser Glu Val Arg Pro Cys Ala Ser Leu Glu Leu Arg Leu Asn  
165 170 175

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1572244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acaacttccc | cattttctgc | ttotttttgt | tcaactccaa | tcacacaatt | cacaacccat | 60  |
| tgagaaacca | ataaaataac | ctcaatcaaa | aaaaaaaaaa | aaaaaagatg | aaaatctcaa | 120 |
| tttagtaaag | gagaaaaaag | ccatttcgaa | taacttgaaa | aggttttggt | tttgcagaag | 180 |

```
aaaatgaagg agaaggcgga gagtggtgga ggagtaggat acgtgagagc agatcagata 240
gatttaaaga gtctggacga gcaattgcag agacacttaa gtaaagcatg gacgatggag 300
aagaggaaga gtttgagtga tggatgaagat aacgtcaata acacccgaca taaccagaac 360
aacttcggac atcgacagct tgtgtttcag aggccgcttc Cttggtggtg gatatagcaa 420
caacaacaac agcagcaaga acgacataat taggtcgacc gaggttgaga agtcgaggag 480
agagtgggag attgatcctt ctaagcttat aatcaaaagt gtgattgcta gaggtacttt 540
tggtacgggt caccgtggaa tctacgatgg tcaagatgtc gccgtaaaac tactagactg 600
gggagaagag gggcacaggt cagacgcaga gatagCttcg cttagagctg ctttcactca 660
agaagtt
```

(2) INFORMATION FOR SEQ ID NO:2253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1572245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:

```
Met Lys Glu Lys Ala Glu Ser Gly Gly Val Gly Tyr Val Arg Ala
1 5 10 15
Asp Gln Ile Asp Leu Lys Ser Leu Asp Glu Gln Leu Gln Arg His Leu
20 25 30
Ser Lys Ala Trp Thr Met Glu Lys Arg Lys Ser Leu Ser Asp Gly Glu
35 40 45
Asp Asn Val Asn Asn Thr Arg His Asn Gln Asn Asn Phe Gly His Arg
50 55 60
Gln Leu Val Phe Gln Arg Pro Leu Pro Trp Trp Trp Ile
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1572246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:

```
Met Val Lys Ile Thr Ser Ile Thr Pro Asp Ile Thr Arg Thr Thr Ser
1 5 10 15
Asp Ile Asp Ser Leu Cys Phe Arg Gly Arg Phe Leu Gly Gly Tyr
20 25 30
Ser Asn Asn Asn Asn Ser Ser Lys Asn Asp Ile Ile Arg Ser Thr Glu
35 40 45
Val Glu Lys Ser Arg Arg Glu Trp Glu Ile Asp Pro Ser Lys Leu Ile
50 55 60
Ile Lys Ser Val Ile Ala Arg Gly Thr Phe Gly Thr Val His Arg Gly
65 70 75 80
Ile Tyr Asp Gly Gln Asp Val Ala Val Lys Leu Leu Asp Trp Gly Glu
85 90 95
Glu Gly His Arg Ser Asp Ala Glu Ile Ala Ser Leu Arg Ala Ala Phe
100 105 110
Thr Gln Glu Val
115
```

(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..619
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| atttccggcg  | actgtgaatt | atgtggtcgg  | cgacgttatt | tttcccttct | tttgtggctt | 60  |
| cttcattctt  | tctacctaat | tacaggaacc  | gtagGtttcc | aaagattaaa | gCttcgctct | 120 |
| ttaattaccc  | tctagcgagc | aaaatcatgg  | tcagaaattt | accgttttct | mcaagtgaag | 180 |
| atttttctaaa | gagagagttt | tcagcttttg  | gagagatagc | tgaagtgaag | cttatcaaag | 240 |
| atgaggcaat  | gcagagatca | aaagggttatg | cttttattca | attcacgtct | caagatgatg | 300 |
| cttttcttgc  | catagagacc | atggaccgtc  | ggatgtacaa | tggaagaatg | atttatatag | 360 |
| acattgcgaa  | acccggtaaa | cgtgatttcc  | aaggactacc | gaggacttct | ggccccctg  | 420 |
| agaagtcgga  | tgtgccagaa | gaagccgcta  | atgatgaggt | tgctgattgc | tggtattagt | 480 |
| tgtagtatc   | aagctcacca | aactgtaact  | gaacttgcac | aaatcagatg | tcaaattatg | 540 |
| cttcttatta  | ggaatttgat | caatgtgaag  | aatgttgttt | actgataaac | aattattgac | 600 |
| acggttccag  | ttacagctc  |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..152
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Ser | Ala | Thr | Leu | Ser | Phe | Pro | Ser | Phe | Val | Ala | Ser | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Pro | Asn | Tyr | Arg | Asn | Arg | Arg | Phe | Pro | Lys | Ile | Lys | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Asn | Tyr | Pro | Leu | Ala | Ser | Lys | Ile | Met | Val | Arg | Asn | Leu | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ser | Xaa | Ser | Glu | Asp | Phe | Leu | Lys | Arg | Glu | Phe | Ser | Ala | Phe | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ile | Ala | Glu | Val | Lys | Leu | Ile | Lys | Asp | Glu | Ala | Met | Gln | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Gly | Tyr | Ala | Phe | Ile | Gln | Phe | Thr | Ser | Gln | Asp | Asp | Ala | Phe | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ile | Glu | Thr | Met | Asp | Arg | Arg | Met | Tyr | Asn | Gly | Arg | Met | Ile | Tyr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asp | Ile | Ala | Lys | Pro | Gly | Lys | Arg | Asp | Phe | Gln | Gly | Leu | Pro | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ser | Gly | Pro | Pro | Glu | Lys | Ser | Asp | Val | Pro | Glu | Glu | Ala | Ala | Asn |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Asp | Glu | Val | Ala | Asp | Cys | Trp | Tyr |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 110 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..110  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Arg | Asn | Leu | Pro | Phe | Ser | Xaa | Ser | Glu | Asp | Phe | Leu | Lys | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Phe | Ser | Ala | Phe | Gly | Glu | Ile | Ala | Glu | Val | Lys | Leu | Ile | Lys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Met | Gln | Arg | Ser | Lys | Gly | Tyr | Ala | Phe | Ile | Gln | Phe | Thr | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gln | Asp | Asp | Ala | Phe | Leu | Ala | Ile | Glu | Thr | Met | Asp | Arg | Arg | Met | Tyr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Asn | Gly | Arg | Met | Ile | Tyr | Ile | Asp | Ile | Ala | Lys | Pro | Gly | Lys | Arg | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Gln | Gly | Leu | Pro | Arg | Thr | Ser | Gly | Pro | Pro | Glu | Lys | Ser | Asp | Val |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| Pro | Glu | Glu | Ala | Ala | Asn | Asp | Glu | Val | Ala | Asp | Cys | Trp | Tyr |     |     |
|     |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:2258:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Arg | Ser | Lys | Gly | Tyr | Ala | Phe | Ile | Gln | Phe | Thr | Ser | Gln | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ala | Phe | Leu | Ala | Ile | Glu | Thr | Met | Asp | Arg | Arg | Met | Tyr | Asn | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Met | Ile | Tyr | Ile | Asp | Ile | Ala | Lys | Pro | Gly | Lys | Arg | Asp | Phe | Gln |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Leu | Pro | Arg | Thr | Ser | Gly | Pro | Pro | Glu | Lys | Ser | Asp | Val | Pro | Glu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Glu | Ala | Ala | Asn | Asp | Glu | Val | Ala | Asp | Cys | Trp | Tyr |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2259:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1386  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

|              |            |             |            |            |             |     |
|--------------|------------|-------------|------------|------------|-------------|-----|
| actggtggtgta | atatacgctg | cgtttcgcaa  | gtatcacccg | gaattgcaaa | gaagcagagg  | 60  |
| accatgtacg   | gagacgctac | aaactggaat  | gaagatgagt | atagagaatc | aattttgaag  | 120 |
| gagcgagaga   | tagagacacg | caccgtcttc  | agaaccgcct | gggctcctcc | ggcgagaatc  | 180 |
| tctaattccag  | acgcatttgt | tgtagcctcc  | agcgatggaa | ctttagcttt | ccattcactg  | 240 |
| aactcgcttg   | tgtctcaatc | ggcgagtttt  | ggctactcga | aaggtcaaga | tgttatggtg  | 300 |
| gctgaacctg   | agagagtgg  | tagggcacac  | gaaggtcctg | cttatgatgt | taagttctat  | 360 |
| ggtgaagacg   | aagatgcttt | gctacttagt  | tgtggtgatg | atggtagagt | taggggatgg  | 420 |
| aaatggagag   | aatttgctga | atcagatgtg  | tctcttcatt | tgaaagagaa | tcatctgaag  | 480 |
| ccattgcttg   | aactgattaa | tcacacaacac | aaaggtcctt | ggggtgcgct | ttcacccgatg | 540 |

```
cctgagatca atgccatgtc tgttgatcct cagtcaggaa gtgtatttac agcagctggt 600
gattcttgcg catattgttg ggacgtggag agtggttaaga ttaaaatgac ctttaaaggt 660
cattcagact atttgcatac tgtagtttct cgtagttctg caagtcagat attgacgggt 720
tcagaggatg ggactgcgag aatctgggat tgcaaaacgg gaaaatgtgt taaagtaatt 780
ggttcccagg ataaaaagtc ccgccttgcg gttagttcta tggcccttga tgggagtga 840
agctggttgg tttgtggaca gggcaaaaat ttagctttat ggaatcttcc cgcctcagaa 900
tgcgtacaaa caatacccat ccctgcacat gtacaggatg tgatgtttga tgaaaagcaa 960
attttgactg taggagcaga accacttcta agacgtttcg acttaaatgg agctttgctt 1020
tctcaaattc actgtgctcc ttgttcagta ttttccattt ccttgcatcc agcaggagta 1080
gttgctgtgg gaggttatgg aggtattgtt gatgtcatct ctcaatttgg aagccatctc 1140
tgcacatttc gtagcagttc attgtaaaac tccttacagt ttcttgattt ggctcgatac 1200
cctaaagagg taccgaaatg tgtcagtcag attattgcag aggttaagaa accttttctt 1260
tggttttctt aggatcttgc tcctgactaa agaccaatta gttgtttggt taagtgtaat 1320
tggtttgtgg ttocgtagtt gctatcaaat ttgaaccatt aaaatgacat tggaccggtt 1380
tagtct
```

(2) INFORMATION FOR SEQ ID NO:2260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..388
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

```
Thr Gly Gly Asn Ile Ala Gly Val Ser Gln Val Ser Pro Gly Ile Ala
1 5 10 15
Lys Lys Gln Arg Thr Met Tyr Gly Asp Ala Thr Asn Trp Asn Glu Asp
20 25 30
Glu Tyr Arg Glu Ser Ile Leu Lys Glu Arg Glu Ile Glu Thr Arg Thr
35 40 45
Val Phe Arg Thr Ala Trp Ala Pro Pro Ala Arg Ile Ser Asn Pro Asp
50 55 60
Ala Phe Val Val Ala Ser Ser Asp Gly Thr Leu Ala Phe His Ser Leu
65 70 75 80
Asn Ser Leu Val Ser Gln Ser Ala Ser Phe Gly Tyr Ser Lys Gly Gln
85 90 95
Asp Val Met Val Ala Glu Pro Glu Arg Val Val Arg Ala His Glu Gly
100 105 110
Pro Ala Tyr Asp Val Lys Phe Tyr Gly Glu Asp Glu Asp Ala Leu Leu
115 120 125
Leu Ser Cys Gly Asp Asp Gly Arg Val Arg Gly Trp Lys Trp Arg Glu
130 135 140
Phe Ala Glu Ser Asp Val Ser Leu His Leu Lys Glu Asn His Leu Lys
145 150 155 160
Pro Leu Leu Glu Leu Ile Asn Pro Gln His Lys Gly Pro Trp Gly Ala
165 170 175
Leu Ser Pro Met Pro Glu Ile Asn Ala Met Ser Val Asp Pro Gln Ser
180 185 190
Gly Ser Val Phe Thr Ala Ala Gly Asp Ser Cys Ala Tyr Cys Trp Asp
195 200 205
Val Glu Ser Gly Lys Ile Lys Met Thr Phe Lys Gly His Ser Asp Tyr
210 215 220
Leu His Thr Val Val Ser Arg Ser Ser Ala Ser Gln Ile Leu Thr Gly
225 230 235 240
Ser Glu Asp Gly Thr Ala Arg Ile Trp Asp Cys Lys Thr Gly Lys Cys
245 250 255
Val Lys Val Ile Gly Ser Gln Asp Lys Lys Ser Arg Leu Arg Val Ser
260 265 270
```



Ser Met Ala Leu Asp Gly Ser Glu Ser Trp Leu Val Cys Gly Gln Gly  
275 280 285  
lys Asn Leu Ala Leu Trp Asn Leu Pro Ala Ser Glu Cys Val Gln Thr  
290 295 300  
Ile Pro Ile Pro Ala His Val Gln Asp Val Met Phe Asp Glu Lys Gln  
305 310 315 320  
Ile Leu Thr Val Gly Ala Glu Pro Leu Leu Arg Arg Phe Asp Leu Asn  
325 330 335  
Gly Ala Leu Leu Ser Gln Ile His Cys Ala Pro Cys Ser Val Phe Ser  
340 345 350  
Ile Ser Leu His Pro Ala Gly Val Val Ala Val Gly Gly Tyr Gly Gly  
355 360 365  
Ile Val Asp Val Ile Ser Gln Phe Gly Ser His Leu Cys Thr Phe Arg  
370 375 380  
Ser Ser Ser Leu  
385

(2) INFORMATION FOR SEQ ID NO:2261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1572340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

Met Tyr Gly Asp Ala Thr Asn Trp Asn Glu Asp Glu Tyr Arg Glu Ser  
1 5 10 15  
Ile Leu Lys Glu Arg Glu Ile Glu Thr Arg Thr Val Phe Arg Thr Ala  
20 25 30  
Trp Ala Pro Pro Ala Arg Ile Ser Asn Pro Asp Ala Phe Val Val Ala  
35 40 45  
Ser Ser Asp Gly Thr Leu Ala Phe His Ser Leu Asn Ser Leu Val Ser  
50 55 60  
Gln Ser Ala Ser Phe Gly Tyr Ser Lys Gly Gln Asp Val Met Val Ala  
65 70 75 80  
Glu Pro Glu Arg Val Val Arg Ala His Glu Gly Pro Ala Tyr Asp Val  
85 90 95  
Lys Phe Tyr Gly Glu Asp Glu Asp Ala Leu Leu Leu Ser Cys Gly Asp  
100 105 110  
Asp Gly Arg Val Arg Gly Trp Lys Trp Arg Glu Phe Ala Glu Ser Asp  
115 120 125  
Val Ser Leu His Leu Lys Glu Asn His Leu Lys Pro Leu Leu Glu Leu  
130 135 140  
Ile Asn Pro Gln His Lys Gly Pro Trp Gly Ala Leu Ser Pro Met Pro  
145 150 155 160  
Glu Ile Asn Ala Met Ser Val Asp Pro Gln Ser Gly Ser Val Phe Thr  
165 170 175  
Ala Ala Gly Asp Ser Cys Ala Tyr Cys Trp Asp Val Glu Ser Gly Lys  
180 185 190  
Ile Lys Met Thr Phe Lys Gly His Ser Asp Tyr Leu His Thr Val Val  
195 200 205  
Ser Arg Ser Ser Ala Ser Gln Ile Leu Thr Gly Ser Glu Asp Gly Thr  
210 215 220  
Ala Arg Ile Trp Asp Cys Lys Thr Gly Lys Cys Val Lys Val Ile Gly  
225 230 235 240  
Ser Gln Asp Lys Lys Ser Arg Leu Arg Val Ser Ser Met Ala Leu Asp  
245 250 255  
Gly Ser Glu Ser Trp Leu Val Cys Gly Gln Gly Lys Asn Leu Ala Leu

2025 RELEASE UNDER E.O. 14176

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 260 |     | 265 |     | 270 |     |     |     |     |     |     |     |     |     |     |
| Trp | Asn | Leu | Pro | Ala | Ser | Glu | Cys | Val | Gln | Thr | Ile | Pro | Ile | Pro | Ala |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| His | Val | Gln | Asp | Val | Met | Phe | Asp | Glu | Lys | Gln | Ile | Leu | Thr | Val | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Glu | Pro | Leu | Leu | Arg | Arg | Phe | Asp | Leu | Asn | Gly | Ala | Leu | Leu | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Gln | Ile | His | Cys | Ala | Pro | Cys | Ser | Val | Phe | Ser | Ile | Ser | Leu | His | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Gly | Val | Val | Ala | Val | Gly | Gly | Tyr | Gly | Gly | Ile | Val | Asp | Val | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Ser | Gln | Phe | Gly | Ser | His | Leu | Cys | Thr | Phe | Arg | Ser | Ser | Ser | Leu |     |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1572341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ala | Glu | Pro | Glu | Arg | Val | Val | Arg | Ala | His | Glu | Gly | Pro | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Asp | Val | Lys | Phe | Tyr | Gly | Glu | Asp | Glu | Asp | Ala | Leu | Leu | Leu | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Cys | Gly | Asp | Asp | Gly | Arg | Val | Arg | Gly | Trp | Lys | Trp | Arg | Glu | Phe | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Ser | Asp | Val | Ser | Leu | His | Leu | Lys | Glu | Asn | His | Leu | Lys | Pro | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Glu | Leu | Ile | Asn | Pro | Gln | His | Lys | Gly | Pro | Trp | Gly | Ala | Leu | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Met | Pro | Glu | Ile | Asn | Ala | Met | Ser | Val | Asp | Pro | Gln | Ser | Gly | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Phe | Thr | Ala | Ala | Gly | Asp | Ser | Cys | Ala | Tyr | Cys | Trp | Asp | Val | Glu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Gly | Lys | Ile | Lys | Met | Thr | Phe | Lys | Gly | His | Ser | Asp | Tyr | Leu | His |
|     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
| Thr | Val | Val | Ser | Arg | Ser | Ser | Ala | Ser | Gln | Ile | Leu | Thr | Gly | Ser | Glu |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Asp | Gly | Thr | Ala | Arg | Ile | Trp | Asp | Cys | Lys | Thr | Gly | Lys | Cys | Val | Lys |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Val | Ile | Gly | Ser | Gln | Asp | Lys | Lys | Ser | Arg | Leu | Arg | Val | Ser | Ser | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Leu | Asp | Gly | Ser | Glu | Ser | Trp | Leu | Val | Cys | Gly | Gln | Gly | Lys | Asn |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Leu | Ala | Leu | Trp | Asn | Leu | Pro | Ala | Ser | Glu | Cys | Val | Gln | Thr | Ile | Pro |
|     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| Ile | Pro | Ala | His | Val | Gln | Asp | Val | Met | Phe | Asp | Glu | Lys | Gln | Ile | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Thr | Val | Gly | Ala | Glu | Pro | Leu | Leu | Arg | Arg | Phe | Asp | Leu | Asn | Gly | Ala |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Leu | Leu | Ser | Gln | Ile | His | Cys | Ala | Pro | Cys | Ser | Val | Phe | Ser | Ile | Ser |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     |     | 255 |     |
| Leu | His | Pro | Ala | Gly | Val | Val | Ala | Val | Gly | Gly | Tyr | Gly | Gly | Ile | Val |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asp | Val | Ile | Ser | Gln | Phe | Gly | Ser | His | Leu | Cys | Thr | Phe | Arg | Ser | Ser |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Ser Leu  
290

(2) INFORMATION FOR SEQ ID NO:2263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| aacaacatct  | ttcacacaac | aattcacaca | atttctcggt | tttttttggt | tatcatcaaa | 60   |
| agttttaatc  | taaattacgt | atcaaattcc | gagcaagatg | actattcttg | ttgaacattt | 120  |
| tgttcctgat  | tcaagagtgg | atgaaaagaa | agtgatagag | gagagggata | atgaattggg | 180  |
| gttggtatga  | ggttttgtgg | ttccaaaatc | aaaggaaact | gatgcattcg | atgctcctga | 240  |
| tatgaatttc  | ttgggccatt | ccttcaggga | ttatgagaat | gatgaaagcg | agagacaaca | 300  |
| aggtgttgag  | gaattttaca | ggatgcaaca | cattcaccag | acctatgact | ttgtgaagaa | 360  |
| gatgaggaaa  | gagtatggaa | aacttaacaa | gatggaaatg | agtatatggg | aatgtttgtg | 420  |
| gttattgaac  | aatgtttgtg | atgaaagcga | tccggatctt | gatgagcctc | aaattcaaca | 480  |
| ccttctccaa  | accgctgaag | ccattcgaag | ggactatccc | gacgaagatt | ggctccatct | 540  |
| cactgcccta  | atccatgata | ttggcaaggt | tctccttctg | ccagaattcg | gtggtcttcc | 600  |
| ccagtgggct  | gtcgttggcg | atacatttcc | agttggatgt | accttcgact | cagccaatat | 660  |
| tcaccacaag  | tatttcaaag | gaaaccatga | tatcaacaac | ccaaagtaca | acacaaaaaa | 720  |
| tgaggtttac  | actgaaggat | gtggtttaga | caatgttctc | atgtcatggg | gtcatgaoga | 780  |
| ctacatgtat  | ttggtggcta | agaagaatgg | cacgacctt  | cctcacgctg | gtctcttcat | 840  |
| tattcgatat  | cattcctttt | atccattgca | caaggcagga | gcctacacac | acttgatgaa | 900  |
| cgatgaggac  | agagatgata | tcaagtggct | ccatgtcttc | aataaatatg | acctatacag | 960  |
| taagagcaaa  | gttctggtag | atgtcgaaca | agtgaagcct | tactacattt | cactcatcaa | 1020 |
| caagtatttt  | cggcgaaaac | taaaatgggt | agataaagct | acgagtcaat | taattaacta | 1080 |
| tcttttatga  | ggagaacgag | atcgaagggt | aacgagtttT | ctattgtata | caacggaaga | 1140 |
| taaattctatc | taataaaaaa | gttggtgtgt | tcatttgtaa | ttttttcccc | catcagttta | 1200 |
| aaagttatgt  | tgt        |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Ile | Leu | Val | Glu | His | Phe | Val | Pro | Asp | Ser | Arg | Val | Asp | Glu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Lys | Val | Ile | Glu | Glu | Arg | Asp | Asn | Glu | Leu | Val | Leu | Asp | Gly | Gly |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Val | Val | Pro | Lys | Ser | Lys | Glu | Thr | Asp | Ala | Phe | Asp | Ala | Pro | Asp |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Asn | Phe | Leu | Gly | His | Ser | Phe | Arg | Asp | Tyr | Glu | Asn | Asp | Glu | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Arg | Gln | Gln | Gly | Val | Glu | Glu | Phe | Tyr | Arg | Met | Gln | His | Ile | His |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gln | Thr | Tyr | Asp | Phe | Val | Lys | Lys | Met | Arg | Lys | Glu | Tyr | Gly | Lys | Leu |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asn | Lys | Met | Glu | Met | Ser | Ile | Trp | Glu | Cys | Cys | Glu | Leu | Leu | Asn | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |

Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu Pro Gln Ile Gln His  
115 120 125  
Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp Tyr Pro Asp Glu Asp  
130 135 140  
Trp Leu His Leu Thr Ala Leu Ile His Asp Leu Gly Lys Val Leu Leu  
145 150 155 160  
Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala Val Val Gly Asp Thr  
165 170 175  
Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn Ile His His Lys Tyr  
180 185 190  
Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys Tyr Asn Thr Lys Asn  
195 200 205  
Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn Val Leu Met Ser Trp  
210 215 220  
Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys Lys Asn Gly Thr Thr  
225 230 235 240  
Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr His Ser Phe Tyr Pro  
245 250 255  
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg  
260 265 270  
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser  
275 280 285  
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile  
290 295 300  
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp  
305 310 315

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1572351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

Met Asn Phe Leu Gly His Ser Phe Arg Asp Tyr Glu Asn Asp Glu Ser  
1 5 10 15  
Glu Arg Gln Gln Gly Val Glu Glu Phe Tyr Arg Met Gln His Ile His  
20 25 30  
Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys Glu Tyr Gly Lys Leu  
35 40 45  
Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys Glu Leu Leu Asn Asn  
50 55 60  
Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu Pro Gln Ile Gln His  
65 70 75 80  
Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp Tyr Pro Asp Glu Asp  
85 90 95  
Trp Leu His Leu Thr Ala Leu Ile His Asp Leu Gly Lys Val Leu Leu  
100 105 110  
Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala Val Val Gly Asp Thr  
115 120 125  
Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn Ile His His Lys Tyr  
130 135 140  
Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys Tyr Asn Thr Lys Asn  
145 150 155 160  
Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn Val Leu Met Ser Trp  
165 170 175  
Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys Lys Asn Gly Thr Thr

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 180                                                             | 185 | 190 |
| Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr His Ser Phe Tyr Pro |     |     |
| 195                                                             | 200 | 205 |
| Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg |     |     |
| 210                                                             | 215 | 220 |
| Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser |     |     |
| 225                                                             | 230 | 235 |
| Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile |     |     |
| 245                                                             | 250 | 255 |
| Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp             |     |     |
| 260                                                             | 265 |     |

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gln His Ile His Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys |     |     |
| 1                                                               | 5   | 10  |
| Glu Tyr Gly Lys Leu Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys |     |     |
| 20                                                              | 25  | 30  |
| Glu Leu Leu Asn Asn Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu |     |     |
| 35                                                              | 40  | 45  |
| Pro Gln Ile Gln His Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp |     |     |
| 50                                                              | 55  | 60  |
| Tyr Pro Asp Glu Asp Trp Leu His Leu Thr Ala Leu Ile His Asp Leu |     |     |
| 65                                                              | 70  | 75  |
| Gly Lys Val Leu Leu Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala |     |     |
| 85                                                              | 90  | 95  |
| Val Val Gly Asp Thr Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn |     |     |
| 100                                                             | 105 | 110 |
| Ile His His Lys Tyr Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys |     |     |
| 115                                                             | 120 | 125 |
| Tyr Asn Thr Lys Asn Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn |     |     |
| 130                                                             | 135 | 140 |
| Val Leu Met Ser Trp Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys |     |     |
| 145                                                             | 150 | 155 |
| Lys Asn Gly Thr Thr Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr |     |     |
| 165                                                             | 170 | 175 |
| His Ser Phe Tyr Pro Leu His Lys Ala Gly Ala Tyr Thr His Leu Met |     |     |
| 180                                                             | 185 | 190 |
| Asn Asp Glu Asp Arg Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys |     |     |
| 195                                                             | 200 | 205 |
| Tyr Asp Leu Tyr Ser Lys Ser Lys Val Leu Val Asp Val Glu Gln Val |     |     |
| 210                                                             | 215 | 220 |
| Lys Pro Tyr Tyr Ile Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu |     |     |
| 225                                                             | 230 | 235 |
| Lys Trp                                                         |     |     |

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

000001-133333

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..629

(D) OTHER INFORMATION: / Ceres Seq. ID 1572364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atccgatttt atttgtttga taagttcgtg tcgtcttcgt ctctctaacc caattctgtg | 60  |
| gtgtctgaag aaagcagaat caaaAtccat gtctttcaga ggacttagca ggccaaatgc | 120 |
| aatatctgga atgggtgttg cagatgagag caaaaccaca tttctagagc ttcaaaggaa | 180 |
| aaaaactcat cgctatgttg tcttcaagat tgatgaatcc aaaaaagaag ttgttgttga | 240 |
| gaaaactgga aaccctacag agagctacga tgatttctta gcttcacttc ctgataatga | 300 |
| ctgcagatac gctgtttatg acttcgattt cgttacttct gagaattgtc aaaagagcaa | 360 |
| aatcttcttc ttttcttggt ctccttcgac ttctccagtt cgggcgaagg tgctttactc | 420 |
| gacttctaaa gaccagctaa gtaaggagct tcaagggtt cactatgaga ttcaagctac  | 480 |
| tgatcctact gaggttgatc ttgaagtgtt acgcgaacga gcgaactgag agcaagcaag | 540 |
| attgctatgt ctattcaaaa cttatggtaa tgtaatgaat aattcgtatt ctctgtggat | 600 |
| tgatttgtgt aaacacagtt tcatgttcc                                   |     |

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1572365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Asp Phe Ile Cys Leu Ile Ser Ser Cys Arg Leu Arg Leu Ser Asn |  |
| 1 5 10 15                                                       |  |
| Pro Ile Leu Trp Cys Leu Lys Lys Ala Glu Ser Lys Ser Met Ser Phe |  |
| 20 25 30                                                        |  |
| Arg Gly Leu Ser Arg Pro Asn Ala Ile Ser Gly Met Gly Val Ala Asp |  |
| 35 40 45                                                        |  |
| Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg Lys Lys Thr His Arg |  |
| 50 55 60                                                        |  |
| Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys Glu Val Val Val Glu |  |
| 65 70 75 80                                                     |  |
| Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp Phe Leu Ala Ser Leu |  |
| 85 90 95                                                        |  |
| Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp Phe Asp Phe Val Thr |  |
| 100 105 110                                                     |  |
| Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe Phe Ser Trp Ser Pro |  |
| 115 120 125                                                     |  |
| Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr Ser Thr Ser Lys Asp |  |
| 130 135 140                                                     |  |
| Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr Glu Ile Gln Ala Thr |  |
| 145 150 155 160                                                 |  |
| Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg Glu Arg Ala Asn     |  |
| 165 170 175                                                     |  |

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

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(D) OTHER INFORMATION: / Ceres Seq. ID 1572366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

Met Ser Phe Arg Gly Leu Ser Arg Pro Asn Ala Ile Ser Gly Met Gly  
1 5 10 15  
Val Ala Asp Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg Lys Lys  
20 25 30  
Thr His Arg Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys Glu Val  
35 40 45  
Val Val Glu Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp Phe Leu  
50 55 60  
Ala Ser Leu Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp Phe Asp  
65 70 75 80  
Phe Val Thr Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe Phe Ser  
85 90 95  
Trp Ser Pro Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr Ser Thr  
100 105 110  
Ser Lys Asp Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr Glu Ile  
115 120 125  
Gln Ala Thr Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg Glu Arg  
130 135 140  
Ala Asn  
145

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1572367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

Met Gly Val Ala Asp Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg  
1 5 10 15  
Lys Lys Thr His Arg Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys  
20 25 30  
Glu Val Val Val Glu Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp  
35 40 45  
Phe Leu Ala Ser Leu Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp  
50 55 60  
Phe Asp Phe Val Thr Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe  
65 70 75 80  
Phe Ser Trp Ser Pro Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr  
85 90 95  
Ser Thr Ser Lys Asp Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr  
100 105 110  
Glu Ile Gln Ala Thr Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg  
115 120 125  
Glu Arg Ala Asn  
130

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..798

(D) OTHER INFORMATION: / Ceres Seq. ID 1572368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| ttgtcaaaaag | ctgattcttc | gccttatggc  | atcgattttg  | caccttcgaa | cggccaaccc | 60  |
| acgggaagat  | tcactaatgg | tcgaaccatt  | tccgatattg  | tgggtgaagc | cttaggagca | 120 |
| aaatcaccac  | caccaccata | tcttgaacca  | aacactgagg  | ctaacacaat | tctcaatgga | 180 |
| atcaactatg  | cttctgggtg | tgctggaatc  | ttggacgaca  | ctggacttct | ggttcatcgg | 240 |
| ggcgagttcc  | gctgagagaa | caagtgaagta | attttgagaa  | gagtagagaa | tatatggtaa | 300 |
| gcgtgattgg  | tgaaaatggg | acaaaagaga  | tgttgaaagaa | tgcaatgttc | acaatcacaa | 360 |
| ttggatcaaa  | tgatattttg | aatttatattc | aaccatcaat  | acctttcttc | tctcaagaca | 420 |
| agctccccac  | tgaAtgtcct | acaagattcc  | atggtcctcc  | atTTTaacca | cacatcttaa | 480 |
| gcgattgcat  | cagctaggag | gtaggaagtt  | cgtgggtggt  | ggagtagggc | cactcggttg | 540 |
| cataccCttt  | gctcgagcgt | tgaatttwat  | accagccgga  | aaatgctccg | aacaAgtcaa | 600 |
| ccaagtagtc  | CgaggtTata | acatgaAgct  | tatacactct  | cttaagacat | tgaacaatga | 660 |
| gttaagatcc  | gaagattaca | acactacatt  | tgtctacgcc  | aactcttacg | acctattctt | 720 |
| gaaactagtt  | ttgaactatc | aactattttg  | cttgaagaac  | gcagacaagc | cgtgttggtg | 780 |
| cggtactttt  | ccaccgtt   |             |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1572369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Lys | Ala | Asp | Ser | Ser | Pro | Tyr | Gly | Ile | Asp | Phe | Ala | Pro | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Gly | Gln | Pro | Thr | Gly | Arg | Phe | Thr | Asn | Gly | Arg | Thr | Ile | Ser | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Val | Gly | Glu | Ala | Leu | Gly | Ala | Lys | Ser | Pro | Pro | Pro | Pro | Tyr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Glu | Pro | Asn | Thr | Glu | Ala | Asn | Thr | Ile | Leu | Asn | Gly | Ile | Asn | Tyr | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Ala | Ala | Gly | Ile | Leu | Asp | Asp | Thr | Gly | Leu | Leu | Val | His | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Glu | Phe | Arg |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1572370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Tyr | Lys | Ile | Pro | Trp | Ser | Ser | Ile | Leu | Thr | Thr | His | Leu | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Leu | His | Gln | Leu | Gly | Gly | Arg | Lys | Phe | Val | Val | Val | Gly | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Leu | Gly | Cys | Ile | Pro | Phe | Ala | Arg | Ala | Leu | Asn | Xaa | Ile | Pro | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Lys | Cys | Ser | Glu | Gln | Val | Asn | Gln | Val | Val | Arg | Gly | Tyr | Asn | Met |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |



Lys Leu Ile His Ser Leu Lys Thr Leu Asn Asn Glu Leu Arg Ser Glu  
65 70 75 80  
Asp Tyr Asn Thr Thr Phe Val Tyr Ala Asn Ser Tyr Asp Leu Phe Leu  
85 90 95  
Lys Leu Val Leu Asn Tyr Gln Leu Phe Gly Leu Lys Asn Ala Asp Lys  
100 105 110  
Pro Cys Cys Gly Gly Tyr Phe Pro Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:2274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1080
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| gatcacaaaa | aattagaatc | atggaggctg | agagagacca | gcacaagcct | ccgttgtctc | 60   |
| tacaaaacaa | caaatccca  | tcatacacia | acttcccagt | cgtcgacct  | agcaacacca | 120  |
| atggggagct | cgtggcgct  | aaagtggcaa | aggcgagcga | agagtgggga | atttttcagg | 180  |
| tagttaacca | cgggatccca | accgaactaa | tccggagggt | gcacaagggt | gatacacagt | 240  |
| tctttgagct | cccagagtcc | aagaaagaag | ccgtggccaa | accagcgaac | tccaaagaga | 300  |
| tacaaggata | tgagatggat | gatgtacaag | gtagaaggag | tcatactctc | cataatctat | 360  |
| atccatcatc | gtcagtcagt | tatgcattct | ggcctaagaa | tcctcctgaa | tacagagagg | 420  |
| tgactgagga | gtttgcaaa  | catgcaaaag | agctagcgga | agagatccct | ggTttgctat | 480  |
| ccgaaggKtt | aggtttacaa | cgtgagatgt | tgaagtttag | attcggggac | gatagtgtct | 540  |
| gttatcttat | gaagatcaac | tattaccggc | cgtgtccaga | gccagattgg | gtcatgggaa | 600  |
| taaaagccca | cactgatttc | aatgaactca | cacttctcat | tcccaatgaa | attttcggac | 660  |
| ttcaagtgtt | caaggaagac | cgctggcttg | atgtagatta | tatatatccc | gcggttatta | 720  |
| tcatacatcg | agatcagatc | atgaagatga | gcaacggaag | gtacaacaat | gtgttgcata | 780  |
| gaaccttgat | ggataaaaag | aaaacgagga | tgtcgtcggt | ggttcataat | aagcctcctt | 840  |
| atgatatggt | tgtgaagcca | tttcccgaac | tcaccagcgg | cgataatcct | cccaagttcg | 900  |
| agcctttaac | ttaccaggat | tacatagaca | ttgaagtccc | caagctttct | cgactgatca | 960  |
| agaattgact | tctttgtcgt | tgtatgtatg | ttgtttgttg | ttgctctgtt | tcatttggcc | 1020 |
| gtttggcatt | gttgaaccg  | gtttctatta | attgaagttc | aaacaaaaaa | aatttgactc | 1080 |

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Ser Gln Lys Ile Arg Ile Met Glu Val Glu Arg Asp Gln His Lys Pro  
1 5 10 15  
Pro Leu Ser Leu Gln Asn Asn Lys Ile Pro Ser Ser Gln Asn Phe Pro  
20 25 30  
Val Val Asp Leu Ser Asn Thr Asn Gly Glu Leu Val Ala Arg Lys Val  
35 40 45  
Ala Lys Ala Ser Glu Glu Trp Gly Ile Phe Gln Val Val Asn His Gly  
50 55 60  
Ile Pro Thr Glu Leu Ile Arg Arg Leu His Lys Val Asp Thr Gln Phe  
65 70 75 80

Phe Glu Leu Pro Glu Ser Lys Lys Glu Ala Val Ala Lys Pro Ala Asn  
85 90 95  
Ser Lys Glu Ile Gln Gly Tyr Glu Met Asp Asp Val Gln Gly Arg Arg  
100 105 110  
Ser His Ile Phe His Asn Leu Tyr Pro Ser Ser Ser Val Asn Tyr Ala  
115 120 125  
Phe Trp Pro Lys Asn Pro Pro Glu Tyr Arg Glu Val Thr Glu Glu Phe  
130 135 140  
Ala Lys His Ala Lys Gln Leu Ala Glu Glu Ile Leu Gly Leu Leu Ser  
145 150 155 160  
Glu Xaa Leu Gly Leu Gln Arg Glu Met Leu Lys Leu Ala Phe Gly Asp  
165 170 175  
Asp Ser Ala Gly Tyr Leu Met Lys Ile Asn Tyr Tyr Arg Pro Cys Pro  
180 185 190  
Glu Pro Asp Trp Val Met Gly Ile Lys Ala His Thr Asp Phe Asn Glu  
195 200 205  
Leu Thr Leu Leu Ile Pro Asn Glu Ile Phe Gly Leu Gln Val Phe Lys  
210 215 220  
Glu Asp Arg Trp Leu Asp Val Asp Tyr Ile Tyr Pro Ala Val Ile Ile  
225 230 235 240  
Ile Ile Gly Asp Gln Ile Met Lys Met Ser Asn Gly Arg Tyr Asn Asn  
245 250 255  
Val Leu His Arg Thr Leu Met Asp Lys Lys Lys Thr Arg Met Ser Ser  
260 265 270  
Val Val His Ile Lys Pro Pro Tyr Asp Met Val Val Lys Pro Phe Pro  
275 280 285  
Glu Leu Thr Ser Gly Asp Asn Pro Pro Lys Phe Glu Pro Leu Thr Tyr  
290 295 300  
Gln Asp Tyr Ile Asp Ile Glu Val Pro Lys Leu Ser Arg Leu Ile Lys  
305 310 315 320  
Asn

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1572377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

Met Glu Val Glu Arg Asp Gln His Lys Pro Pro Leu Ser Leu Gln Asn  
1 5 10 15  
Asn Lys Ile Pro Ser Ser Gln Asn Phe Pro Val Val Asp Leu Ser Asn  
20 25 30  
Thr Asn Gly Glu Leu Val Ala Arg Lys Val Ala Lys Ala Ser Glu Glu  
35 40 45  
Trp Gly Ile Phe Gln Val Val Asn His Gly Ile Pro Thr Glu Leu Ile  
50 55 60  
Arg Arg Leu His Lys Val Asp Thr Gln Phe Phe Glu Leu Pro Glu Ser  
65 70 75 80  
Lys Lys Glu Ala Val Ala Lys Pro Ala Asn Ser Lys Glu Ile Gln Gly  
85 90 95  
Tyr Glu Met Asp Asp Val Gln Gly Arg Arg Ser His Ile Phe His Asn  
100 105 110  
Leu Tyr Pro Ser Ser Ser Val Asn Tyr Ala Phe Trp Pro Lys Asn Pro  
115 120 125  
Pro Glu Tyr Arg Glu Val Thr Glu Glu Phe Ala Lys His Ala Lys Gln

|                     |                     |                         |
|---------------------|---------------------|-------------------------|
| 130                 | 135                 | 140                     |
| Leu Ala Glu Glu Ile | Leu Gly Leu Leu Ser | Glu Xaa Leu Gly Leu Gln |
| 145                 | 150                 | 155                     |
| Arg Glu Met Leu Lys | Leu Ala Phe Gly Asp | Ser Ala Gly Tyr Leu     |
| 165                 | 170                 | 175                     |
| Met Lys Ile Asn Tyr | Tyr Arg Pro Cys Pro | Glu Pro Asp Trp Val Met |
| 180                 | 185                 | 190                     |
| Gly Ile Lys Ala His | Thr Asp Phe Asn Glu | Leu Thr Leu Leu Ile Pro |
| 195                 | 200                 | 205                     |
| Asn Glu Ile Phe Gly | Leu Gln Val Phe Lys | Glu Asp Arg Trp Leu Asp |
| 210                 | 215                 | 220                     |
| Val Asp Tyr Ile Tyr | Pro Ala Val Ile Ile | Ile Gly Asp Gln Ile     |
| 225                 | 230                 | 235                     |
| Met Lys Met Ser Asn | Gly Arg Tyr Asn Asn | Val Leu His Arg Thr Leu |
| 245                 | 250                 | 255                     |
| Met Asp Lys Lys Lys | Thr Arg Met Ser Ser | Val Val His Ile Lys Pro |
| 260                 | 265                 | 270                     |
| Pro Tyr Asp Met Val | Val Lys Pro Phe Pro | Glu Leu Thr Ser Gly Asp |
| 275                 | 280                 | 285                     |
| Asn Pro Pro Lys Phe | Glu Pro Leu Thr Tyr | Gln Asp Tyr Ile Asp Ile |
| 290                 | 295                 | 300                     |
| Glu Val Pro Lys Leu | Ser Arg Leu Ile Lys | Asn                     |
| 305                 | 310                 | 315                     |

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Asp Asp Val Gln Gly Arg Arg Ser His Ile Phe His Asn Leu Tyr |             |
| 1                                                               | 5 10 15     |
| Pro Ser Ser Ser Val Asn Tyr Ala Phe Trp Pro Lys Asn Pro Pro Glu |             |
|                                                                 | 20 25 30    |
| Tyr Arg Glu Val Thr Glu Glu Phe Ala Lys His Ala Lys Gln Leu Ala |             |
|                                                                 | 35 40 45    |
| Glu Glu Ile Leu Gly Leu Leu Ser Glu Xaa Leu Gly Leu Gln Arg Glu |             |
|                                                                 | 50 55 60    |
| Met Leu Lys Leu Ala Phe Gly Asp Asp Ser Ala Gly Tyr Leu Met Lys |             |
| 65                                                              | 70 75 80    |
| Ile Asn Tyr Tyr Arg Pro Cys Pro Glu Pro Asp Trp Val Met Gly Ile |             |
|                                                                 | 85 90 95    |
| Lys Ala His Thr Asp Phe Asn Glu Leu Thr Leu Leu Ile Pro Asn Glu |             |
|                                                                 | 100 105 110 |
| Ile Phe Gly Leu Gln Val Phe Lys Glu Asp Arg Trp Leu Asp Val Asp |             |
|                                                                 | 115 120 125 |
| Tyr Ile Tyr Pro Ala Val Ile Ile Ile Ile Gly Asp Gln Ile Met Lys |             |
|                                                                 | 130 135 140 |
| Met Ser Asn Gly Arg Tyr Asn Asn Val Leu His Arg Thr Leu Met Asp |             |
| 145                                                             | 150 155 160 |
| Lys Lys Lys Thr Arg Met Ser Ser Val Val His Ile Lys Pro Pro Tyr |             |
|                                                                 | 165 170 175 |
| Asp Met Val Val Lys Pro Phe Pro Glu Leu Thr Ser Gly Asp Asn Pro |             |
|                                                                 | 180 185 190 |
| Pro Lys Phe Glu Pro Leu Thr Tyr Gln Asp Tyr Ile Asp Ile Glu Val |             |
|                                                                 | 195 200 205 |

(2) INFORMATION FOR SEO ID NO:2278:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..729

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572397

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| acactcatct | cctaaattcc | ttacataata  | ttttcttaag | ataagcaaaa | aaatcatggc | 60  |
| agaagcgtct | agtttggtgg | ggaaacttga  | gacagaagtg | gagatcaaag | cttcggccaa | 120 |
| aaagttcoat | cacatgttta | cggagagacc  | acaccatgtc | tccaaagcaa | ctccagataa | 180 |
| aattcatgga | tgtgagctgc | acgaaggcga  | ctggggcaaa | gtcgggtcta | tcgtcatctg | 240 |
| gaaatacgtt | catgatggaa | agttaacagt  | ggggaagaat | aagatcgagg | cgttggaatc | 300 |
| ggagaagaac | ctgatcacgt | tcaaggtttt  | agaagggtat | ctgatgaatg | agtcaaaag  | 360 |
| cttcgcattt | acactccaag | tgacccttaa  | gcaaggggag | tcagggaata | ttgcgcactg | 420 |
| gcacctggag | tatgagaaaa | ttagcggagga | ggtagctcat | cccgaaaacc | ttctccaatt | 480 |
| ctgtgtcgag | atctccaaag | agatcgacga  | acatctcttg | gccgaggaat | agaaaaatac | 540 |
| tcctcgtctg | tgtgtgggtc | tttgaaactt  | aagcaagtct | ttgaaactgc | aataataaat | 600 |
| gaacgggtcc | gtctttatgt | aagagaaaaag | agatatatat | atatgtgttg | gtgtgtgtaa | 660 |
| tgcggtgatg | cctactacta | cggttgagtt  | atgttggaat | agtaaaaRgc | atataatcta | 720 |
| ttttgtccc  |            |             |            |            |            |     |

(2) INFORMATION FOR SEO ID NO:2279:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids

- (B) TYPE: amino acid

- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..158

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572398

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Ala | Ser | Ser | Leu | Val | Gly | Lys | Leu | Glu | Thr | Glu | Val | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Lys | Ala | Ser | Ala | Lys | Lys | Phe | His | His | Met | Phe | Thr | Glu | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | His | Val | Ser | Lys | Ala | Thr | Pro | Asp | Lys | Ile | His | Gly | Cys | Glu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Glu | Gly | Asp | Trp | Gly | Lys | Val | Gly | Ser | Ile | Val | Ile | Trp | Lys | Tyr |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Val | His | Asp | Gly | Lys | Leu | Thr | Val | Gly | Lys | Asn | Lys | Ile | Glu | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Pro | Glu | Lys | Asn | Leu | Ile | Thr | Phe | Lys | Val | Leu | Glu | Gly | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Asn | Glu | Tyr | Lys | Ser | Phe | Ala | Phe | Thr | Leu | Gln | Val | Thr | Pro | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Gly | Glu | Ser | Gly | Ser | Ile | Ala | His | Trp | His | Leu | Glu | Tyr | Glu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Glu | Glu | Val | Ala | His | Pro | Glu | Thr | Leu | Leu | Gln | Phe | Cys | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ile | Ser | Lys | Glu | Ile | Asp | Glu | His | Leu | Leu | Ala | Glu | Glu |     |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2280:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..132
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572399
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

Met Phe Thr Glu Arg Pro His His Val Ser Lys Ala Thr Pro Asp Lys  
1 5 10 15  
Ile His Gly Cys Glu Leu His Glu Gly Asp Trp Gly Lys Val Gly Ser  
20 25 30  
Ile Val Ile Trp Lys Tyr Val His Asp Gly Lys Leu Thr Val Gly Lys  
35 40 45  
Asn Lys Ile Glu Ala Val Asp Pro Glu Lys Asn Leu Ile Thr Phe Lys  
50 55 60  
Val Leu Glu Gly Asp Leu Met Asn Glu Tyr Lys Ser Phe Ala Phe Thr  
65 70 75 80  
Leu Gln Val Thr Pro Lys Gln Gly Glu Ser Gly Ser Ile Ala His Trp  
85 90 95  
His Leu Glu Tyr Glu Lys Ile Ser Glu Glu Val Ala His Pro Glu Thr  
100 105 110  
Leu Leu Gln Phe Cys Val Glu Ile Ser Lys Glu Ile Asp Glu His Leu  
115 120 125  
Leu Ala Glu Glu  
130

(2) INFORMATION FOR SEQ ID NO:2281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 572 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..572

(D) OTHER INFORMATION: / Ceres Seq. ID 1572400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

attcataaat ctctcaaagt aagaactaag agcttttacta cagtcctact ctctacacat 60  
cttctctTct ctctcaagag ctagtcatgg ccaaactcat aacttctttt ctcttactca 120  
caattttatt cactttcggt tgtctcacta tgtcaaaaga agctgagtag catccagaaa 180  
gtgtaagttt ttatttttttg gtaaaataga aagttatgga ccaggaagtc tgaaatcata 240  
ccaatgtgga ggacaatgca caaggagatg tagcaatata aagtatcata agccatgcat 300  
gttcttctgc caaaagtgtt gtgctaaatg cctttgtgtc cctccaggca cgtacggcaa 360  
caaacaagtg tgtccttggt acaacaactg gaagactcaa caaggtggac caaaatgtcc 420  
ataaacaaaa agagagaaaac cccaatctgt ttctattttt atttaattat ttccagtagt 480  
cttttggtgt cgtgatggtt aaattatagt gtttttgcag gtatcattta tcatcgataa 540  
acaatatcat ataaaaatctt ctatgtttct tg

(2) INFORMATION FOR SEQ ID NO:2282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1572401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

Met Ala Lys Leu Ile Thr Ser Phe Leu Leu Thr Ile Leu Phe Thr  
1 5 10 15  
Phe Val Cys Leu Thr Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser  
20 25 30  
Val Ser Phe Tyr Phe Leu Val Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

Met Phe Phe Cys Gln Lys Cys Cys Ala Lys Cys Leu Cys Val Pro Pro  
1 5 10 15  
Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro Cys Tyr Asn Asn Trp Lys  
20 25 30  
Thr Gln Gln Gly Gly Pro Lys Cys Pro  
35 40

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

Met Pro Leu Cys Pro Ser Arg His Val Arg Gln Gln Thr Ser Val Ser  
1 5 10 15  
Leu Leu Gln Gln Leu Glu Asp Ser Thr Arg Trp Thr Lys Met Ser Ile  
20 25 30  
Asn Lys Lys Arg Glu Thr Pro Ile Cys Phe Leu Phe Tyr Leu Ile Ile  
35 40 45  
Ser Ser Met Leu Leu Leu Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

cggaggtgat cggttgctc tgggttaatg aagctgccac gaattggcgt attttagatt 60  
gatacgtcaa agctcctcct cgcgcacgtt agctaaagga atgtcttgta ctctttttgt 120  
tgttggtggt gattttttga acaaagaaag aaactaatca aaaagacgaa gaggaagagg 180  
aagctcaccg tttctatctc tcattttaac cactgatctt ctccgattgc gtcttgcttc 240

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| togtgcgtttg | cttccgatct | ctctctggat | tttctcaatt | togtacggat | taggttaatt | 300  |
| gtgtataaag  | gagtttagtt | gatcattggt | ttgtacattt | gggatgatga | tgcgtactgt | 360  |
| tgttttacca  | ttgtcccatg | atctgaatgt | tcataagatc | catgaagctt | ctggattcca | 420  |
| taatagtgtc  | gctggtaaaa | atcgtgtgta | tctgactcgg | actggtcttt | catcatgtgc | 480  |
| cacgagacaa  | gacgtttgga | gtcttcagct | actagagagc | ttgagtgggt | caatagtacc | 540  |
| tgtatcatct  | aggtgtaatg | catttgtttg | ccggtcagct | ctctctcctg | ggaatggaaa | 600  |
| tgaaggccct  | attcttaaat | caactgcagt | aatattcaca | agggtatatg | atgctttagg | 660  |
| tggaaatcct  | catttagtga | aactaattcc | agcggttggg | attcttgcac | ttgctacatg | 720  |
| gggtcttaga  | ccccttctgc | gccttgccag | aactaccctg | tttgagaagg | ggaatgatgc | 780  |
| aaattcacag  | aagagtagca | cgcagtagat | tgttggtgtc | tatcttcaac | ctttgctgct | 840  |
| ttggagcgga  | gcaatccttt | tatgcagaac | attggaccca | atagtattgc | cttcaagtgc | 900  |
| cggccaggct  | attaaacagc | gtcttctgat | ctttgctcgg | tccatatcaa | cgggtgttgc | 960  |
| attttcctgc  | tgtttatcaa | gcctacttca | gcagggtcag | aaatttttta | tggagacaaa | 1020 |
| taatcctgct  | gataccagaa | atatgggttt | cagttttgct | ggaaaagctg | tttacactgc | 1080 |
| tgcgtgggtt  | gctgctgctt | cattgtttat | ggaactgtta | ggcttctcta | cccaaaaatg | 1140 |
| gctaacggct  | gggggtctgg | ggacagtact | gctaactctt | gctggccgtg | agatacttac | 1200 |
| taactttctt  | tcaagcatta | tgattcatgc | tacacggccc | tttgttctga | atgagtggat | 1260 |
| ccagaccaag  | ataggaggct | atgaagtttc | tggcacagta | gagcaagtcg | gttggtggtc | 1320 |
| acctacaatt  | atcagagggt | atgaccggga | agcagttcat | attcctaacc | accagttcag | 1380 |
| tgtaaatatt  | gtgagaaatc | tcactcagaa | gacgcattgg | cgcacaaaaa | cacatcttgc | 1440 |
| catcagtcac  | cttgatgtc  |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1572405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Met | Arg | Thr | Val | Ala | Leu | Pro | Leu | Ser | His | Asp | Leu | Asn | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Lys | Ile | His | Glu | Ala | Ser | Gly | Phe | His | Asn | Ser | Ala | Ala | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Arg | Val | Tyr | Leu | Thr | Arg | Thr | Gly | Leu | Ser | Ser | Cys | Ala | Thr | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Asp | Val | Trp | Ser | Leu | Gln | Leu | Leu | Glu | Ser | Leu | Ser | Gly | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Pro | Val | Ser | Ser | Arg | Cys | Asn | Ala | Phe | Val | Cys | Arg | Ser | Ala | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Pro | Gly | Asn | Gly | Asn | Glu | Gly | Pro | Ile | Leu | Lys | Ser | Thr | Ala | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Phe | Thr | Arg | Val | Tyr | Asp | Ala | Leu | Gly | Gly | Asn | Pro | His | Leu | Val |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Ile | Pro | Ala | Val | Gly | Ile | Leu | Ala | Phe | Ala | Thr | Trp | Gly | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Leu | Leu | Arg | Leu | Ala | Arg | Thr | Thr | Leu | Phe | Glu | Lys | Gly | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ala | Asn | Ser | Gln | Lys | Ser | Ser | Thr | Gln | Tyr | Ile | Val | Val | Ser | Tyr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Gln | Pro | Leu | Leu | Trp | Ser | Gly | Ala | Ile | Leu | Leu | Cys | Arg | Thr |     |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |
| Leu | Asp | Pro | Ile | Val | Leu | Pro | Ser | Ser | Ala | Gly | Gln | Ala | Ile | Lys | Gln |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Arg | Leu | Leu | Ile | Phe | Ala | Arg | Ser | Ile | Ser | Thr | Val | Leu | Ala | Phe | Ser |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Cys | Cys | Leu | Ser | Ser | Leu | Leu | Gln | Gln | Val | Gln | Lys | Phe | Phe | Met | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Arg | Thr | Val | Ala | Leu | Pro | Leu | Ser | His | Asp | Leu | Asn | Val | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ile | His | Glu | Ala | Ser | Gly | Phe | His | Asn | Ser | Ala | Ala | Gly | Lys | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Tyr | Leu | Thr | Arg | Thr | Gly | Leu | Ser | Ser | Cys | Ala | Thr | Arg | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Val | Trp | Ser | Leu | Gln | Leu | Leu | Glu | Ser | Leu | Ser | Gly | Ser | Ile | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Val | Ser | Ser | Arg | Cys | Asn | Ala | Phe | Val | Cys | Arg | Ser | Ala | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Gly | Asn | Gly | Asn | Glu | Gly | Pro | Ile | Leu | Lys | Ser | Thr | Ala | Val | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Thr | Arg | Val | Tyr | Asp | Ala | Leu | Gly | Gly | Asn | Pro | His | Leu | Val | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ile | Pro | Ala | Val | Gly | Ile | Leu | Ala | Phe | Ala | Thr | Trp | Gly | Leu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Leu | Leu | Arg | Leu | Ala | Arg | Thr | Thr | Leu | Phe | Glu | Lys | Gly | Asn | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Asn | Ser | Gln | Lys | Ser | Ser | Thr | Gln | Tyr | Ile | Val | Val | Ser | Tyr | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Pro | Leu | Leu | Leu | Trp | Ser | Gly | Ala | Ile | Leu | Leu | Cys | Arg | Thr | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Pro | Ile | Val | Leu | Pro | Ser | Ser | Ala | Gly | Gln | Ala | Ile | Lys | Gln | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Ile | Phe | Ala | Arg | Ser | Ile | Ser | Thr | Val | Leu | Ala | Phe | Ser | Cys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Leu | Ser | Ser | Leu | Leu | Gln | Gln | Val | Gln | Lys | Phe | Phe | Met | Glu | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Asn | Pro | Ala | Asp | Thr | Arg | Asn | Met | Gly | Phe | Ser | Phe | Ala | Gly | Lys |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Ala | Val | Tyr | Thr | Ala | Ala | Trp | Val | Ala | Ala | Ser | Leu | Phe | Met | Glu |     |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Leu | Leu | Gly | Phe | Ser | Thr | Gln | Lys | Trp | Leu | Thr | Ala | Gly | Gly | Leu | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Val | Leu | Leu | Thr | Leu | Ala | Gly | Arg | Glu | Ile | Leu | Thr | Asn | Phe | Leu |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Ser | Ser | Ile | Met | Ile | His | Ala | Thr | Arg | Pro | Phe | Val | Leu | Asn | Glu | Trp |
|     |     |     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |
| Ile | Gln | Thr | Lys | Ile | Gly | Gly | Tyr | Glu | Val | Ser | Gly | Thr | Val | Glu | Gln |
|     |     |     | 305 |     |     |     |     | 310 |     |     |     | 315 |     |     | 320 |
| Val | Gly | Trp | Trp | Ser | Pro | Thr | Ile | Ile | Arg | Gly | Asp | Asp | Arg | Glu | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | His | Ile | Pro | Asn | His | Gln | Phe | Ser | Val | Asn | Ile | Val | Arg | Asn | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Gln | Lys | Thr | His | Trp | Arg | Ile | Lys | Thr | His | Leu | Ala | Ile | Ser | His |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |
| Leu | Asp | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 370 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..370

(D) OTHER INFORMATION: / Ceres Seq. ID 1572407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Thr | Val | Ala | Leu | Pro | Leu | Ser | His | Asp | Leu | Asn | Val | His | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | His | Glu | Ala | Ser | Gly | Phe | His | Asn | Ser | Ala | Ala | Gly | Lys | Asn | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Tyr | Leu | Thr | Arg | Thr | Gly | Leu | Ser | Ser | Cys | Ala | Thr | Arg | Gln | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Val | Trp | Ser | Leu | Gln | Leu | Leu | Glu | Ser | Leu | Ser | Gly | Ser | Ile | Val | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Ser | Arg | Cys | Asn | Ala | Phe | Val | Cys | Arg | Ser | Ala | Leu | Ser | Pro |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Asn | Gly | Asn | Glu | Gly | Pro | Ile | Leu | Lys | Ser | Thr | Ala | Val | Ile | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Arg | Val | Tyr | Asp | Ala | Leu | Gly | Gly | Asn | Pro | His | Leu | Val | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Pro | Ala | Val | Gly | Ile | Leu | Ala | Phe | Ala | Thr | Trp | Gly | Leu | Arg | Pro |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Leu | Leu | Arg | Leu | Ala | Arg | Thr | Thr | Leu | Phe | Glu | Lys | Gly | Asn | Asp | Ala |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Asn | Ser | Gln | Lys | Ser | Ser | Thr | Gln | Tyr | Ile | Val | Val | Ser | Tyr | Leu | Gln |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Pro | Leu | Leu | Leu | Trp | Ser | Gly | Ala | Ile | Leu | Leu | Cys | Arg | Thr | Leu | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ile | Val | Leu | Pro | Ser | Ser | Ala | Gly | Gln | Ala | Ile | Lys | Gln | Arg | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ile | Phe | Ala | Arg | Ser | Ile | Ser | Thr | Val | Leu | Ala | Phe | Ser | Cys | Cys |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Leu | Ser | Ser | Leu | Leu | Gln | Gln | Val | Gln | Lys | Phe | Phe | Met | Glu | Thr | Asn |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |
| Asn | Pro | Ala | Asp | Thr | Arg | Asn | Met | Gly | Phe | Ser | Phe | Ala | Gly | Lys | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |

225 230 235 240

Val Tyr Thr Ala Ala Trp Val Ala Ala Ala Ser Leu Phe Met Glu Leu  
245 250 255  
Leu Gly Phe Ser Thr Gln Lys Trp Leu Thr Ala Gly Gly Leu Gly Thr  
260 265 270  
Val Leu Leu Thr Leu Ala Gly Arg Glu Ile Leu Thr Asn Phe Leu Ser  
275 280 285  
Ser Ile Met Ile His Ala Thr Arg Pro Phe Val Leu Asn Glu Trp Ile  
290 295 300  
Gln Thr Lys Ile Gly Gly Tyr Glu Val Ser Gly Thr Val Glu Gln Val  
305 310 315 320  
Gly Trp Trp Ser Pro Thr Ile Ile Arg Gly Asp Asp Arg Glu Ala Val  
325 330 335  
His Ile Pro Asn His Gln Phe Ser Val Asn Ile Val Arg Asn Leu Thr  
340 345 350  
Gln Lys Thr His Trp Arg Ile Lys Thr His Leu Ala Ile Ser His Leu  
355 360 365  
Asp Val  
370

(2) INFORMATION FOR SEQ ID NO:2289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..605
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gcaccccttt tattgtagcg acgcaagaag aagcagctat agcgtacgat atcgcagcta  | 60  |
| tcgagtaaccg tggactcaac gccgttacta acttcgacat cagccgttat ctgaaactcc | 120 |
| cgggtgccgga gaacctatc gataccgcga ataatctcct cgagagtcgg cattctgatc  | 180 |
| ttagccatt tataaaacct aaccacgagt ctgacttatc acagagtcaa tcttcgtcag   | 240 |
| aggacaacga tgatcggaaa acaaagctct tgaagtcgtc accttagtg gcagaggagg   | 300 |
| taatcggacc atcgacgcca cctgagattg ctccgcctcg tcggagcttc ccggaagata  | 360 |
| tccagacgta tttcgggtgt caaaactccg gcaagttaac ggccgaggaa gatgatgta   | 420 |
| tcttcgggtga ttttagattct ttccttacgc ctgatttcta cagcgagta aatgattgct | 480 |
| aaagtgttgt tcttctgata agttttgttt tttagttgtt cagaatctcg gttgtgaaaA  | 540 |
| tcaacattga cacatcgatt attctttctt gtgacaatct tatataataa agtttgaatc  | 600 |
| ttttt                                                              |     |

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Pro Phe Ile Val Ala Thr Gln Glu Ala Ala Ile Ala Tyr Asp     |  |
| 1 5 10 15                                                       |  |
| Ile Ala Ala Ile Glu Tyr Arg Gly Leu Asn Ala Val Thr Asn Phe Asp |  |
| 20 25 30                                                        |  |
| Ile Ser Arg Tyr Leu Lys Leu Pro Val Pro Glu Asn Pro Ile Asp Thr |  |
| 35 40 45                                                        |  |
| Ala Asn Asn Leu Leu Glu Ser Pro His Ser Asp Leu Ser Pro Phe Ile |  |
| 50 55 60                                                        |  |

Lys Pro Asn His Glu Ser Asp Leu Ser Gln Ser Gln Ser Ser Ser Glu  
65 70 75 80  
Asp Asn Asp Asp Arg Lys Thr Lys Leu Leu Lys Ser Ser Pro Leu Val  
85 90 95  
Ala Glu Glu Val Ile Gly Pro Ser Thr Pro Pro Glu Ile Ala Pro Pro  
100 105 110  
Arg Arg Ser Phe Pro Glu Asp Ile Gln Thr Tyr Phe Gly Cys Gln Asn  
115 120 125  
Ser Gly Lys Leu Thr Ala Glu Glu Asp Asp Val Ile Phe Gly Asp Leu  
130 135 140  
Asp Ser Phe Leu Thr Pro Asp Phe Tyr Ser Glu Leu Asn Asp Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

aagccataga tattgacgaa atacactttt tgtctttttg ttgctgtgcA acgtcataga 60  
tctaactccg gaagaagaag aagatgagtg acgaaacgac gtcattctccg tccccagctc 120  
cggcgaagaa gaagcagaat ctgggatgga tggagtgatg gaggggatgg agcagtgttt 180  
tcggggagat tctcttcacag aggatcacag cttctcattt ggagaatcct cttcctcttc 240  
cttcctcaa cgacctcact tgcgttgta cttggtccac cagcggcatt ggccgtgaaa 300  
ccgcgaggca gcttgacgaa gctggtgctc atgttgatg ggccgtaagg aacacaaagg 360  
cggctcagga gctgatactg caatggcaga acgaatggtc tggtaaaggc ctcccactca 420  
atattgaggc aatggagatt gatctactct cactggattc tgtcgcgaga tttgctgagg 480  
ctttcaacgc tcggttagga cctttgcatg ttctgattaa caatgctggg atgtttgcta 540  
tgggagaggc gcaaaaattc tcagaggaag gatattgagca gcacatgcaa gtgaatcatt 600  
tagctccagc gctgctttca gtactctctt tgcctgtctc gatccgaggc tctcctagcc 660  
gaatcattaa tgtgaattcc gttatgcata gtgtcggttt tgttgacccg gatgacatga 720  
atgttgtttc tggtagacgt aagtactcaa gccttatagg atactcaagc agcaagcttg 780  
cccagattat gtttagtagc attcttttca aaaagcttcc tctggaaaca ggagtcagcg 840  
tcgtatgtct atcccctggt gttgtcctaa caaatgttgc cagggatcta tccaggattc 900  
ttcaagctct ttacgcagtg ataccttatt tcatattttc accccaagaa ggttgtagaa 960  
gttctctatt ctgcgccaca gatcctcaga ttccagagta ctgggaaaca ctaaaaaacg 1020  
atgattggcc tgtttgccc aatcatctctc aagattgccg ccctgcaaat ccttccgaag 1080  
aagcacacaa cacagaaact gcacagagag tgtggaaaaa gacgttagag ctggtgggtc 1140  
ttcctctcga tgcagttgag aagctcatag aaggggaaaa tatccaatgc cggtagtgag 1200  
cacaacacga atagtctttc aaaattacca cagggttaagt gacccattac agatcaaagg 1260  
gtaggtaatt gagaaaatat cttttttttt tgtttccttg tattaatcta cacgatacag 1320  
tggggaatgg atcccccagg catgtagttt gcttgagaat gtttgattgt tggataaaaag 1380  
tcaagcttta gct

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..376
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

Met Ser Asp Glu Thr Thr Ser Ser Pro Ser Pro Ala Pro Ala Lys Lys

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Lys | Gln | Asn | Leu | Gly | Trp | Met |
|     |     | 20  |     |     | 25  |     |
| Phe | Gly | Glu | Ile | Leu | Phe | Gln |
|     |     | 35  |     |     | 40  |     |
| Pro | Leu | Pro | Leu | Pro | Ser | Val |
|     |     | 50  |     |     | 55  |     |
| Ser | Thr | Ser | Gly | Ile | Gly | Arg |
|     |     | 65  |     |     | 70  |     |
| Gly | Ala | His | Val | Val | Met | Ala |
|     |     |     | 85  |     |     | 90  |
| Leu | Ile | Leu | Gln | Trp | Gln | Asn |
|     |     | 100 |     |     | 105 |     |
| Asn | Ile | Glu | Ala | Met | Glu | Ile |
|     |     | 115 |     |     | 120 |     |
| Arg | Phe | Ala | Glu | Ala | Phe | Asn |
|     |     | 130 |     |     | 135 |     |
| Ile | Asn | Asn | Ala | Gly | Met | Phe |
|     |     | 145 |     |     | 150 |     |
| Glu | Glu | Gly | Tyr | Glu | Gln | His |
|     |     |     | 165 |     |     | 170 |
| Leu | Leu | Ser | Val | Leu | Leu | Leu |
|     |     | 180 |     |     | 185 |     |
| Arg | Ile | Ile | Asn | Val | Asn | Ser |
|     |     | 195 |     |     | 200 |     |
| Pro | Asp | Asp | Met | Asn | Val | Val |
|     |     | 210 |     |     | 215 |     |
| Ile | Gly | Tyr | Ser | Ser | Ser | Lys |
|     |     | 225 |     |     | 230 |     |
| Leu | Phe | Lys | Lys | Leu | Pro | Leu |
|     |     |     | 245 |     |     | 250 |
| Ser | Pro | Gly | Val | Val | Leu | Thr |
|     |     | 260 |     |     | 265 |     |
| Leu | Gln | Ala | Leu | Tyr | Ala | Val |
|     |     | 275 |     |     | 280 |     |
| Glu | Gly | Cys | Arg | Ser | Ser | Leu |
|     |     | 290 |     |     | 295 |     |
| Glu | Tyr | Trp | Glu | Thr | Leu | Lys |
|     |     | 305 |     |     | 310 |     |
| Ile | Ser | Gln | Asp | Cys | Arg | Pro |
|     |     |     | 325 |     |     | 330 |
| Thr | Glu | Thr | Ala | Gln | Arg | Val |
|     |     | 340 |     |     | 345 |     |
| Leu | Pro | Leu | Asp | Ala | Val | Glu |
|     |     | 355 |     |     | 360 |     |
| Cys | Arg | Tyr | Gly | Ala | Gln | His |
|     |     | 370 |     |     | 375 |     |

(2) INFORMATION FOR SEQ ID NO:2293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1572452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Trp | Met | Arg | Gly | Trp | Ser | Ser | Val | Phe | Gly | Glu | Ile | Leu | Phe |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |

Gln Arg Ile Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser  
20 25 30  
Val Asn Asp Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly  
35 40 45  
Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met  
50 55 60  
Ala Val Arg Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln  
65 70 75 80  
Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu  
85 90 95  
Ile Asp Leu Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe  
100 105 110  
Asn Ala Arg Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met  
115 120 125  
Phe Ala Met Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln  
130 135 140  
His Met Gln Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu  
145 150 155 160  
Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser Arg Ile Ile Asn Val Asn  
165 170 175  
Ser Val Met His Ser Val Gly Phe Val Asp Pro Asp Asp Met Asn Val  
180 185 190  
Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu Ile Gly Tyr Ser Ser Ser  
195 200 205  
Lys Leu Ala Gln Ile Met Phe Ser Ser Ile Leu Phe Lys Lys Leu Pro  
210 215 220  
Leu Glu Thr Gly Val Ser Val Val Cys Leu Ser Pro Gly Val Val Leu  
225 230 235 240  
Thr Asn Val Ala Arg Asp Leu Ser Arg Ile Leu Gln Ala Leu Tyr Ala  
245 250 255  
Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln Glu Gly Cys Arg Ser Ser  
260 265 270  
Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro Glu Tyr Trp Glu Thr Leu  
275 280 285  
Lys Asn Asp Asp Trp Pro Val Cys Pro Phe Ile Ser Gln Asp Cys Arg  
290 295 300  
Pro Ala Asn Pro Ser Glu Glu Ala His Asn Thr Glu Thr Ala Gln Arg  
305 310 315 320  
Val Trp Lys Lys Thr Leu Glu Leu Val Gly Leu Pro Leu Asp Ala Val  
325 330 335  
Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln Cys Arg Tyr Gly Ala Gln  
340 345 350  
His Glu

(2) INFORMATION FOR SEQ ID NO:2294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..351
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe Gln Arg Ile  
1 5 10 15  
Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser Val Asn Asp  
20 25 30  
Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly Arg Glu Thr

|                 |                             |                     |
|-----------------|-----------------------------|---------------------|
| 35              | 40                          | 45                  |
| Ala Arg Gln Leu | Ala Glu Ala Gly Ala His Val | Val Met Ala Val Arg |
| 50              | 55                          | 60                  |
| Asn Thr Lys Ala | Ala Gln Leu Ile Leu Gln     | Trp Gln Asn Glu Trp |
| 65              | 70                          | 75                  |
| Ser Gly Lys Gly | Leu Pro Leu Asn Ile Glu Ala | Met Glu Ile Asp Leu |
| 85              | 90                          | 95                  |
| Leu Ser Leu Asp | Ser Val Ala Arg Phe Ala Glu | Ala Phe Asn Ala Arg |
| 100             | 105                         | 110                 |
| Leu Gly Pro Leu | His Val Leu Ile Asn Asn Ala | Gly Met Phe Ala Met |
| 115             | 120                         | 125                 |
| Gly Glu Ala Gln | Lys Phe Ser Glu Glu Gly Tyr | Glu Gln His Met Gln |
| 130             | 135                         | 140                 |
| Val Asn His Leu | Ala Pro Ala Leu Leu Ser Val | Leu Leu Leu Pro Ser |
| 145             | 150                         | 155                 |
| Leu Ile Arg Gly | Ser Pro Ser Arg Ile Ile Asn | Val Asn Ser Val Met |
| 165             | 170                         | 175                 |
| His Ser Val Gly | Phe Val Asp Pro Asp Asp Met | Asn Val Val Ser Gly |
| 180             | 185                         | 190                 |
| Arg Arg Lys Tyr | Ser Ser Leu Ile Gly Tyr Ser | Ser Ser Lys Leu Ala |
| 195             | 200                         | 205                 |
| Gln Ile Met Phe | Ser Ser Ile Leu Phe Lys Lys | Leu Pro Leu Glu Thr |
| 210             | 215                         | 220                 |
| Gly Val Ser Val | Val Cys Leu Ser Pro Gly Val | Val Leu Thr Asn Val |
| 225             | 230                         | 235                 |
| Ala Arg Asp Leu | Ser Arg Ile Leu Gln Ala Leu | Tyr Ala Val Ile Pro |
| 245             | 250                         | 255                 |
| Tyr Phe Ile Phe | Ser Pro Gln Glu Gly Cys Arg | Ser Ser Leu Phe Ser |
| 260             | 265                         | 270                 |
| Ala Thr Asp Pro | Gln Ile Pro Glu Tyr Trp Glu | Thr Leu Lys Asn Asp |
| 275             | 280                         | 285                 |
| Asp Trp Pro Val | Cys Pro Phe Ile Ser Gln Asp | Cys Arg Pro Ala Asn |
| 290             | 295                         | 300                 |
| Pro Ser Glu Glu | Ala His Asn Thr Glu Thr Ala | Gln Arg Val Trp Lys |
| 305             | 310                         | 315                 |
| Lys Thr Leu Glu | Leu Val Gly Leu Pro Leu Asp | Ala Val Glu Lys Leu |
| 325             | 330                         | 335                 |
| Ile Glu Gly Glu | Asn Ile Gln Cys Arg Tyr Gly | Ala Gln His Glu     |
| 340             | 345                         | 350                 |

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1506
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

|                       |            |             |            |             |     |
|-----------------------|------------|-------------|------------|-------------|-----|
| accgagaaat gggatcgta  | gcgaatacac | aaaccaacgg  | caacgcaccg | ccaccgtcgt  | 60  |
| cgaatcaaaa gcctccggct | acgaacggcg | ttgatgggtc  | tcatcctcct | cctcctcctt  | 120 |
| taactcctga tcaagctatt | atagagtcgg | atccgtcgaa  | gaagaggaaa | atgggggatgc | 180 |
| ttcctctaga agtgggtact | cgtgtgatgt | gtcgggtggag | agacgggaaa | caccatccgg  | 240 |
| tgaaagtaat tgagcgccgg | cggataYcat | aacggcggtc  | aaaatgatta | cgagtattac  | 300 |
| gttcattaca ctgagtttaa | taggaggctg | gatgaatgga  | ctcagctgga | ccaactggac  | 360 |
| cttgattcag tagagtgcgc | tgtagatgaa | aaattggaag  | acaaggtaac | aagcttgaaG  | 420 |
| gatgacacgt caccagaaga | ggaagatcga | tgaGgacaca  | tatagagggt | catgaagagc  | 480 |
| tggatgcagc aagtttgctg | gaacatgaag | agttcacgaa  | agtgaagaac | atatcaacaa  | 540 |
| ttgagcttgg aaaatatgag | attgagactt | ggtactttctc | cccttttccg | ccagaataca  | 600 |

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| atgactgtgt  | gaagctcttt | ttttgtgagt  | tttgccctgaa | cttcatgaaa  | cgcaaagagc | 660  |
| agcttcaaag  | gcatatgagr | aagtgtgacc  | tgaagcaccc  | acctgggtgat | gaaatttacc | 720  |
| gaagtggtag  | cttgtcaatg | tttgaggtag  | atggcaaaaa  | gaacaagggt  | tatgcacaga | 780  |
| atctctgcta  | cctggcaaa  | ttatttcttg  | accacaaaac  | tctttactac  | gatgttgatt | 840  |
| tgtttctatt  | ctacgttctt | tgcgaaatgtg | atgaccgagg  | atgccacatg  | gttgggtact | 900  |
| tttcaaagga  | gaagcattcg | gaagaagcat  | acaacttagc  | ttgcattcta  | acctgcctt  | 960  |
| catatcaaag  | aaaaggctat | ggaaagtctt  | taatagcctt  | ttcctatgaa  | ctgtcaaaga | 1020 |
| aagagggaaa  | agttgggaca | ccggRaaaga  | cccttgctcg  | atctaggctt  | actaagctac | 1080 |
| agaggttatt  | ggactcgtgt | tctattagaa  | atcttgaaaa  | aacataaggg  | aaacatttct | 1140 |
| atcaaggagc  | tgagcgacgt | gacagcaatc  | aaagcggaag  | atatattaag  | cacacttcag | 1200 |
| agcctagaac  | tgatacagta | caggaaagga  | cagcatgtga  | tctgtgcgga  | tccaaagggt | 1260 |
| ctggaccgac  | atctgaaagc | tgaggccga   | ggtggtcttg  | atgtagatgc  | tagcaaactg | 1320 |
| atgttgacac  | cttacaagga | ccagagttaa  | gagtaagtac  | actcctcttg  | tgccattgga | 1380 |
| tttgatttga  | gtgtgtaagt | aaggggtgt   | cttattctcc  | tgaaatgtaa  | gtgtacttta | 1440 |
| cttgtaaattg | ttgaaatcgt | acttggaatg  | gtgtttgttt  | acaactNctt  | ataatgagga | 1500 |
| aatttg      |            |             |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1572459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Thr | His | Ile | Glu | Gly | His | Glu | Leu | Asp | Ala | Ala | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | His | Glu | Phe | Thr | Lys | Val | Lys | Asn | Ile | Ser | Thr | Ile | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Lys | Tyr | Glu | Ile | Glu | Thr | Trp | Tyr | Phe | Ser | Pro | Phe | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Glu | Tyr | Asn | Asp | Cys | Val | Lys | Leu | Phe | Phe | Cys | Glu | Phe | Cys | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     | Asn |
| Phe | Met | Lys | Arg | Lys | Glu | Gln | Leu | Gln | Arg | His | Met | Xaa | Lys | Cys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Lys | His | Pro | Pro | Gly | Asp | Glu | Ile | Tyr | Arg | Ser | Gly | Thr | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |
| Met | Phe | Glu | Val | Asp | Gly | Lys | Lys | Asn | Lys | Val | Tyr | Ala | Gln | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 | Leu |
| Cys | Tyr | Leu | Ala | Lys | Leu | Phe | Leu | Asp | His | Lys | Thr | Leu | Tyr | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     | Asp |
| Val | Asp | Leu | Phe | Leu | Phe | Tyr | Val | Leu | Cys | Glu | Cys | Asp | Asp | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     | Gly |
| Cys | His | Met | Val | Gly | Tyr | Phe | Ser | Lys | Glu | Lys | His | Ser | Glu | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Tyr | Asn | Leu | Ala | Cys | Ile | Leu | Thr | Leu | Pro | Ser | Tyr | Gln | Arg | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |
| Tyr | Gly | Lys | Phe | Leu | Ile | Ala | Phe | Ser | Tyr | Glu | Leu | Ser | Lys | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 | Glu |
| Gly | Lys | Val | Gly | Thr | Pro | Xaa | Lys | Thr | Leu | Val | Gly | Ser | Arg | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     | Thr |
| Lys | Leu | Gln | Arg | Leu | Leu | Asp | Ser | Cys | Ser | Ile | Arg | Asn | Leu | Glu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     | Lys |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids

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- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..160  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572460  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:

Met Lys Arg Lys Glu Gln Leu Gln Arg His Met Xaa Lys Cys Asp Leu  
1                   5                   10                   15  
Lys His Pro Pro Gly Asp Glu Ile Tyr Arg Ser Gly Thr Leu Ser Met  
                  20                   25                   30  
Phe Glu Val Asp Gly Lys Lys Asn Lys Val Tyr Ala Gln Asn Leu Cys  
                  35                   40                   45  
Tyr Leu Ala Lys Leu Phe Leu Asp His Lys Thr Leu Tyr Tyr Asp Val  
50                   55                   60  
Asp Leu Phe Leu Phe Tyr Val Leu Cys Glu Cys Asp Asp Arg Gly Cys  
65                   70                   75                   80  
His Met Val Gly Tyr Phe Ser Lys Glu Lys His Ser Glu Glu Ala Tyr  
                  85                   90                   95  
Asn Leu Ala Cys Ile Leu Thr Leu Pro Ser Tyr Gln Arg Lys Gly Tyr  
                  100                   105                   110  
Gly Lys Phe Leu Ile Ala Phe Ser Tyr Glu Leu Ser Lys Lys Glu Gly  
                  115                   120                   125  
Lys Val Gly Thr Pro Xaa Lys Thr Leu Val Gly Ser Arg Leu Thr Lys  
130                   135                   140  
Leu Gln Arg Leu Leu Asp Ser Cys Ser Ile Arg Asn Leu Glu Lys Thr  
145                   150                   155                   160

(2) INFORMATION FOR SEQ ID NO:2298:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 150 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..150  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572461  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

Met Xaa Lys Cys Asp Leu Lys His Pro Pro Gly Asp Glu Ile Tyr Arg  
1                   5                   10                   15  
Ser Gly Thr Leu Ser Met Phe Glu Val Asp Gly Lys Lys Asn Lys Val  
                  20                   25                   30  
Tyr Ala Gln Asn Leu Cys Tyr Leu Ala Lys Leu Phe Leu Asp His Lys  
                  35                   40                   45  
Thr Leu Tyr Tyr Asp Val Asp Leu Phe Leu Phe Tyr Val Leu Cys Glu  
50                   55                   60  
Cys Asp Asp Arg Gly Cys His Met Val Gly Tyr Phe Ser Lys Glu Lys  
65                   70                   75                   80  
His Ser Glu Glu Ala Tyr Asn Leu Ala Cys Ile Leu Thr Leu Pro Ser  
                  85                   90                   95  
Tyr Gln Arg Lys Gly Tyr Gly Lys Phe Leu Ile Ala Phe Ser Tyr Glu  
                  100                   105                   110  
Leu Ser Lys Lys Glu Gly Lys Val Gly Thr Pro Xaa Lys Thr Leu Val  
115                   120                   125  
Gly Ser Arg Leu Thr Lys Leu Gln Arg Leu Leu Asp Ser Cys Ser Ile  
130                   135                   140



Arg Asn Leu Glu Lys Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..889
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

|                                             |     |
|---------------------------------------------|-----|
| aaaacgaact agagacagtt tgattcgaaa atcttgctcg | 60  |
| ccaagaatta agcaattact gggaacctag ctcttgctc  | 120 |
| cgacagctgg cctttggaag aagccatttc tgggtcgat  | 180 |
| agctgcttcg tcgccggtt ctaagaatat tgtgtcggag  | 240 |
| taaccagaga ctcttcgctc ttcgatcagt tggtcccaat | 300 |
| ctcaataatc aaagatgcta ttagttacat agaaggatta | 360 |
| cgaagctgag atcagagAAC ttgaatctac accaaagagt | 420 |
| atcttgatcg tgatttactt gttcctgtca catccaagaa | 480 |
| gttcttccac ttctctcatc gaagttctcg aattgaaggt | 540 |
| caatggtggt gagtgtAAC tgtaataaga ggacagatac  | 600 |
| tctttgagtc attgaatctc aaatcctca cttccaatct  | 660 |
| tcttccacac tgtctttatt gaggcggatg aagaagaaca | 720 |
| tagaaacagg aataggagct tataatgaaa ctcaaagccc | 780 |
| tttactaata atactttttt tcttcctttt ttggttcatt | 840 |
| aatgtatgtc tctcttttca tttttatgat ctctacgtt  |     |
| tgtttgtcc                                   |     |

(2) INFORMATION FOR SEQ ID NO:2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Arg Thr Arg Asp Ser Leu Ile Arg Lys Ser Cys Arg Lys Met Glu |  |
| 1 5 10 15                                                       |  |
| Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser Ser Leu |  |
| 20 25 30                                                        |  |
| Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu Glu Ala |  |
| 35 40 45                                                        |  |
| Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala Ser Ser |  |
| 50 55 60                                                        |  |
| Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln Lys Leu |  |
| 65 70 75 80                                                     |  |
| Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile Thr Lys |  |
| 85 90 95                                                        |  |
| Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile Glu Gly |  |
| 100 105 110                                                     |  |
| Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu Leu Glu |  |
| 115 120 125                                                     |  |
| Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe             |  |
| 130 135 140                                                     |  |

(2) INFORMATION FOR SEQ ID NO:2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..127  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572464  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

Met Glu Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser  
1 5 10 15  
Ser Leu Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu  
20 25 30  
Glu Ala Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala  
35 40 45  
Ser Ser Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln  
50 55 60  
Lys Leu Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile  
65 70 75 80  
Thr Lys Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile  
85 90 95  
Glu Gly Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu  
100 105 110  
Leu Glu Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2302:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1572465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Met Lys Lys Arg Ser Ser Lys Leu Arg Ser Glu Asn Leu Asn Leu His  
1 5 10 15  
Gln Arg Val Ala Leu Val Ser Ala Lys Asp Phe Asp Arg Asp Leu Leu  
20 25 30  
Val Pro Val Thr Ser Lys Lys Met Lys Gln Leu Asp Ser Gly Ser Ser  
35 40 45  
Thr Ser Leu Ile Glu Val Leu Glu Leu Lys Val Thr Phe Met Gly Glu  
50 55 60  
Arg Thr Met Val Val Ser Val Thr Cys Asn Lys Arg Thr Asp Thr Met  
65 70 75 80  
Val Lys Leu Cys Glu Val Phe Glu Ser Leu Asn Leu Lys Ile Leu Thr  
85 90 95  
Ser Asn Leu Thr Ser Phe Ser Gly Met Ile Phe His Thr Val Phe Ile  
100 105 110  
Glu Ala Asp Glu Glu Glu Gln Glu Val Leu Arg Leu Lys Ile Glu Thr  
115 120 125  
Gly Ile Gly Ala Tyr Asn Glu Thr Gln Ser Pro Thr Leu Ser Ile Asp  
130 135 140  
Ser Leu Tyr  
145

(2) INFORMATION FOR SEQ ID NO:2303:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1010 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

(2) INFORMATION FOR SEQ ID NO:2304:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

| (X1) SEQUENCE DESCRIPTION: Seq 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser                              | Ile | Arg | Gly | Gly | Ala | Asp | Val | Ser | Ala | Ser | Met | Val | Thr | Leu | Ser |  |
| 1                                |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser                              | Pro | Ser | Pro | Ser | Leu | Ser | Cys | Val | Glu | Asn | Val | Thr | Cys | Lys | Ser |  |
|                                  |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser                              | His | Val | Ser | Arg | Val | Leu | Ile | Ser | Gly | Thr | Asp | Asn | Ile | Asn | His |  |
|                                  |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly                              | Glu | Ser | Ser | Glu | Ala | Lys | Ile | Leu | Arg | Asp | Val | His | Ile | Ser | Glu |  |
|                                  | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg                              | Leu | Leu | Glu | Asp | Phe | Thr | Glu | Leu | Ala | Arg | Glu | Asn | Thr | Glu | Lys |  |
| 65                               |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asp                              | Leu | Glu | Thr | Cys | Gly | Thr | Leu | Ala | Ala | Phe | Leu | Glu | Arg | Gly | Ile |  |
|                                  |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Phe                              | Tyr | Val | Thr | Thr | Leu | Ile | Ile | Pro | Lys | Gln | Glu | Ser | Thr | Ser | Asn |  |
|                                  |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser                              | Cys | Gln | Ala | Met | Asn | Glu | Val | Glu | Val | Phe | Ser | Ile | Gln | Asn | Glu |  |
|                                  |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg                              | Glu | Leu | Tyr | Pro | Val | Gly | Trp | Ile | His | Thr | His | Pro | Ser | Gln | Gly |  |
|                                  | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Cys                              | Phe | Met | Ser | Ser | Val | Asp | Leu | His | Thr | His | Tyr | Ser | Tyr | Gln | Val |  |
| 145                              |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Met                              | Val | Pro | Glu | Ala | Phe | Ala | Ile | Val | Val | Ala | Pro | Thr | Asp | Ser | Ser |  |
|                                  |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asn                              | Tyr | Gly | Ile | Phe | Lys | Leu | Thr | Asp | Pro | Gly | Gly | Met | Glu | Val | Leu |  |

180 185 190  
Arg Gly Cys Ser Glu Thr Gly Phe His Pro His Lys Glu Pro Glu Asp  
195 200 205  
Gly Asn Pro Val Tyr Glu His Cys Ser Asn Val Tyr Lys Asn Ser Asn  
210 215 220  
Leu Arg Phe Glu Ile Phe Asp Leu Arg  
225 230

(2) INFORMATION FOR SEQ ID NO:2305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1572489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:

Met Val Thr Leu Ser Ser Pro Ser Pro Ser Leu Ser Cys Val Glu Asn  
1 5 10 15  
Val Thr Cys Lys Ser Ser His Val Ser Arg Val Leu Ile Ser Gly Thr  
20 25 30  
Asp Asn Ile Asn His Gly Glu Ser Ser Glu Ala Lys Ile Leu Arg Asp  
35 40 45  
Val His Ile Ser Glu Arg Leu Leu Glu Asp Phe Thr Glu Leu Ala Arg  
50 55 60  
Glu Asn Thr Glu Lys Asp Leu Glu Thr Cys Gly Thr Leu Ala Ala Phe  
65 70 75 80  
Leu Glu Arg Gly Ile Phe Tyr Val Thr Thr Leu Ile Ile Pro Lys Gln  
85 90 95  
Glu Ser Thr Ser Asn Ser Cys Gln Ala Met Asn Glu Val Glu Val Phe  
100 105 110  
Ser Ile Gln Asn Glu Arg Glu Leu Tyr Pro Val Gly Trp Ile His Thr  
115 120 125  
His Pro Ser Gln Gly Cys Phe Met Ser Ser Val Asp Leu His Thr His  
130 135 140  
Tyr Ser Tyr Gln Val Met Val Pro Glu Ala Phe Ala Ile Val Val Ala  
145 150 155 160  
Pro Thr Asp Ser Ser Asn Tyr Gly Ile Phe Lys Leu Thr Asp Pro Gly  
165 170 175  
Gly Met Glu Val Leu Arg Gly Cys Ser Glu Thr Gly Phe His Pro His  
180 185 190  
Lys Glu Pro Glu Asp Gly Asn Pro Val Tyr Glu His Cys Ser Asn Val  
195 200 205  
Tyr Lys Asn Ser Asn Leu Arg Phe Glu Ile Phe Asp Leu Arg  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1572490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:

Met Asn Glu Val Glu Val Phe Ser Ile Gln Asn Glu Arg Glu Leu Tyr  
1 5 10 15

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Pro Val Gly Trp Ile His Thr His Pro Ser Gln Gly Cys Phe Met Ser  
20 25 30  
Ser Val Asp Leu His Thr His Tyr Ser Tyr Gln Val Met Val Pro Glu  
35 40 45  
Ala Phe Ala Ile Val Val Ala Pro Thr Asp Ser Ser Asn Tyr Gly Ile  
50 55 60  
Phe Lys Leu Thr Asp Pro Gly Gly Met Glu Val Leu Arg Gly Cys Ser  
65 70 75 80  
Glu Thr Gly Phe His Pro His Lys Glu Pro Glu Asp Gly Asn Pro Val  
85 90 95  
Tyr Glu His Cys Ser Asn Val Tyr Lys Asn Ser Asn Leu Arg Phe Glu  
100 105 110  
Ile Phe Asp Leu Arg  
115

(2) INFORMATION FOR SEQ ID NO:2307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..868
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aatcacttgt taattctaag cttcttctct ttccaaaaat ggcgtcatca tcggcttttag | 60  |
| ctctcaggag acttctctct tcttccaccg tcgccgtccc tcgcgcctta agagccgttc  | 120 |
| gtccggtgtc tgcttcttct cgctcttcca ataccaacgc cgccagaaac tatgaagacg  | 180 |
| gtgtgatag gaaccatcac tcaaaccgac atgtttctcg ccacggcggc gatttcttct   | 240 |
| cagatatact cgatccgttt actccaacga gaagcttgag ccagatgctg aatttcatgg  | 300 |
| accaggtaag cgaaatccct ttggtatcag ctactcgtgg aatgggagct tctggagtta  | 360 |
| gacgtgggtg gaacgtgaaa gagaaagacg acgcgttgca tctaaggata gatatgccgg  | 420 |
| gactaagcag agaggatgtg aaattggctt tggaacagaa cacattggtg attagaggag  | 480 |
| aaggggaaac agaggaggga gaagatgttt ctggagatgg acggaggttt acgagtagga  | 540 |
| ttgagttacc ggagaaagta tacaagactg atgagatTaa ggcggaaAtg aagaatggtg  | 600 |
| tgtTgaaAgt ggtgatTCca aagattaaAg agGatgagcg taAcaAtatT cgtcacataa  | 660 |
| acgttgacta gagtgtttta ttttgattg tttgagatgg aatggaagta agtgagtga    | 720 |
| tttgtgaact ttaaggtgtc ctttggtgaa tcaaggagaa tgacatttcc cacggtccta  | 780 |
| tgtgttcggg attttgactt ttttcgttac atcaatgac tatgtacgtt tgactacttt   | 840 |
| catatcatag gttcggattt tgtttccc                                     |     |

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

Ser Leu Val Asn Ser Lys Leu Leu Leu Phe Pro Lys Met Ala Ser Ser  
1 5 10 15  
Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser Thr Val Ala Val  
20 25 30  
Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala Ser Ser Arg Leu  
35 40 45  
Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly Val Asp Arg Asn  
50 55 60

His His Ser Asn Arg His Val Ser Arg His Gly Gly Asp Phe Phe Ser  
65 70 75 80  
Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu Ser Gln Met Leu  
85 90 95  
Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala Thr Arg  
100 105 110  
Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys Glu Lys  
115 120 125  
Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser Arg Glu  
130 135 140  
Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg Gly Glu  
145 150 155 160  
Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg Arg Phe  
165 170 175  
Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp Glu Ile  
180 185 190  
Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro Lys Ile  
195 200 205  
Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn Val Asp  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1572497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Met Ala Ser Ser Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser  
1 5 10 15  
Thr Val Ala Val Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala  
20 25 30  
Ser Ser Arg Leu Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly  
35 40 45  
Val Asp Arg Asn His His Ser Asn Arg His Val Ser Arg His Gly Gly  
50 55 60  
Asp Phe Phe Ser Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu  
65 70 75 80  
Ser Gln Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val  
85 90 95  
Ser Ala Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn  
100 105 110  
Val Lys Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly  
115 120 125  
Leu Ser Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val  
130 135 140  
Ile Arg Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp  
145 150 155 160  
Gly Arg Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys  
165 170 175  
Thr Asp Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val  
180 185 190  
Ile Pro Lys Ile Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn  
195 200 205  
Val Asp  
210

(2) INFORMATION FOR SEQ ID NO:2310:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 128 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..128  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572498  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala  
1                  5                  10                  15  
Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys  
                  20                  25                  30  
Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser  
                  35                  40                  45  
Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg  
                  50                  55                  60  
Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg  
65                  70                  75                  80  
Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp  
                  85                  90                  95  
Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro  
                  100                  105                  110  
Lys Ile Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn Val Asp  
                  115                  120                  125

(2) INFORMATION FOR SEQ ID NO:2311:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 911 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..911  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572503  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

agtgaaccgg agggagacag cgagatgagg ccggagatag ttctgttcgg cgactcgatc 60  
acggcgcagt ctttttaggtc cggcggttgg ggatctgctc ttgccgacgc ttactctcgc 120  
aaggctgatg ttgtggttcg aggctacggc ggctacaaca cccgatgggc tctcttcttg 180  
cttcatacaca tcttccctct cggtctcttcg tctcctcctg ttgctacgac gatattcttc 240  
ggtgcaaacg atgcagctct caaaggaaga accagtgata gacaacatgt gccggtggaa 300  
gagtacacag ataattgtcag aaagattggt cagcatttga agaaatgttc acctacaatg 360  
ctaattgtgc ttataactcc accaccaatt gatgaagctg gacgGtcaaa gttatgcaga 420  
atcaatctac ggtgagaaag ctatgaaaga gcctgagaga acaaacgaaa caacaggggt 480  
atatgcacaa catttgtgtg cattggccga ggaactcggc ctgcgatgtg tcaacttatg 540  
gtctaagatg caggaaacca attattggca gaaaaagtac ctaagtgatg ggctccatct 600  
cacgcctgaa ggcaatgggg tagtttttga tgaagtctcg agagttttta gagaagcttg 660  
gctctctccc gaagaaatgc cgtttgattt ccccatcatc tcgcatatcg atggtaaaaa 720  
cccatggaaa gcttttgaag agcgttgctt ataacgatca tccccaaatt aatgagcagg 780  
tttgttttga tttaaattca tgaacacgtt tcaatgttgt gatttagaaa actctcgat 840  
gtgaataaat acctaaaaag tgcatacatc ctagagatcg ttttcaagag aaatgaactt 900  
atgatgtact t

(2) INFORMATION FOR SEQ ID NO:2312:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 144 amino acids  
    (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572504  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:

Ser Glu Pro Glu Gly Asp Ser Glu Met Arg Pro Glu Ile Val Leu Phe  
1 5 10 15  
Gly Asp Ser Ile Thr Ala Gln Ser Phe Arg Ser Gly Gly Trp Gly Ser  
20 25 30  
Ala Leu Ala Asp Ala Tyr Ser Arg Lys Ala Asp Val Val Val Arg Gly  
35 40 45  
Tyr Gly Gly Tyr Asn Thr Arg Trp Ala Leu Phe Leu Leu His His Ile  
50 55 60  
Phe Pro Leu Gly Ser Ser Ser Pro Pro Val Ala Thr Thr Ile Phe Phe  
65 70 75 80  
Gly Ala Asn Asp Ala Ala Leu Lys Gly Arg Thr Ser Asp Arg Gln His  
85 90 95  
Val Pro Val Glu Tyr Thr Asp Asn Val Arg Lys Ile Val Gln His  
100 105 110  
Leu Lys Lys Cys Ser Pro Thr Met Leu Ile Val Leu Ile Thr Pro Pro  
115 120 125  
Pro Ile Asp Glu Ala Gly Arg Ser Lys Leu Cys Arg Ile Asn Leu Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2313:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572505  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:

Met Arg Pro Glu Ile Val Leu Phe Gly Asp Ser Ile Thr Ala Gln Ser  
1 5 10 15  
Phe Arg Ser Gly Gly Trp Gly Ser Ala Leu Ala Asp Ala Tyr Ser Arg  
20 25 30  
Lys Ala Asp Val Val Val Arg Gly Tyr Gly Gly Tyr Asn Thr Arg Trp  
35 40 45  
Ala Leu Phe Leu Leu His His Ile Phe Pro Leu Gly Ser Ser Ser Pro  
50 55 60  
Pro Val Ala Thr Thr Ile Phe Phe Gly Ala Asn Asp Ala Ala Leu Lys  
65 70 75 80  
Gly Arg Thr Ser Asp Arg Gln His Val Pro Val Glu Glu Tyr Thr Asp  
85 90 95  
Asn Val Arg Lys Ile Val Gln His Leu Lys Lys Cys Ser Pro Thr Met  
100 105 110  
Leu Ile Val Leu Ile Thr Pro Pro Ile Asp Glu Ala Gly Arg Ser  
115 120 125  
Lys Leu Cys Arg Ile Asn Leu Arg  
130 135

(2) INFORMATION FOR SEQ ID NO:2314:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:

Met Lys Leu Asp Gly Gln Ser Tyr Ala Glu Ser Ile Tyr Gly Glu Lys  
1 5 10 15  
Ala Met Lys Glu Pro Glu Arg Thr Asn Glu Thr Thr Gly Val Tyr Ala  
20 25 30  
Gln His Cys Val Ala Leu Ala Glu Glu Leu Gly Leu Arg Cys Val Asn  
35 40 45  
Leu Trp Ser Lys Met Gln Glu Thr Asn Tyr Trp Gln Lys Lys Tyr Leu  
50 55 60  
Ser Asp Gly Leu His Leu Thr Pro Glu Gly Asn Gly Val Val Phe Asp  
65 70 75 80  
Glu Val Ser Arg Val Phe Arg Glu Ala Trp Leu Ser Pro Glu Glu Met  
85 90 95  
Pro Phe Asp Phe Pro His His Ser His Ile Asp Gly Lys Asn Pro Trp  
100 105 110  
Lys Ala Phe Glu Glu Arg Cys Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:2315:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 538 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

atcaaaacRa tcacatacac tatttttctc ctctccttat tgtctatata tttttcctct 60  
ttagcttttt catttcgaaa tggccaccgt tgagggttgaa caagtcactc cagtagcagt 120  
agagaacggt gaggtaccaa caaagacagt ggaggagaca gtggtggaga cagagaagaa 180  
agatgaagaa accgagaaga aaacagagga gaaagacgag aagacagaag tgatcacgga 240  
aactccggtg gttgaggagg aggagaagaa agctgaggaa gtgaccgaaa ctccggcggt 300  
tgtggaggag gagaagaaga cagaggtggt tgaggagaaa cagactgagg ttgcggctgc 360  
tgaggaagtc gccgttgaga aggccgagga gtaaagagga aggaagaagc tatatatgac 420  
cttttttggt ctcatatcgt tttctgttta ttttatttta tcaacatttc ataagtattt 480  
tctatgtttg ttgggtttgt tatgatgaaa tcagatgttt ggatctttta atggttgc

(2) INFORMATION FOR SEQ ID NO:2316:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Val Glu Asn  
1 5 10 15  
Val Glu Val Pro Thr Lys Thr Val Glu Glu Thr Val Val Glu Thr Glu

20 25 30  
Lys Lys Asp Glu Glu Thr Glu Lys Thr Glu Glu Lys Asp Glu Lys  
35 40 45  
Thr Glu Val Ile Thr Glu Thr Pro Val Val Glu Glu Glu Lys Lys  
50 55 60  
Ala Glu Glu Val Thr Glu Thr Pro Ala Val Val Glu Glu Glu Lys Lys  
65 70 75 80  
Thr Glu Val Val Glu Glu Lys Gln Thr Glu Val Ala Ala Ala Glu Glu  
85 90 95  
Val Ala Val Glu Lys Ala Glu Glu  
100

(2) INFORMATION FOR SEQ ID NO:2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

|             |            |             |            |            |             |      |
|-------------|------------|-------------|------------|------------|-------------|------|
| gcagtggaga  | gagagcatgt | gaataaaaag  | cgtgaagctt | tttgatatct | ctttctcttc  | 60   |
| ctcttccttt  | ctcctccgat | agatttcgcc  | ggcgatggcg | gtggactcct | tagaaacgga  | 120  |
| gattgacacg  | gcggtgcgtg | ttgtccacct  | cgcttcttct | ctctgtgtta | aagttcaaga  | 180  |
| gaagcttcat  | cttcctaacg | gtggtcacgt  | taagtctaaa | gacgatgatt | ccctgtcac   | 240  |
| cgtcgcgtgat | tttggtgtac | aagcaattgt  | gagctgggtt | ttagctgaag | tgtttggtga  | 300  |
| tcaaaacctt  | tcaattgttg | ctgaagaaga  | cactgagaca | ctctctgagg | ctgattcttt  | 360  |
| aggctcttta  | ggagctgtgt | cgaatgcggt  | taatgaagca | ttgtccgaag | ctcagaacta  | 420  |
| cgggcttcgg  | aagccagtta | agccattggg  | gtctagttaa | attcttaagg | ctattagtag  | 480  |
| atgtaactct  | gttggaggac | ctaaaggaag  | gcattgggtt | cttgatcctg | ttgatggaac  | 540  |
| gtaggggttt  | gttcgtgggg | atcagtatgc  | tggtgcttta | gctttgatag | agaatggtaa  | 600  |
| agttcttttg  | ggtgtactag | gatgtcctaa  | ttatccgggt | aagaaagaat | gtttaagtaa  | 660  |
| tggttgtaac  | caagctatga | agacgaaagc  | tggtgctggt | tcagtatcga | aaggatgtgt  | 720  |
| tatgtatgca  | aagagaggta | gtggtcgaagc | ttggatgcaa | cctttgatcg | ttggagggaat | 780  |
| accagaatct  | gcaacacttc | ttaaggtttc  | ttcagttgat | gacccggttt | tagctacagt  | 840  |
| ttgtgagcca  | gtagagagag | caaactcaaa  | ccacttggtc | actgcaggac | ttgccaatag  | 900  |
| catgggagtt  | agaaagcagc | ctatgcgagt  | gtatagcatg | gtgaaatatg | cagcgaTtgc  | 960  |
| acgtggagac  | gctgaagtgt | ttatgaagtt  | tgcacagtca | agttacaaag | agaagatatg  | 1020 |
| ggatcacgca  | gctggagttg | ttattgtgga  | agaagctggt | ggtgtggtga | ctgatgcggg  | 1080 |
| agggagaaac  | ttagacttct | cgaaagggtg  | ttacttgga  | ggtcttgacc | gtggaatcat  | 1140 |
| cgcatgttct  | ggtcaagttt | tacatgagaa  | gattataggt | gctgtttatg | ctagttggga  | 1200 |
| atcttccagt  | ctctgaaaaa | gcttatccac  | aatccgtagt | ttggtgcagc | atcatcgagc  | 1260 |
| caaagcaaag  | gaggaacaag | ggccattacg  | gtttaggatg | agcaagggcc | agtttcaatg  | 1320 |
| aatgtgaatg  | gcggagaagt | aaatatagtc  | gaggaagcag | cggtaaaagt | aagaatctag  | 1380 |
| tttatttacc  | tatctaagag | taataaagct  | gctgcatttc | acgaaccctt | atgttctatg  | 1440 |
| atctttaatg  | gatgatatca | ttttt       |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

Met Ala Val Asp Ser Leu Glu Thr Glu Ile Asp Thr Ala Val Arg Val

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|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Val His Leu Ala Ser Ser Leu Cys Val Lys Val Gln Glu Lys Leu His |     |     |     |
| 20                                                              | 25  | 30  |     |
| Leu Pro Asn Gly Gly His Val Lys Ser Lys Asp Asp Asp Ser Pro Val |     |     |     |
| 35                                                              | 40  | 45  |     |
| Thr Val Ala Asp Phe Gly Val Gln Ala Ile Val Ser Trp Val Leu Ala |     |     |     |
| 50                                                              | 55  | 60  |     |
| Glu Val Phe Gly Asp Gln Asn Leu Ser Ile Val Ala Glu Glu Asp Thr |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Glu Thr Leu Ser Glu Ala Asp Ser Leu Gly Leu Leu Gly Ala Val Ser |     |     |     |
| 85                                                              | 90  | 95  |     |
| Asn Ala Val Asn Glu Ala Leu Ser Glu Ala Gln Asn Tyr Gly Leu Pro |     |     |     |
| 100                                                             | 105 | 110 |     |
| Lys Pro Val Lys Pro Leu Gly Ser Ser Glu Ile Leu Lys Ala Ile Ser |     |     |     |
| 115                                                             | 120 | 125 |     |
| Arg Cys Asn Ser Val Gly Gly Pro Lys Gly Arg His Trp Val Leu Asp |     |     |     |
| 130                                                             | 135 | 140 |     |
| Pro Val Asp Gly Thr Leu Gly Phe Val Arg Gly Asp Gln Tyr Ala Val |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Ala Leu Ala Leu Ile Glu Asn Gly Lys Val Leu Leu Gly Val Leu Gly |     |     |     |
| 165                                                             | 170 | 175 |     |
| Cys Pro Asn Tyr Pro Val Lys Lys Glu Cys Leu Ser Asn Gly Cys Asn |     |     |     |
| 180                                                             | 185 | 190 |     |
| Gln Ala Met Lys Thr Lys Ala Val Ala Gly Ser Val Ser Lys Gly Cys |     |     |     |
| 195                                                             | 200 | 205 |     |
| Val Met Tyr Ala Lys Arg Gly Ser Gly Gln Ala Trp Met Gln Pro Leu |     |     |     |
| 210                                                             | 215 | 220 |     |
| Ile Val Gly Gly Ile Pro Glu Ser Ala Thr Leu Leu Lys Val Ser Ser |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Val Asp Asp Pro Val Leu Ala Thr Val Cys Glu Pro Val Glu Arg Ala |     |     |     |
| 245                                                             | 250 | 255 |     |
| Asn Ser Asn His Leu Phe Thr Ala Gly Leu Ala Asn Ser Met Gly Val |     |     |     |
| 260                                                             | 265 | 270 |     |
| Arg Lys Gln Pro Met Arg Val Tyr Ser Met Val Lys Tyr Ala Ala Ile |     |     |     |
| 275                                                             | 280 | 285 |     |
| Ala Arg Gly Asp Ala Glu Val Phe Met Lys Phe Ala Gln Ser Ser Tyr |     |     |     |
| 290                                                             | 295 | 300 |     |
| Lys Glu Lys Ile Trp Asp His Ala Ala Gly Val Val Ile Val Glu Glu |     |     |     |
| 305                                                             | 310 | 315 | 320 |
| Ala Gly Gly Val Val Thr Asp Ala Gly Gly Arg Asn Leu Asp Phe Ser |     |     |     |
| 325                                                             | 330 | 335 |     |
| Lys Gly Val Tyr Leu Glu Gly Leu Asp Arg Gly Ile Ile Ala Cys Ser |     |     |     |
| 340                                                             | 345 | 350 |     |
| Gly Gln Val Leu His Glu Lys Ile Ile Gly Ala Val Tyr Ala Ser Trp |     |     |     |
| 355                                                             | 360 | 365 |     |
| Glu Ser Ser Ser Leu                                             |     |     |     |
| 370                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atctacaact | ttcattcttc | cactacattt | ctctccttga | gtatcttctt | atcctatttt | 60  |
| ccaaattcca | aaacaattca | caaatggct  | acatgctggc | ctgagccgat | tgtttcogtg | 120 |

caatccttgt cccaaaccgg tgtaccaact gtaccaaacc gctatgtgaa gccggctcat 180  
cagagaccgg tctttaacac cacccaatcc gatgctggga tagaaatccc tggtctagac 240  
atgaacgacg ttggggggaa accagagggg ctaaggctcg tgaggagcgc gtgtgaggag 300  
tgggggtttct tccaaatggg gaaccatggg gtgacccact cgttgatgga gagagtgaga 360  
ggagcgtggc gagagttctt cgagctaccg ctgaggagga aacggaagta tgcaaactca 420  
ccggacacgt acgaggggata tgggaagccgc cttgggggtt tgagagatgc taaattagat 480  
tggagtgatt atttcttcct caattacttg cttctctcca taagaaaccc ttccaagtgg 540  
ccatActcag cctcctaaga tcagagaatt gatcgaaaag tacggagaag aagtgagaaa 600  
actgtgcgaa aggctaacag agacgttgtc agagagttta gggtttaaacc caaacaagct 660  
catgcaggct ttaggaggag gcgacaaagt cggagcttct ctgaggacaa acttctaccc 720  
aaaatgccct cagccgcagc tcactttagg tctctcttct cattctgacc ctggaggcat 780  
caccattctt ctcccggacg agaaggtcgc tggccttcag gtcgctcgtg gtgatggctg 840  
ggtcaccatt aaatcagtc ctaatgcttt gatcgttaac attggagatc aacttcagat 900  
acttagcaat ggaatttaca aaagcgtgga acatcaagtg atcggttaatt ccggtatgga 960  
acgagtctct ttggcattct tctataaccc gagaagtgat atcccgggtt gaccaatcga 1020  
agaactagta actgcaaacc gacctgctct ttataaacca atcaggttcg acgagtaccg 1080  
ttctctgata aggcaaaagg gtccttggtg aaaaaaccaa gtcgactcac tgttattaac 1140  
tagataataa ttgataaaca ttccaagtat tatctgttat tcctatgtcc ttgatatagt 1200  
cgttactaaa taatatgtaa accgtatctt cactttttct tattatattg ctgctctctc 1260  
ttgaggtttg

(2) INFORMATION FOR SEQ ID NO:2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1572529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

Ile Tyr Asn Phe His Ser Ser Thr Thr Phe Leu Ser Leu Ser Ile Phe  
1 5 10 15  
Leu Ser Tyr Phe Pro Asn Ser Lys Thr Ile His Lys Met Ala Thr Cys  
20 25 30  
Trp Pro Glu Pro Ile Val Ser Val Gln Ser Leu Ser Gln Thr Gly Val  
35 40 45  
Pro Thr Val Pro Asn Arg Tyr Val Lys Pro Ala His Gln Arg Pro Val  
50 55 60  
Phe Asn Thr Thr Gln Ser Asp Ala Gly Ile Glu Ile Pro Val Leu Asp  
65 70 75 80  
Met Asn Asp Val Trp Gly Lys Pro Glu Gly Leu Arg Leu Val Arg Ser  
85 90 95  
Ala Cys Glu Glu Trp Gly Phe Phe Gln Met Val Asn His Gly Val Thr  
100 105 110  
His Ser Leu Met Glu Arg Val Arg Gly Ala Trp Arg Glu Phe Phe Glu  
115 120 125  
Leu Pro Leu Glu Glu Lys Arg Lys Tyr Ala Asn Ser Pro Asp Thr Tyr  
130 135 140  
Glu Gly Tyr Gly Ser Arg Leu Gly Val Val Arg Asp Ala Lys Leu Asp  
145 150 155 160  
Trp Ser Asp Tyr Phe Phe Leu Asn Tyr Leu Pro Ser Ser Ile Arg Asn  
165 170 175  
Pro Ser Lys Trp Pro Tyr Ser Ala Ser  
180 185

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

acaagtcaca accccacccat gcatgtcata tctctttcgt tctcctcaat attctttttc 60  
ctcttcctca catcaacccat tttgatttct ccggtacaac ccacaacctc taagcctccg 120  
gcaccacggc cccacagaga gctctccgcc gattactact ccaagaaatg tcttcagctt 180  
gaaactctcg tcggttccgt cacttctcag cggttcaaag aagtcccat ctcagctcca 240  
gccaccattc gcctcttctt tcacgactgc ttcggtgagg gttgtgatgg gtcgatattg 300  
atagaaacaa agaaaggaag caagaaatta gcagagagag aagcatatga gaataaggaa 360  
ttgagagagg aaggatttga tagtatcatc aaggcgaagg ccttggttga gtctcattgc 420  
ccttctctcg tctcTtscct tgatattctc gctattgccg ctcgagattt cattcatctg 480  
gcagggtgggc cttactatca agtgaaaaaa ggaagggtgg acggaaaaag atcaacggca 540  
aagaacgtcc ctccaaacat acctcgatca aactccaccg ttgatcaact catcaagctc 600  
ttcgcgctcca aaggactaac cgtagaggaa ctgcgtctcc tttctggttc ccacaccatc 660  
ggttcgccca ttgtaaaaat ttccttggtc gtctctacga ctacaaaggc acaaaacgac 720  
ccgacccgag tcttgaccaa agattactaa aagagctccg gatgtcttgt cctttttccg 780  
gcggaagctc tggagtcgtc cttccgctcg acgctacaac tccgtttggtg tttgataatg 840  
gatatttcac aggtctagga accaaccatgg gccttctcgg gtcggaccaaa gctttgttcc 900  
ttgacccgag gacgaagccc attgcacttg agatggcaag agataagcag aagtttctca 960  
aggcgtttgg agacgctatg gataaaatgg gttccattgg tgtaaagaga gggaagagac 1020  
atggggaaat acgtacggat tgtcagatct ttttatagat tttctttatt gtcttgctg 1080  
atgggttttg tcttgatctt gatgtgttct gtgtcatgtg tcttttaatt tattagcatt 1140  
ttogtgattg ttttgttgat agtataaggt attttttt

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

Thr Ser His Asn Pro Thr Met His Val Ile Ser Leu Ser Leu Ser Ser  
1 5 10 15  
Ile Phe Phe Phe Leu Phe Leu Thr Ser Thr Ile Leu Ile Ser Pro Val  
20 25 30  
Gln Pro Thr Thr Ser Lys Pro Pro Ala Pro Arg Pro His Arg Glu Leu  
35 40 45  
Ser Ala Asp Tyr Tyr Ser Lys Lys Cys Pro Gln Leu Glu Thr Leu Val  
50 55 60  
Gly Ser Val Thr Ser Gln Arg Phe Lys Glu Val Pro Ile Ser Ala Pro  
65 70 75 80  
Ala Thr Ile Arg Leu Phe Phe His Asp Cys Phe Val Glu Gly Cys Asp  
85 90 95  
Gly Ser Ile Leu Ile Glu Thr Lys Lys Gly Ser Lys Lys Leu Ala Glu  
100 105 110  
Arg Glu Ala Tyr Glu Asn Lys Glu Leu Arg Glu Glu Gly Phe Asp Ser  
115 120 125  
Ile Ile Lys Ala Lys Ala Leu Val Glu Ser His Cys Pro Ser Leu Val

130 135 140  
Ser Xaa Ser Asp Ile Leu Ala Ile Ala Ala Arg Asp Phe Ile His Leu  
145 150 155 160  
Ala Gly Gly Pro Tyr Gln Val Lys Lys Gly Arg Trp Asp Gly Lys  
165 170 175  
Arg Ser Thr Ala Lys Asn Val Pro Pro Asn Ile Pro Arg Ser Asn Ser  
180 185 190  
Thr Val Asp Gln Leu Ile Lys Leu Phe Ala Ser Lys Gly Leu Thr Val  
195 200 205  
Glu Glu Leu Val Val Leu Ser Gly Ser His Thr Ile Gly Ser Pro Ile  
210 215 220  
Val Lys Ile Ser Leu Val Ser Thr Thr Thr Lys Ala Gln Asn Asp  
225 230 235 240  
Pro Thr Arg Val Leu Thr Lys Asp Tyr  
245

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1572540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

Met His Val Ile Ser Leu Ser Leu Ser Ser Ile Phe Phe Phe Leu Phe  
1 5 10 15  
Leu Thr Ser Thr Ile Leu Ile Ser Pro Val Gln Pro Thr Thr Ser Lys  
20 25 30  
Pro Pro Ala Pro Arg Pro His Arg Glu Leu Ser Ala Asp Tyr Tyr Ser  
35 40 45  
Lys Lys Cys Pro Gln Leu Glu Thr Leu Val Gly Ser Val Thr Ser Gln  
50 55 60  
Arg Phe Lys Glu Val Pro Ile Ser Ala Pro Ala Thr Ile Arg Leu Phe  
65 70 75 80  
Phe His Asp Cys Phe Val Glu Gly Cys Asp Gly Ser Ile Leu Ile Glu  
85 90 95  
Thr Lys Lys Gly Ser Lys Lys Leu Ala Glu Arg Glu Ala Tyr Glu Asn  
100 105 110  
Lys Glu Leu Arg Glu Glu Gly Phe Asp Ser Ile Ile Lys Ala Lys Ala  
115 120 125  
Leu Val Glu Ser His Cys Pro Ser Leu Val Ser Xaa Ser Asp Ile Leu  
130 135 140  
Ala Ile Ala Ala Arg Asp Phe Ile His Leu Ala Gly Gly Pro Tyr Tyr  
145 150 155 160  
Gln Val Lys Lys Gly Arg Trp Asp Gly Lys Arg Ser Thr Ala Lys Asn  
165 170 175  
Val Pro Pro Asn Ile Pro Arg Ser Asn Ser Thr Val Asp Gln Leu Ile  
180 185 190  
Lys Leu Phe Ala Ser Lys Gly Leu Thr Val Glu Glu Leu Val Val Leu  
195 200 205  
Ser Gly Ser His Thr Ile Gly Ser Pro Ile Val Lys Ile Ser Leu Val  
210 215 220  
Val Ser Thr Thr Thr Lys Ala Gln Asn Asp Pro Thr Arg Val Leu Thr  
225 230 235 240  
Lys Asp Tyr

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1239  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572569  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

acaattcaga ttccaatttt ctcaaactct aaaatcaatc tctcaaactct ctcaaccgtg 60  
atcaaggtag attttctgagt tcttattgta tttcttcgat ttgtttcgtt cgatcgcaat 120  
ttaggctctg ttcttttgatt ttgatctcgt taatctctga tcggaggcaa attacatagt 180  
ttcatcgta gatctcttct tatttctcga ttagggttcg tatttttcgc agatctgttt 240  
attttcttgt tgtttccttg tatttgatcc gatttggtga aagaatttgt gtgttctcga 300  
ttatttatgc ttgatctgt gatttttata tagatttggg gttagtcttct tgtttgtgcg 360  
atcgaatttg tcgattaatc tcgggttttc tgattaacag atgcagatct tcgttaagac 420  
tctcacccga aagactatca ccctcgagggt ggaaagctct gacaccatcg acaacgttaa 480  
ggccaagatc caggataagg aagggtattcc tccggatcag cagaggctta tcttcgccgg 540  
aaagcagttg gaggatggcc gcacgttggc ggattacaat atccagaagg aatccaccct 600  
ccacttggtt ctcaggctcc gtggtggtat gcagattttc gttaaaacc taacgggaaa 660  
gacgattact cttgaggtgg agagctctga caccattgac aacgtcaagg ccaagatcca 720  
agataaggag ggtattcctc cggaccagca gaggttgatc ttcgccggaa agcaacttga 780  
ggacggcaga actttggcgg attacaacat ccagaaggag tctacgcttc atttggtcTt 840  
tgctctgcg tggagggtat cagatcttcg taaagacttt gaccggaaag accatcactc 900  
ttgaagttga gagctccgac accattgata acgtgaaggc taagatccag gacaaggaa 960  
gcattcctcc ggaccagcag cgtctcatct tcgctggaaa gcagcttgag gatggacgta 1020  
ctttggccga ctacaacatc cagaaggagt ctactcttca cttggtcctc cgtctccgtg 1080  
gtggtttcta aaccttgtct ctctctctta tggttactga accaagttca tgtatcgttt 1140  
catctagtac tttggtggtt tatgttttgg ggccatgtac agcctctgat aaataattga 1200  
tcgactatgt ttccgtttct ttcactctctc ttttcttcc

(2) INFORMATION FOR SEQ ID NO:2327:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 167 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..167  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572570  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe  
65 70 75 80  
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser  
85 90 95  
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile  
100 105 110  
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp  
115 120 125  
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His  
130 135 140



Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu Arg Lys Asp Phe  
145 150 155 160  
Asp Arg Lys Asp His His Ser  
165

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu  
1 5 10 15  
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp  
20 25 30  
Lys Glu Gly Ile Pro Pro Asp Gln Arg Leu Ile Phe Ala Gly Lys  
35 40 45  
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu  
50 55 60  
Ser Thr Leu His Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu  
65 70 75 80  
Arg Lys Asp Phe Asp Arg Lys Asp His His Ser  
85 90

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

aaaataaaga accttgacaa cttctctaca acactcactt tttctctcta atggtggaag 60  
caagaagctt gaagaaacca atccaattgg gtaataaaga agatcaaaac cctagaaaat 120  
tctactctcg attcatcttt aaagctctta tcctcaccgt gctctgcgcc gtcgtacctg 180  
tcttcccttc tcagacacca gagcttgcta accaaacaag actcctcgag cttctccacc 240  
ttgttttctg cggatctgca gtctcttacg gtctcttcag ccgcaggaac tacgacggag 300  
gaggaggtgg aggaacaagc aatagtgtac acaacaaagc tgatcatagt aataataatt 360  
cgcatctata tgtgcctaag attcttgaag tatcctctgt ttttaacgtg ggtcacgaga 420  
gtgaatctga accgtccgat gattcctccg gtgatcaacg taagtttcag acatggaaga 480  
acaagtacca catgaaaatc cccgaggttg agactcgttt cgttgatcga gttagttcag 540  
aaaacagaga gaagcctctg cttttgccgg ttcggagctt gaattattct cgtgtttctg 600  
attcttccgg cgataattcc ggtcgtatgg agaaagttag atctaagaga gaacttctga 660  
agactcttgg cgatgataat agtgatgtgc ttccttctcc gattccatgg aggtcaagat 720  
catcttcata atcatcatca tcatcaaagg aggttgatca tctaccgtcc gttagaatc 780  
tgactacagt tgaatcacag ccgttgatca agaactctgac accatcttct tctttctctt 840  
ctccaagaaa gtggaatcct atacctaatc tcgcatctga gttccatcca tctccgccac 900  
cgctcctcc gccgcgcgca ccactaccgg cgttttataa ctctcgtcgc agaaaagatc 960  
atcccggaat ttacagggtt gagaggagag aatcatcagt tcacaagacg aaatttgcag 1020  
gaggtgagtt tcatcctccg ccgcctcctc ctccaccacc tccggtggag tattataagt 1080  
cacctccgac aaaattcaga ctaagtaacg aacggagaaa gtcctcggag caaaagatgW 1140  
aaagaaacgc tcctaaaaag gtttggtggt ccgatccaat cgtggaatcg aaggaacaag 1200  
acacagagaa gaatgatcaa agaagtaact tgggaagcaa ggcagtggaa gaatccgaga 1260

(2) INFORMATION FOR SEQ ID NO:2330:

(A) LENGTH: 473 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(11) MOLECULE TYPE: peptide  
(ix) FEATURE:

(IX) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1572577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Ala | Arg | Ser | Leu | Lys | Lys | Pro | Ile | Gln | Leu | Gly | Asn | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Gln | Asn | Pro | Arg | Lys | Phe | Tyr | Ser | Arg | Phe | Ile | Phe | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Leu | Thr | Val | Leu | Cys | Ala | Val | Val | Pro | Val | Phe | Leu | Ser | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Pro | Glu | Leu | Ala | Asn | Gln | Thr | Arg | Leu | Leu | Glu | Leu | Leu | His | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Val | Phe | Val | Gly | Ile | Ala | Val | Ser | Tyr | Gly | Leu | Phe | Ser | Arg | Arg | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | Asp | Gly | Gly | Gly | Gly | Gly | Gly | Thr | Ser | Asn | Ser | Asp | His | Asn | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Asp | His | Ser | Asn | Asn | Asn | Ser | His | Ser | Tyr | Val | Pro | Lys | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Val | Ser | Ser | Val | Phe | Asn | Val | Gly | His | Glu | Ser | Glu | Ser | Glu | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Asp | Asp | Ser | Ser | Gly | Asp | Gln | Arg | Lys | Phe | Gln | Thr | Trp | Lys | Asn |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Lys | Tyr | His | Met | Lys | Ile | Pro | Glu | Val | Glu | Thr | Arg | Phe | Val | Asp | Arg |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Ser | Ser | Glu | Asn | Arg | Glu | Lys | Pro | Leu | Leu | Leu | Pro | Val | Arg | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Asn | Tyr | Ser | Arg | Val | Ser | Asp | Ser | Ser | Gly | Asp | Asn | Ser | Gly | Arg |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Trp | Glu | Lys | Val | Arg | Ser | Lys | Arg | Glu | Leu | Leu | Lys | Thr | Leu | Gly | Asp |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Asn | Ser | Asp | Val | Leu | Pro | Ser | Pro | Ile | Pro | Trp | Arg | Ser | Arg | Ser |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Lys | Glu | Val | Glu | Ser | Leu | Pro | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Lys | Asn | Leu | Thr | Thr | Val | Glu | Ser | Gln | Pro | Leu | Ile | Lys | Asn | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Thr | Pro | Ser | Ser | Ser | Phe | Ser | Ser | Pro | Arg | Lys | Ser | Asn | Pro | Ile | Pro |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Leu | Ala | Ser | Glu | Phe | His | Pro | Ser | Pro | Pro | Pro | Pro | Pro | Pro | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Pro | Pro | Pro | Leu | Pro | Ala | Phe | Tyr | Asn | Ser | Ser | Ser | Arg | Lys | Asp | His |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Pro | Gly | Ile | Tyr | Arg | Val | Glu | Arg | Arg | Glu | Ser | Ser | Val | His | Lys | Thr |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Phe | Ala | Gly | Gly | Glu | Phe | His | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Pro | Pro | Val | Glu | Tyr | Tyr | Lys | Ser | Pro | Pro | Thr | Lys | Phe | Arg | Leu | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Pro | Glu | Val | Glu | Thr | Arg | Phe | Val | Asp | Arg | Val | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | Arg | Glu | Lys | Pro | Leu | Leu | Leu | Pro | Val | Arg | Ser | Leu | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Arg | Val | Ser | Asp | Ser | Ser | Gly | Asp | Asn | Ser | Gly | Arg | Trp | Glu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Ser | Lys | Arg | Glu | Leu | Leu | Lys | Thr | Leu | Gly | Asp | Asp | Asn | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Val | Leu | Pro | Ser | Pro | Ile | Pro | Trp | Arg | Ser | Arg | Ser | Ser | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ser | Ser | Ser | Ser | Lys | Glu | Val | Glu | Ser | Leu | Pro | Ser | Val | Lys | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Thr | Val | Glu | Ser | Gln | Pro | Leu | Ile | Lys | Asn | Leu | Thr | Pro | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Phe | Ser | Ser | Pro | Arg | Lys | Ser | Asn | Pro | Ile | Pro | Asn | Leu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Glu | Phe | His | Pro | Ser | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Leu | Pro | Ala | Phe | Tyr | Asn | Ser | Ser | Ser | Arg | Lys | Asp | His | Pro | Gly | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Arg | Val | Glu | Arg | Arg | Glu | Ser | Ser | Val | His | Lys | Thr | Lys | Phe | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Gly | Glu | Phe | His | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Tyr | Tyr | Lys | Ser | Pro | Pro | Thr | Lys | Phe | Arg | Leu | Ser | Asn | Glu | Arg |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Lys | Ser | Ser | Glu | Gln | Lys | Met | Xaa | Arg | Asn | Ala | Pro | Lys | Lys | Val |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Trp | Trp | Ser | Asp | Pro | Ile | Val | Glu | Ser | Lys | Glu | Gln | Asp | Thr | Glu | Lys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Asn | Asp | Gln | Arg | Ser | Asn | Leu | Gly | Ser | Lys | Ala | Val | Glu | Glu | Ser | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |

Asn Gly Glu Gln Arg Arg Gly Glu Asn Glu Ile His Asp Glu Val Glu  
260 265 270  
Lys Lys Ile Val Glu Glu Glu Gly Val Ser Glu Ile Asn Asn Gly Ser  
275 280 285  
Asp Val Asp Lys Lys Ala Asp Glu Phe Ile Ala Lys Phe Arg Glu Gln  
290 295 300  
Ile Arg Leu Gln Arg Ile Glu Ser Ile Lys Arg Ser Thr Asn Lys Ile  
305 310 315 320  
Ser Ala Asn Ser Ser Arg  
325

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..783
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attgaagtct gcgctctgtga gatcacgctt tagctttgtg gatgcagaat tgcagactat | 60  |
| acattctttt ttaagttctt gagcttggaa caataccttt ttcactctag ttgtttcttc  | 120 |
| aactaaatgg atactggtgg gttttagat gaaaaagggtg agaacagatt atatgttgga  | 180 |
| aacctggatc ttagaataaaa cgaggcttcg ttgataaaaa tgttttctcc atatgggaag | 240 |
| atcatatcag aagacttcct ttggcacaca cgcgggccaa agaaaggaga acctcggggt  | 300 |
| tatgctttca ttcaatacag ccttaaagag tgagcataca ggaagctgaa ttggcgaaag  | 360 |
| agaagatgca tgggagatta gcttgtggtg ggcctttagt ggtgcgtcta gctagtgaga  | 420 |
| agcatctaga agattcctct catgatcact ccaaaagatc attaccagaa ggaacagaa   | 480 |
| ccagatttgt aaacgggagc agctcaggac aaatgagccg agacgaaaaa gtaactgcca  | 540 |
| ttaagaacaa actcaaagct ttggaagaag atgagaaacg tgatccCaag aaacagaaaa  | 600 |
| tttaagaaaa cggttttcaa acacacaact ttgggtctat gtgactctgt gactctgacc  | 660 |
| atttttcagt tttggtttga tttgatttgg tttaccggtt taatcgaaac caattttgat  | 720 |
| ttaatatattc ggtttggctc agtgtgatat ataaaatttg taatggaaag caaaagttag | 780 |

cgc

(2) INFORMATION FOR SEQ ID NO:2333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Asp Thr Gly Gly Phe Val Asp Glu Lys Gly Glu Asn Arg Leu Tyr |  |
| 1 5 10 15                                                       |  |
| Val Gly Asn Leu Asp Leu Arg Ile Asn Glu Ala Ser Leu Ile Lys Met |  |
| 20 25 30                                                        |  |
| Phe Ser Pro Tyr Gly Lys Ile Ile Ser Glu Asp Phe Leu Trp His Thr |  |
| 35 40 45                                                        |  |
| Arg Gly Pro Lys Lys Gly Glu Pro Arg Gly Tyr Ala Phe Ile Gln Tyr |  |
| 50 55 60                                                        |  |
| Ser Leu Lys Glu                                                 |  |
| 65                                                              |  |

(2) INFORMATION FOR SEQ ID NO:2334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..79
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572629
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:

Met His Gly Arg Leu Ala Cys Gly Arg Pro Leu Val Val Arg Leu Ala  
1 5 10 15  
Ser Glu Lys His Leu Glu Asp Ser Ser His Asp His Ser Lys Arg Ser  
20 25 30  
Leu Pro Glu Gly Asn Arg Thr Arg Phe Val Asn Gly Ser Ser Ser Gly  
35 40 45  
Gln Met Ser Arg Asp Glu Lys Val Thr Ala Ile Lys Asn Lys Leu Lys  
50 55 60  
Ala Leu Glu Glu Asp Glu Lys Arg Asp Pro Lys Lys Gln Lys Ile  
65 70 75

- (2) INFORMATION FOR SEQ ID NO:2335:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 58 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..58
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1572630
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

Met Arg Asn Val Ile Pro Arg Asn Arg Lys Phe Lys Lys Thr Val Phe  
1 5 10 15  
Lys His Thr Thr Leu Gly Leu Cys Asp Ser Val Thr Leu Thr Ile Phe  
20 25 30  
Gln Phe Trp Phe Asp Leu Ile Trp Phe Thr Gly Leu Ile Glu Thr Asn  
35 40 45  
Phe Asp Leu Ile Phe Arg Phe Gly Ser Val  
50 55

- (2) INFORMATION FOR SEQ ID NO:2336:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 910 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..910
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1572643
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atcaactctc tctctcactt tcacaactct cctttctctat ttctctctct agaaaaatat | 60  |
| catcatctat caattatata gactacttat ttagattcat ttcataaaaa tggagaaaag  | 120 |
| agaaagtagt ggtggttctg gatcaggaga tgcagagggtg agaaaagggc catggacgat | 180 |
| ggaagaagat ttgattctca tcaattatat cgccaatcat ggtgaagggtg tttggaactc | 240 |
| tctcgccaaa tctgcaggac taaaacgcac cgggaaaagt tgccggctcc ggtggctgaa  | 300 |
| ctacctccga cctgatgtgc gacggggaaa tatcacacca gaagaacagc tcaccatcat  | 360 |
| ggaacttcat gcaaaatggg gaaatagggt gtcaaaaatt gcaaaagcatt taccaggaag | 420 |
| gaccgacaat gagataaaga acttttggag gactaagatc cagaaataca tcatcaagag  | 480 |
| cggagaaaacg acgaccgttg gatcacaaag ctccgagttt ataaaccatc atgcgacaac | 540 |
| gagccatgtc atgaatgata ctcaagaaac Catggatatg tattctccaa cgacgtcgta  | 600 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcaacatgcc agcaatatta atcagcagct taattatggt aattatgtgc ctgaatccag  | 660 |
| ttcgatcatg atgccattat ctgttgatca atccgaacaa aactattgga gcgtcgatga  | 720 |
| tctttggccc atgaatatat ataatggtaa ttaataaata agttcggttaa aacttatata | 780 |
| tatttacggt ccaaagaggg ttctatataa acagagtact gtatgggttt gcctcattgt  | 840 |
| ttagaggtag gtacttaata taaggttgga gatcttatat gaattaataa ataactcgta  | 900 |
| tttactagat                                                         |     |

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1572644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Lys | Arg | Glu | Ser | Ser | Gly | Gly | Ser | Gly | Ser | Gly | Asp | Ala | Glu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Arg | Lys | Gly | Pro | Trp | Thr | Met | Glu | Glu | Asp | Leu | Ile | Leu | Ile | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Tyr | Ile | Ala | Asn | His | Gly | Glu | Gly | Val | Trp | Asn | Ser | Leu | Ala | Lys | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Ala | Gly | Leu | Lys | Arg | Thr | Gly | Lys | Ser | Cys | Arg | Leu | Arg | Trp | Leu | Asn |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Tyr | Leu | Arg | Pro | Asp | Val | Arg | Arg | Gly | Asn | Ile | Thr | Pro | Glu | Glu | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Leu | Thr | Ile | Met | Glu | Leu | His | Ala | Lys | Trp | Gly | Asn | Arg | Trp | Ser | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ile | Ala | Lys | His | Leu | Pro | Gly | Arg | Thr | Asp | Asn | Glu | Ile | Lys | Asn | Phe |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Trp | Arg | Thr | Lys | Ile | Gln | Lys | Tyr | Ile | Ile | Lys | Ser | Gly | Glu | Thr | Thr |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Thr | Val | Gly | Ser | Gln | Ser | Ser | Glu | Phe | Ile | Asn | His | His | Ala | Thr | Thr |  |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | His | Val | Met | Asn | Asp | Thr | Gln | Glu | Thr | Met | Asp | Met | Tyr | Ser | Pro |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Thr | Ser | Tyr | Gln | His | Ala | Ser | Asn | Ile | Asn | Gln | Gln | Leu | Asn | Tyr |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Asn | Tyr | Val | Pro | Glu | Ser | Ser | Ser | Ile | Met | Met | Pro | Leu | Ser | Val |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asp | Gln | Ser | Glu | Gln | Asn | Tyr | Trp | Ser | Val | Asp | Asp | Leu | Trp | Pro | Met |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Asn | Ile | Tyr | Asn | Gly | Asn |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1572645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Glu | Asp | Leu | Ile | Leu | Ile | Asn | Tyr | Ile | Ala | Asn | His | Gly | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Val | Trp | Asn | Ser | Leu | Ala | Lys | Ser | Ala | Gly | Leu | Lys | Arg | Thr | Gly |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Lys | Ser | Cys | Arg | Leu | Arg | Trp | Leu | Asn | Tyr | Leu | Arg | Pro | Asp | Val | Arg |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Gly | Asn | Ile | Thr | Pro | Glu | Glu | Gln | Leu | Thr | Ile | Met | Glu | Leu | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Lys | Trp | Gly | Asn | Arg | Trp | Ser | Lys | Ile | Ala | Lys | His | Leu | Pro | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Thr | Asp | Asn | Glu | Ile | Lys | Asn | Phe | Trp | Arg | Thr | Lys | Ile | Gln | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Ile | Ile | Lys | Ser | Gly | Glu | Thr | Thr | Thr | Val | Gly | Ser | Gln | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Phe | Ile | Asn | His | His | Ala | Thr | Thr | Ser | His | Val | Met | Asn | Asp | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Glu | Thr | Met | Asp | Met | Tyr | Ser | Pro | Thr | Thr | Ser | Tyr | Gln | His | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Asn | Ile | Asn | Gln | Gln | Leu | Asn | Tyr | Gly | Asn | Tyr | Val | Pro | Glu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ser | Ile | Met | Met | Pro | Leu | Ser | Val | Asp | Gln | Ser | Glu | Gln | Asn | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Trp | Ser | Val | Asp | Asp | Leu | Trp | Pro | Met | Asn | Ile | Tyr | Asn | Gly | Asn |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:2339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1572646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | His | Ala | Lys | Trp | Gly | Asn | Arg | Trp | Ser | Lys | Ile | Ala | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Leu | Pro | Gly | Arg | Thr | Asp | Asn | Glu | Ile | Lys | Asn | Phe | Trp | Arg | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Gln | Lys | Tyr | Ile | Ile | Lys | Ser | Gly | Glu | Thr | Thr | Thr | Val | Gly |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gln | Ser | Ser | Glu | Phe | Ile | Asn | His | His | Ala | Thr | Thr | Ser | His | Val |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Met | Asn | Asp | Thr | Gln | Glu | Thr | Met | Asp | Met | Tyr | Ser | Pro | Thr | Thr | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Tyr | Gln | His | Ala | Ser | Asn | Ile | Asn | Gln | Gln | Leu | Asn | Tyr | Gly | Asn | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Pro | Glu | Ser | Ser | Ile | Met | Met | Pro | Leu | Ser | Val | Asp | Gln | Ser |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Gln | Asn | Tyr | Trp | Ser | Val | Asp | Asp | Leu | Trp | Pro | Met | Asn | Ile | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gly | Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1928 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1928

(D) OTHER INFORMATION: / Ceres Seq. ID 1572647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:

|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| tttctctctt | ttccatctcc  | acaaattcca  | aacatctctc | tctctttctc  | tctcacacac  | 60   |
| aaaattgcag | aagaagaaga  | gtcatgaatg  | gtgaagaaag | ctttgtagaa  | gattgctctg  | 120  |
| tttttggtga | gattgatcct  | tctggaagat  | atggaagata | cgatgaaata  | cttggcaaag  | 180  |
| gagcttcaaa | gacagtatac  | agagcatttg  | atgagtatga | aggtatagaa  | gtagcatgga  | 240  |
| accaagtaaa | gcttcgaaat  | ttcacaagga  | atcctgagga | attagagaag  | tttttcagag  | 300  |
| agattcatct | tctcaagact  | ttgaatcatc  | aaaacattat | gaaattctac  | acttcttggg  | 360  |
| ttgataccaa | caatttatca  | atcaattttg  | tcactgaact | cttcacctct  | ggtactctca  | 420  |
| gacagtatag | gttgagacat  | agaagagtga  | atattagagc | agtgaagcaa  | tggtgcaagc  | 480  |
| agattttaaa | agggtctctt  | tatttacata  | gtcgttctcc | accaattata  | catagagatc  | 540  |
| tcaaagtga  | taacattttc  | atcaatggaa  | accaaggtga | agtoaagatc  | ggtgaccttg  | 600  |
| gactcgctgc | gattcttctg  | aaatcacatg  | ccgttcggtg | cgttggaacc  | cctgagttta  | 660  |
| tggctccaga | agtgtatgat  | gaggaatata  | atgagttggt | tgatgtatat  | gcttttggca  | 720  |
| tgtgtgtggt | ggagatgggt  | acttttgatt  | atccttacag | tgaatgtact  | cacccgccac  | 780  |
| aaatctacaa | gaaagttacc  | tcggggaaaa  | agcctgaagc | tttttactta  | gtgaaggatc  | 840  |
| ctgaggttcg | tgagtttggt  | gagaagtgtt  | tagctaacgt | gacgtgtagg  | ctaacggcat  | 900  |
| tggagctttt | acaagaccct  | tttctacaag  | atgataatat | ggatggattt  | gttatgagac  | 960  |
| ctattgatta | ctacaatggt  | tatgatgaaa  | ctgggtgtgt | ccttagacat  | cctttgattg  | 1020 |
| atgatcctct | ttaccatgat  | cagtttgagt  | cgtcacagat | atgtgagatc  | gatccttttcg | 1080 |
| ctaacgatga | tgaagatcat  | gtcgacattt  | cgattaaagg | gaagagaaac  | ggtgatgatg  | 1140 |
| ggatattctt | gagacttaga  | atatctgatg  | ctgaaggacg | gataaggaaac | atttacttcc  | 1200 |
| cgtttgagac | ggctattgat  | actgcatgga  | gtgtagcggg | tgagatgggtg | tcagagctcg  | 1260 |
| acataacgaa | tcaagatggt  | gcgaaaatcg  | cggagatgat | cgatgcagag  | attgctgcat  | 1320 |
| tggtgcctga | ttggaaaaat  | gatacagaaa  | gtTcccaaaa | tgtaaacaac  | aacaagaaca  | 1380 |
| acaacactgc | aggattctgt  | ggagagtgtg  | cttcaaacgg | gtatatacaa  | gagactgtat  | 1440 |
| catcaggaga | aaaatctcat  | cataatcatc  | atgagttcga | tagttctgaa  | gacaagagct  | 1500 |
| gttcttcggg | tcacggtagg  | tttgccggata | tgtgggggtt | gcgagaatca  | tattctgatg  | 1560 |
| atggagaaaa | acagagctca  | aggaagggtta | gaagtggacg | gtggtcggag  | aatgagatga  | 1620 |
| gacgagaact | gagatggctt  | aaggcaaggc  | acaagattca | acttatgaaa  | atgagagggtc | 1680 |
| aaacgatctg | cgagacaccg  | atagagatct  | ctcttacacc | gggaacttca  | gtttcggttac | 1740 |
| ctcttcttta | cagggtctata | tcacttctctg | tggatgccgt | ggatatgtga  | cattatttgta | 1800 |
| aagtctgatg | atagttatca  | cttatatttg  | tatgtttcga | catttttaac  | ttttgttaag  | 1860 |
| ttaaaagtta | atgacatagt  | gtactttatt  | taaagagaag | aagagtaaac  | gaaaaacata  | 1920 |
| aattagtc   |             |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 595 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1572648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ser | Ser | Ser | Thr | Asn | Ser | Lys | His | Leu | Ser | Leu | Phe | Leu |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | His | Thr | Gln | Asn | Cys | Arg | Arg | Arg | Arg | Val | Met | Asn | Gly | Glu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Val | Glu | Asp | Cys | Ser | Val | Phe | Val | Glu | Ile | Asp | Pro | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Tyr | Gly | Arg | Tyr | Asp | Glu | Ile | Leu | Gly | Lys | Gly | Ala | Ser | Lys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Tyr | Arg | Ala | Phe | Asp | Glu | Tyr | Glu | Gly | Ile | Glu | Val | Ala | Trp | Asn |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Val | Lys | Leu | Arg | Asn | Phe | Thr | Arg | Asn | Pro | Glu | Glu | Leu | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Phe | Arg | Glu | Ile | His | Leu | Leu | Lys | Thr | Leu | Asn | His | Gln | Asn | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Tyr | Thr | Ser | Trp | Val | Asp | Thr | Asn | Asn | Leu | Ser | Ile | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Val | Thr | Glu | Leu | Phe | Thr | Ser | Gly | Thr | Leu | Arg | Gln | Tyr | Arg | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | His | Arg | Arg | Val | Asn | Ile | Arg | Ala | Val | Lys | Gln | Trp | Cys | Lys | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Leu | Lys | Gly | Leu | Leu | Tyr | Leu | His | Ser | Arg | Ser | Pro | Pro | Ile | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Arg | Asp | Leu | Lys | Cys | Asp | Asn | Ile | Phe | Ile | Asn | Gly | Asn | Gln | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Lys | Ile | Gly | Asp | Leu | Gly | Leu | Ala | Ala | Ile | Leu | Arg | Lys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Ala | Val | Arg | Cys | Val | Gly | Thr | Pro | Glu | Phe | Met | Ala | Pro | Glu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Asp | Glu | Glu | Tyr | Asn | Glu | Leu | Val | Asp | Val | Tyr | Ala | Phe | Gly | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Cys | Val | Leu | Glu | Met | Val | Thr | Phe | Asp | Tyr | Pro | Tyr | Ser | Glu | Cys | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Pro | Ala | Gln | Ile | Tyr | Lys | Lys | Val | Thr | Ser | Gly | Lys | Lys | Pro | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Phe | Tyr | Leu | Val | Lys | Asp | Pro | Glu | Val | Arg | Glu | Phe | Val | Glu | Lys |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Cys | Leu | Ala | Asn | Val | Thr | Cys | Arg | Leu | Thr | Ala | Leu | Glu | Leu | Leu | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Pro | Phe | Leu | Gln | Asp | Asp | Asn | Met | Asp | Gly | Phe | Val | Met | Arg | Pro |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Ile | Asp | Tyr | Tyr | Asn | Gly | Tyr | Asp | Glu | Thr | Gly | Val | Phe | Leu | Arg | His |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Pro | Leu | Ile | Asp | Asp | Pro | Leu | Tyr | His | Asp | Gln | Phe | Glu | Ser | Ser | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Cys | Glu | Ile | Asp | Leu | Phe | Ala | Asn | Asp | Asp | Glu | Asp | His | Val | Asp |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Ser | Ile | Lys | Gly | Lys | Arg | Asn | Gly | Asp | Asp | Gly | Ile | Phe | Leu | Arg |
|     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |
| Leu | Arg | Ile | Ser | Asp | Ala | Glu | Gly | Arg | Ile | Arg | Asn | Ile | Tyr | Phe | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Phe | Glu | Thr | Ala | Ile | Asp | Thr | Ala | Trp | Ser | Val | Ala | Val | Glu | Met | Val |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ser | Glu | Leu | Asp | Ile | Thr | Asn | Gln | Asp | Val | Ala | Lys | Ile | Ala | Glu | Met |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ile | Asp | Ala | Glu | Ile | Ala | Ala | Leu | Val | Pro | Asp | Trp | Lys | Asn | Asp | Thr |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Ser | Ser | Gln | Asn | Val | Asn | Asn | Asn | Lys | Asn | Asn | Asn | Thr | Ala | Gly |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Phe | C   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

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(2) INFORMATION FOR SEQ ID NO:2342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 568 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..568

(D) OTHER INFORMATION: / Ceres Seq. ID 1572649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Glu | Glu | Ser | Phe | Val | Glu | Asp | Cys | Ser | Val | Phe | Val | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Asp | Pro | Ser | Gly | Arg | Tyr | Gly | Arg | Tyr | Asp | Glu | Ile | Leu | Gly | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Ala | Ser | Lys | Thr | Val | Tyr | Arg | Ala | Phe | Asp | Glu | Tyr | Glu | Gly | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Glu | Val | Ala | Trp | Asn | Gln | Val | Lys | Leu | Arg | Asn | Phe | Thr | Arg | Asn | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Glu | Glu | Leu | Glu | Lys | Phe | Arg | Glu | Ile | His | Leu | Leu | Lys | Thr | Leu |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Asn | His | Gln | Asn | Ile | Met | Lys | Phe | Tyr | Thr | Ser | Trp | Val | Asp | Thr | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Leu | Ser | Ile | Asn | Phe | Val | Thr | Glu | Leu | Phe | Thr | Ser | Gly | Thr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gln | Tyr | Arg | Leu | Arg | His | Arg | Arg | Val | Asn | Ile | Arg | Ala | Val | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Trp | Cys | Lys | Gln | Ile | Leu | Lys | Gly | Leu | Leu | Tyr | Leu | His | Ser | Arg |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ser | Pro | Pro | Ile | Ile | His | Arg | Asp | Leu | Lys | Cys | Asp | Asn | Ile | Phe | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Gly | Asn | Gln | Gly | Glu | Val | Lys | Ile | Gly | Asp | Leu | Gly | Leu | Ala | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ile | Leu | Arg | Lys | Ser | His | Ala | Val | Arg | Cys | Val | Gly | Thr | Pro | Glu | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Met | Ala | Pro | Glu | Val | Tyr | Asp | Glu | Glu | Tyr | Asn | Glu | Leu | Val | Asp | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Ala | Phe | Gly | Met | Cys | Val | Leu | Glu | Met | Val | Thr | Phe | Asp | Tyr | Pro |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Ser | Glu | Cys | Thr | His | Pro | Ala | Gln | Ile | Tyr | Lys | Lys | Val | Thr | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Lys | Lys | Pro | Glu | Ala | Phe | Tyr | Leu | Val | Lys | Asp | Pro | Glu | Val | Arg |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Glu | Phe | Val | Glu | Lys | Cys | Leu | Ala | Asn | Val | Thr | Cys | Arg | Leu | Thr | Ala |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Glu | Leu | Leu | Gln | Asp | Pro | Phe | Leu | Gln | Asp | Asp | Asn | Met | Asp | Gly |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Phe | Val | Met | Arg | Pro | Ile | Asp | Tyr | Tyr | Asn | Gly | Tyr | Asp | Glu | Thr | Gly |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Phe | Leu | Arg | His | Pro | Leu | Ile | Asp | Asp | Pro | Leu | Tyr | His | Asp | Gln |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Phe | Glu | Ser | Ser | Gln | Ile | Cys | Glu | Ile | Asp | Leu | Phe | Ala | Asn | Asp | Asp |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Glu | Asp | His | Val | Asp | Ile | Ser | Ile | Lys | Gly | Lys | Arg | Asn | Gly | Asp | Asp |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Gly | Ile | Phe | Leu | Arg | Leu | Arg | Ile | Ser | Asp | Ala | Glu | Gly | Arg | Ile | Arg |
|     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |
| Asn | Ile | Tyr | Phe | Pro | Phe | Glu | Thr | Ala | Ile | Asp | Thr | Ala | Trp | Ser | Val |
| 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

Ala Val Glu Met Val Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala  
385 390 395 400  
Lys Ile Ala Glu Met Ile Asp Ala Glu Ile Ala Ala Leu Val Pro Asp  
405 410 415  
Trp Lys Asn Asp Thr Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn  
420 425 430  
Asn Asn Thr Ala Gly Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile  
435 440 445  
Gln Glu Thr Val Ser Ser Gly Glu Lys Ser His His Asn His His Glu  
450 455 460  
Phe Asp Ser Ser Glu Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe  
465 470 475 480  
Ala Asp Met Trp Gly Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys  
485 490 495  
Gln Ser Ser Arg Lys Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met  
500 505 510  
Arg Arg Glu Leu Arg Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met  
515 520 525  
Lys Met Arg Gly Gln Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu  
530 535 540  
Thr Pro Gly Thr Ser Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser  
545 550 555 560  
Leu Pro Val Asp Ala Val Asp Met  
565

(2) INFORMATION FOR SEQ ID NO:2343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1572650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

Met Lys Phe Tyr Thr Ser Trp Val Asp Thr Asn Asn Leu Ser Ile Asn  
1 5 10 15  
Phe Val Thr Glu Leu Phe Thr Ser Gly Thr Leu Arg Gln Tyr Arg Leu  
20 25 30  
Arg His Arg Arg Val Asn Ile Arg Ala Val Lys Gln Trp Cys Lys Gln  
35 40 45  
Ile Leu Lys Gly Leu Leu Tyr Leu His Ser Arg Ser Pro Pro Ile Ile  
50 55 60  
His Arg Asp Leu Lys Cys Asp Asn Ile Phe Ile Asn Gly Asn Gln Gly  
65 70 75 80  
Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ala Ile Leu Arg Lys Ser  
85 90 95  
His Ala Val Arg Cys Val Gly Thr Pro Glu Phe Met Ala Pro Glu Val  
100 105 110  
Tyr Asp Glu Glu Tyr Asn Glu Leu Val Asp Val Tyr Ala Phe Gly Met  
115 120 125  
Cys Val Leu Glu Met Val Thr Phe Asp Tyr Pro Tyr Ser Glu Cys Thr  
130 135 140  
His Pro Ala Gln Ile Tyr Lys Lys Val Thr Ser Gly Lys Lys Pro Glu  
145 150 155 160  
Ala Phe Tyr Leu Val Lys Asp Pro Glu Val Arg Glu Phe Val Glu Lys  
165 170 175  
Cys Leu Ala Asn Val Thr Cys Arg Leu Thr Ala Leu Glu Leu Leu Gln  
180 185 190  
Asp Pro Phe Leu Gln Asp Asp Asn Met Asp Gly Phe Val Met Arg Pro

195 200 205  
Ile Asp Tyr Tyr Asn Gly Tyr Asp Glu Thr Gly Val Phe Leu Arg His  
210 215 220  
Pro Leu Ile Asp Asp Pro Leu Tyr His Asp Gln Phe Glu Ser Ser Gln  
225 230 235 240  
Ile Cys Glu Ile Asp Leu Phe Ala Asn Asp Asp Glu Asp His Val Asp  
245 250 255  
Ile Ser Ile Lys Gly Lys Arg Asn Gly Asp Asp Gly Ile Phe Leu Arg  
260 265 270  
Leu Arg Ile Ser Asp Ala Glu Gly Arg Ile Arg Asn Ile Tyr Phe Pro  
275 280 285  
Phe Glu Thr Ala Ile Asp Thr Ala Trp Ser Val Ala Val Glu Met Val  
290 295 300  
Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala Lys Ile Ala Glu Met  
305 310 315 320  
Ile Asp Ala Glu Ile Ala Ala Leu Val Pro Asp Trp Lys Asn Asp Thr  
325 330 335  
Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn Asn Asn Thr Ala Gly  
340 345 350  
Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile Gln Glu Thr Val Ser  
355 360 365  
Ser Gly Glu Lys Ser His His Asn His His Glu Phe Asp Ser Ser Glu  
370 375 380  
Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe Ala Asp Met Trp Gly  
385 390 395 400  
Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys Gln Ser Ser Arg Lys  
405 410 415  
Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met Arg Arg Glu Leu Arg  
420 425 430  
Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met Lys Met Arg Gly Gln  
435 440 445  
Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu Thr Pro Gly Thr Ser  
450 455 460  
Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser Leu Pro Val Asp Ala  
465 470 475 480  
Val Asp Met

(2) INFORMATION FOR SEQ ID NO:2344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aagatgggga  | cgaaattgag | ctggatatag | aagctgtcga | caatgagact | ctatgggagc | 60  |
| ttgatcgttt  | tgtgacgaac | tacaagaaga | tggctagcaa | aatcaagcgc | caagggttta | 120 |
| tcaggaacgt  | gtcaactcca | cttaggaaca | tggcttcggt | agcagaaatg | ggtagtgcgg | 180 |
| agaagagaac  | aaggagagga | gatgcagggg | aagaggatgt | tgacattgga | gaggacatac | 240 |
| caatcgaaga  | ttatccatct | stagagatcg | aaagagatgg | Gtactgcagt | tgacgtctgt | 300 |
| gctagttagt  | gttctagtgc | ttcaggcagt | tccagttcta | gtggtggtag | ttcctcgtct | 360 |
| agtgattcag  | ggtcaggtgg | gagttcatca | ggtagtgtat | ctgatgcaga | tagtgttcaa | 420 |
| tcgccatttg  | tggaagcaaa | agaagcccaa | tgttaaaatc | atttggaat  | ttaacggttg | 480 |
| attctgtcct  | gaagtactag | gaacgtttag | ctgaggggtg | aaagggagga | atgaagggga | 540 |
| aaactgaagg  | aaaggatttg | ttttttcttt | cgatgataaa | cttaggaagc | agatgtagtt | 600 |
| agaaagamaa  | aatgtaatat | gtagatagaa | agagaatgct | agtttaagca | agaagaagag | 660 |
| ttcgttatatt | aatacctttt | acatttagga | gttggttagt | gtatttgtga | gatgctgaac | 720 |

(2) INFORMATION FOR SEQ ID NO:2345:

- (2) INFORMATION FOR SEQ ID NO:2346:

- [illegible]

- [illegible]

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1572665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:

Met Gly Thr Ala Val Ala Ala Ala Ser Ser Gly Ser Ser Ser Ser  
1 5 10 15  
Gly Ser Ser Ser Ser Ser Gly Gly Ser Ser Ser Ser Ser Asp Ser Gly  
20 25 30  
Ser Gly Gly Ser Ser Ser Gly Ser Asp Ser Asp Ala Asp Ser Val Gln  
35 40 45  
Ser Pro Phe Val Glu Ala Lys Glu Ala Gln Cys  
50 55

(2) INFORMATION FOR SEQ ID NO:2348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1281

(D) OTHER INFORMATION: / Ceres Seq. ID 1572694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:

gttcgaggta tgaacttcaa attcgattac gtttttatca gggaagatgc aaggaggtgg 60  
tggtagagat ccttttggtg gtggttttgg gggtcctttt ggtggttttg gaggtggctc 120  
ttttggtggt ttggaagag gttccttttg tggatttggg ggccctaata gtcctccgag 180  
tctcatgtct aattttttcg gaggaagaga tccatttgac gaccctttct tcaactcagcc 240  
ttttggtggt ggcatgtttc aatccaactt ctttggfccc agcatgaatc cttttgcaga 300  
aatgcatcgt ctgccacagg gttttattga gaataatcag cctccaggac cgagtagatc 360  
acgcggaccg gttattgaag agattgattc agatgatgag aaagaaggag aagggtgataa 420  
agagaagaaa ggaagtctag ggaacatgg caggtcaagc agtgaggctg aaactgaaga 480  
tgctagagtg cgagagagaa gaaaccggca aatgcaaagc atgaatgtaa atgcagagag 540  
aaggaaccga gaaatgcaga acatgaatgt gaatgcagag agaaggaacc cacaaatgca 600  
gaacatgaat gtgaatgcta tggatgaaca tggacagtgg caacctcaaa ccggtagtta 660  
tagttttcag agctcgactg ttacatacgg tggtcagaac ggcaactact atacttcctc 720  
aaagaccaga aggacaggaa gtgatgggtt aactcttgaa gaaagcagag aagccaacac 780  
tgcaacgcgg gaagcagcgc atatgatttc aagaggcctt cataacaagg gtcacacagt 840  
tgcgcgtaaa cttaactcag atggccgtgt tgatacaact cagacottgc acaatttgaa 900  
tgaagatgaa ttggctggtt ttgaacagtc ttggagtggg aatgctagaa ggcaaatgca 960  
gttaccagct cgctctggtt catttggaag tggctctgtg aacagagagc aaccaatgtt 1020  
acttccctyk actgatccaa gtccttctca tgcacgagca gaatcatccc gaagaccGva 1080  
agctgcaatg aatgtaagag gacatggtac aaactaatct ccgcctatat gtatggtttc 1140  
gaaaatcttt agtgaatgta accaaagact aattacttta cttaggttgc atcatcatta 1200  
ctgtaactgt atgatgacat gatttgaggg ttttaaacac tgctccttga tgattattat 1260  
atatgtatct tttgttacat t

(2) INFORMATION FOR SEQ ID NO:2349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..356

(D) OTHER INFORMATION: / Ceres Seq. ID 1572695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

Met Gln Gly Gly Gly Gly Arg Asp Pro Phe Gly Gly Gly Phe Gly Gly  
1 5 10 15  
Pro Phe Gly Gly Phe Gly Gly Gly Ser Phe Gly Gly Phe Gly Arg Gly  
20 25 30

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[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1572696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Phe | Phe | Gly | Gly | Arg | Asp | Pro | Phe | Asp | Asp | Pro | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gln | Pro | Phe | Gly | Gly | Gly | Met | Phe | Gln | Ser | Asn | Phe | Phe | Gly | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Met | Asn | Pro | Phe | Ala | Glu | Met | His | Arg | Leu | Pro | Gln | Gly | Phe | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Asn | Gln | Pro | Pro | Gly | Pro | Ser | Arg | Ser | Arg | Gly | Pro | Val | Ile |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Glu | Glu | Ile | Asp | Ser | Asp | Asp | Glu | Lys | Glu | Gly | Glu | Gly | Asp | Lys | Glu |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Lys | Lys | Gly | Ser | Leu | Gly | Lys | His | Gly | Arg | Ser | Ser | Ser | Glu | Ala | Glu |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Thr | Glu | Asp | Ala | Arg | Val | Arg | Glu | Arg | Arg | Asn | Arg | Gln | Met | Gln | Ser |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Met | Asn | Val | Asn | Ala | Glu | Arg | Arg | Asn | Arg | Glu | Met | Gln | Asn | Met | Asn |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Val | Asn | Ala | Glu | Arg | Arg | Asn | Pro | Gln | Met | Gln | Asn | Met | Asn | Val | Asn |  |  |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |  |
| Ala | Met | Val | Asn | Asn | Gly | Gln | Trp | Gln | Pro | Gln | Thr | Gly | Ser | Tyr | Ser |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Phe | Gln | Ser | Ser | Thr | Val | Thr | Tyr | Gly | Gly | Gln | Asn | Gly | Asn | Tyr | Tyr |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Thr | Ser | Ser | Lys | Thr | Arg | Arg | Thr | Gly | Ser | Asp | Gly | Leu | Thr | Leu | Glu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Glu | Ser | Arg | Glu | Ala | Asn | Thr | Ala | Thr | Arg | Glu | Ala | Ala | His | Met | Ile |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Ser | Arg | Gly | Leu | His | Asn | Lys | Gly | His | Thr | Val | Ala | Arg | Lys | Leu | Asn |  |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |  |
| Ser | Asp | Gly | Arg | Val | Asp | Thr | Thr | Gln | Thr | Leu | His | Asn | Leu | Asn | Glu |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Asp | Glu | Leu | Ala | Gly | Phe | Glu | Gln | Ser | Trp | Ser | Gly | Asn | Ala | Arg | Arg |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Gln | Met | Gln | Leu | Pro | Ser | Arg | Ser | Gly | Ser | Phe | Gly | Ser | Gly | Leu | Val |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Asn | Arg | Glu | Gln | Pro | Met | Leu | Leu | Pro | Xaa | Thr | Asp | Pro | Ser | Pro | Ser |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| His | Ala | Arg | Ala | Glu | Ser | Ser | Arg | Arg | Pro | Xaa | Ala | Ala | Met | Asn | Val |  |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Arg | Gly | His | Gly | Thr | Asn |     |     |     |     |     |     |     |     |     |     |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1572697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Phe | Gln | Ser | Asn | Phe | Phe | Gly | Pro | Ser | Met | Asn | Pro | Phe | Ala | Glu |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Met | His | Arg | Leu | Pro | Gln | Gly | Phe | Ile | Glu | Asn | Asn | Gln | Pro | Pro | Gly |  |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Pro | Ser | Arg | Ser | Arg | Gly | Pro | Val | Ile | Glu | Glu | Ile | Asp | Ser | Asp | Asp |  |  |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Glu | Lys | Glu | Gly | Glu | Gly | Asp | Lys | Glu | Lys | Lys | Gly | Ser | Leu | Gly | Lys |  |  |
|     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |  |
| His | Gly | Arg | Ser | Ser | Ser | Glu | Ala | Glu | Thr | Glu | Asp | Ala | Arg | Val | Arg |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Glu | Arg | Arg | Asn | Arg | Gln | Met | Gln | Ser | Met | Asn | Val | Asn | Ala | Glu | Arg |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Arg | Asn | Arg | Glu | Met | Gln | Asn | Met | Asn | Val | Asn | Ala | Glu | Arg | Arg | Asn |  |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Pro | Gln | Met | Gln | Asn | Met | Asn | Val | Asn | Ala | Met | Val | Asn | Asn | Gly | Gln |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |



Trp Gln Pro Gln Thr Gly Ser Tyr Ser Phe Gln Ser Ser Thr Val Thr  
130 135 140  
Tyr Gly Gly Gln Asn Gly Asn Tyr Tyr Thr Ser Ser Lys Thr Arg Arg  
145 150 155 160  
Thr Gly Ser Asp Gly Leu Thr Leu Glu Glu Ser Arg Glu Ala Asn Thr  
165 170 175  
Ala Thr Arg Glu Ala Ala His Met Ile Ser Arg Gly Leu His Asn Lys  
180 185 190  
Gly His Thr Val Ala Arg Lys Leu Asn Ser Asp Gly Arg Val Asp Thr  
195 200 205  
Thr Gln Thr Leu His Asn Leu Asn Glu Asp Glu Leu Ala Gly Phe Glu  
210 215 220  
Gln Ser Trp Ser Gly Asn Ala Arg Arg Gln Met Gln Leu Pro Ser Arg  
225 230 235 240  
Ser Gly Ser Phe Gly Ser Gly Leu Val Asn Arg Glu Gln Pro Met Leu  
245 250 255  
Leu Pro Xaa Thr Asp Pro Ser Pro Ser His Ala Arg Ala Glu Ser Ser  
260 265 270  
Arg Arg Pro Xaa Ala Ala Met Asn Val Arg Gly His Gly Thr Asn  
275 280 285

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tccacacttt catatccaca aaataaaata aaaaaatggc ctcaaagagc tcaaccacca  | 60  |
| tttccctcat catcatcctc ctcatcagcc tcgcagaagc aaatctctta agctcgctta  | 120 |
| caccgaccaa caactttggc tcatgtccca gaaaccatt gcaactaggc gtatgtgcca   | 180 |
| acgtccttgg cctagccaat gttacagctg ggcaccccag agcacgacag tgttgcaactg | 240 |
| ccctcaatgg cctcactaat gttcaagtaa ccgattgtct ctgctttatc ttcaggccga  | 300 |
| ttccgttggt ttccggtatt gatgtggccg ttagagaaat cttttttgct tgcaataggg  | 360 |
| tttttctat cggtttccag tgtccaccac cacagtaact actacttaat tcccctaaat   | 420 |
| aagagcccta tccggtggtt ccttgcaact taagtttgct ggtacaaaaa gtatgggttt  | 480 |
| atctattaat gttttacagt gttggtgtgt gtttcgttgt tgattagaac gtaattataa  | 540 |
| ggactatcga tgcttactaa aaagttgtta agcatatcta ttaatgtcta Mtgaagaata  | 600 |
| atattaaata aagtataaca ctttgtgtc                                    |     |

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

Met Ala Ser Lys Ser Ser Thr Thr Ile Ser Leu Ile Ile Ile Leu Leu  
1 5 10 15  
Ile Ser Leu Ala Glu Ala Asn Leu Leu Ser Ser Pro Thr Pro Thr Asn  
20 25 30  
Asn Phe Gly Ser Cys Pro Arg Asn Pro Leu Gln Leu Gly Val Cys Ala  
35 40 45

Asn Val Leu Gly Leu Ala Asn Val Thr Ala Gly Asp Pro Arg Ala Arg  
50 55 60  
Gln Cys Cys Thr Ala Leu Asn Gly Leu Thr Asn Val Gln Val Thr Asp  
65 70 75 80  
Cys Leu Cys Phe Ile Phe Arg Pro Ile Pro Leu Val Phe Gly Ile Asp  
85 90 95  
Val Ala Val Arg Glu Ile Phe Phe Ala Cys Asn Arg Val Phe Pro Ile  
100 105 110  
Gly Phe Gln Cys Pro Pro Pro Gln  
115 120

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..954
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acattacgaa aagtactagt ttattggtgt tattcatcgc tgctcaaggt ggcaaacc    | 60  |
| ggagaacaag aagagtccag ggccaatgag cctgagggtg tcaaatacagt gattgatgac | 120 |
| atctacaatt ttgaagacga ccctgtggtt gatagattca atagatttgg aacggagatg  | 180 |
| tctgocatgg tctcggcctt gacacagggtg gtttctgctc gctctcagac tgaagctgaa | 240 |
| ggtgctcact cttcttcctc ctcggtctga cataagagag aatggcttgg aatcgattct  | 300 |
| gttcctatct cctcatcatt tgctcgtgta gactcttcac ataataccgat cgaagaatcc | 360 |
| ataagaaaag catttccaga ggaagcaagg gagaaaaaaa ggaggtacag aggagtaagg  | 420 |
| cagagaccat ggggcaaatg ggcagctgag atacgtgatc cacatagagc cgctaRggtt  | 480 |
| tggctcggga cgtttgatac agcggaggcc gcggctagag cctacgacga ggctgcactc  | 540 |
| cggttccgtg gaaataaagc aaagctaaat ttcccagagg atgtaaggat tcttcctcct  | 600 |
| ccccctcctc ttcttcgttc accagctgac acggtggcga ataaagcaga agaggatctg  | 660 |
| ataaattatt ggagttatac aaagttgttg caaagttcag gccaacggtc atttctcgag  | 720 |
| cgaggacaag aagagagtaa taacatattt gaacattcac caatggaaca acctctgcct  | 780 |
| ccttcaagtt ctggtccaag ttctctctaat tttcctgcac cttctctacc taatacatag | 840 |
| tttcactttt attaaagctc taaaaatata attaaatata tagctaaaatg aaaatgattt | 900 |
| tcttgtctgt ataccttctt aagtgtctaa caatatattg tactctttgt ttcc        |     |

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

Thr Leu Arg Lys Val Leu Val Tyr Trp Cys Tyr Ser Ser Leu Leu Lys  
1 5 10 15  
Val Ala Asn Gln Gly Glu Gln Glu Glu Ser Arg Ala Asn Glu Pro Glu  
20 25 30  
Gly Ile Lys Ser Val Ile Asp Asp Ile Tyr Asn Phe Glu Asp Asp Pro  
35 40 45  
Val Val Asp Arg Phe Asn Arg Phe Gly Thr Glu Met Ser Ala Met Val  
50 55 60  
Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser Gln Thr Glu Ala Glu  
65 70 75 80  
Gly Ala His Ser Ser Ser Ser Ser Ala Gly His Lys Arg Glu Trp Leu

(2) INFORMATION FOR SEQ ID NO:2356:

(A) LENGTH: 220 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1572752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Met | Val | Ser | Ala | Leu | Thr | Gln | Val | Val | Ser | Ala | Arg | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Thr | Glu | Ala | Glu | Gly | Ala | His | Ser | Ser | Ser | Ser | Ser | Ala | Gly | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Arg | Glu | Trp | Leu | Gly | Ile | Asp | Ser | Val | Pro | Ile | Pro | Ser | Ser | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Val | Asp | Ser | Ser | His | Asn | Pro | Ile | Glu | Glu | Ser | Ile | Arg | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Phe | Pro | Glu | Glu | Ala | Arg | Glu | Lys | Lys | Arg | Arg | Tyr | Arg | Gly | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Gln | Arg | Pro | Trp | Gly | Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | His |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Ala | Ala | Xaa | Val | Trp | Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Arg | Ala | Tyr | Asp | Glu | Ala | Ala | Leu | Arg | Phe | Arg | Gly | Asn | Lys | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Leu | Asn | Phe | Pro | Glu | Asp | Val | Arg | Ile | Leu | Pro | Pro | Pro | Pro | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Leu | Arg | Ser | Pro | Ala | Asp | Thr | Val | Ala | Asn | Lys | Ala | Glu | Glu | Asp |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Ile | Asn | Tyr | Trp | Ser | Tyr | Thr | Lys | Leu | Leu | Gln | Ser | Ser | Gly | Gln |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Ser | Phe | Leu | Glu | Arg | Gly | Gln | Glu | Glu | Ser | Asn | Asn | Ile | Phe | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

His Ser Pro Met Glu Gln Pro Leu Pro Pro Ser Ser Ser Gly Pro Ser  
195 200 205  
Ser Ser Asn Phe Pro Ala Pro Ser Leu Pro Asn Thr  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

Met Val Ser Ala Leu Thr Gln Val Val Ser Ala Arg Ser Gln Thr Glu  
1 5 10 15  
Ala Glu Gly Ala His Ser Ser Ser Ser Ser Ala Gly His Lys Arg Glu  
20 25 30  
Trp Leu Gly Ile Asp Ser Val Pro Ile Pro Ser Ser Phe Ala Arg Val  
35 40 45  
Asp Ser Ser His Asn Pro Ile Glu Glu Ser Ile Arg Lys Ala Phe Pro  
50 55 60  
Glu Glu Ala Arg Glu Lys Lys Arg Arg Tyr Arg Gly Val Arg Gln Arg  
65 70 75 80  
Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp Pro His Arg Ala Ala  
85 90 95  
Xaa Val Trp Leu Gly Thr Phe Asp Thr Ala Glu Ala Ala Ala Arg Ala  
100 105 110  
Tyr Asp Glu Ala Ala Leu Arg Phe Arg Gly Asn Lys Ala Lys Leu Asn  
115 120 125  
Phe Pro Glu Asp Val Arg Ile Leu Pro Pro Pro Pro Pro Leu Leu Arg  
130 135 140  
Ser Pro Ala Asp Thr Val Ala Asn Lys Ala Glu Glu Asp Leu Ile Asn  
145 150 155 160  
Tyr Trp Ser Tyr Thr Lys Leu Leu Gln Ser Ser Gly Gln Arg Ser Phe  
165 170 175  
Leu Glu Arg Gly Gln Glu Glu Ser Asn Ile Phe Glu His Ser Pro  
180 185 190  
Met Glu Gln Pro Leu Pro Pro Ser Ser Ser Gly Pro Ser Ser Ser Asn  
195 200 205  
Phe Pro Ala Pro Ser Leu Pro Asn Thr  
210 215

(2) INFORMATION FOR SEQ ID NO:2358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1072

(D) OTHER INFORMATION: / Ceres Seq. ID 1572762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acacatctca ctgctcacta ctctcactgt aatcccttag atcttctttt caaatttcaa  | 60  |
| tggcgctccgg tgatgttgag tatcggtgct tcggttgagg tctagcatgg gccactgatg | 120 |
| acagagctct tgagactgcc ttcgctcaat acggcgacgt tattgattcc aaggtctgtt  | 180 |
| acacgccgag atcggactcc gagtgatata gatgatctca tctcgacgg atctgttccg   | 240 |
| atcttgtgtt tctctgttac ttgattcgat tactctgtta ctattctogt tctttgttac  | 300 |

```
tactactact actactgtta cttgtatttt cccaaatcgg tacgttcac ttcctgcttc 360
tgtgagcccg gagatcgatc ggattttttt gtattttgta tatttggtgt agatctaaat 420
gcttttgttc agttttgttg gattgttttg ctgatctggg ttttgattta tttggataac 480
agatcattaa cgatcgtgag actggaagat caaggggatt cggattcgtc accttcaagg 540
atgagaaaagc catgaaggat gcgattgagg gaatgaacgg acaagatctc gatggccgta 600
gcatcactgt taacgaggct cagtcacgag gaagcgggtg cggcggaggc caccgtggag 660
gtggtggcgg tggataCgc agcggcgggtg gtggagggtta ctccgggtga ggtggtagct 720
acggagggtg cggcggtaga cgcgagggtg gaggaggata cagcggcggc gccgggtact 780
cctcaagagg tgggtgggtgg ggaagctacg gtggtggaag acgtgaggga ggaggaggat 840
acgggtgggtg tgaaggagga ggttacggag gaagcgggtg tgggtggagga tggtaattcc 900
tttaattagg tttgggatta ccaatgaatg ttctctctct cgcttggtat gcttctactt 960
ggttttgtgt gttctctatt ttgtcttggg tctgctttag atttgatgta acagttcgtg 1020
attagggtatt ttggatatctg gaaacgtaat gttaagtcac ttgtcattct cc
```

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

```
Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg
1 5 10 15
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly
20 25 30
Gly His Arg Gly Gly Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly
35 40 45
Gly Tyr Ser Gly Gly Gly Gly Ser Tyr Gly Gly Gly Gly Gly Arg Arg
50 55 60
Glu Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Tyr Ser Ser Arg Gly
65 70 75 80
Gly Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly
85 90 95
Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly
100 105 110
Gly Trp
```

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

```
Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr Val Asn Glu Ala
1 5 10 15
Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly His Arg Gly Gly Gly Gly
20 25 30
Gly Gly Tyr Arg Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly
35 40 45
Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Ser
50 55 60
```

Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly  
65 70 75 80  
Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Glu Gly Gly  
85 90 95  
Gly Tyr Gly Gly Ser Gly Gly Gly Gly Gly Trp  
100 105

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1572765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

Met Ala Val Ala Ser Leu Leu Thr Arg Leu Ser His Glu Glu Ala Val  
1 5 10 15  
Ala Ala Glu Ala Thr Val Glu Val Val Ala Val Asp Thr Ala Ala Ala  
20 25 30  
Val Val Glu Val Thr Pro Val Glu Val Val Ala Thr Glu Val Ala Ala  
35 40 45  
Val Asp Ala Arg Val Glu Glu Asp Thr Ala Ala Ala Ala Val Thr Pro  
50 55 60  
Gln Glu Val Val Val Ala Glu Ala Thr Val Val Glu Asp Val Arg Glu  
65 70 75 80  
Glu Glu Asp Thr Val Val Val Lys Glu Glu Val Thr Glu Glu Ala Val  
85 90 95  
Val Val Glu Asp Gly Asn Ser Phe Asn  
100 105

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629

(D) OTHER INFORMATION: / Ceres Seq. ID 1572774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

gcttctctag ggtttcagcc accagactca aacagagagt gaaaatgccg gcgggacacg 60  
gagtgagggc gagaacaaga gatctgttcg cgagaccatt caggaagaag gggtatattc 120  
cactctccac ttacctcaga accttcaagg tcggcgatta cgtcgatgtc aagggttaatg 180  
gagctatcca caaggggtatg cctcataagt tctaccatgg tcgtactggc cgcactctgga 240  
atgtcactaa gcgtgccgtt ggtgttgaag tcaacaaaca gattgggaac agaatacataa 300  
ggaagaggat acatgtgcgt gtggagcatg tgcaacagtc aaggtgtgct gaggagtta 360  
aactcagaaa gaagcagaac gatgtgctta aggctgatgc taaagccaga ggagagacta 420  
tcagaccaa gagacagcct aaaggctcta aaccgggttt catggctcga ggatgacat 480  
tgagactgt cactccatt ccttacgatg ttgtcaacga tctcaagggt gggtattgag 540  
ttttttccat ttattatca ttctttactc agaatttttg cacttgcttt tttaatgatg 600  
ttttgtatc aattaagact aattBStct

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..178  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572775  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

Phe Ser Arg Val Ser Ala Thr Arg Leu Lys Gln Arg Val Lys Met Pro  
1                  5                  10                  15  
Ala Gly His Gly Val Arg Ala Arg Thr Arg Asp Leu Phe Ala Arg Pro  
                  20                  25                  30  
Phe Arg Lys Lys Gly Tyr Ile Pro Leu Ser Thr Tyr Leu Arg Thr Phe  
                  35                  40                  45  
Lys Val Gly Asp Tyr Val Asp Val Lys Val Asn Gly Ala Ile His Lys  
50                  55                  60  
Gly Met Pro His Lys Phe Tyr His Gly Arg Thr Gly Arg Ile Trp Asn  
65                  70                  75                  80  
Val Thr Lys Arg Ala Val Gly Val Glu Val Asn Lys Gln Ile Gly Asn  
                  85                  90                  95  
Arg Ile Ile Arg Lys Arg Ile His Val Arg Val Glu His Val Gln Gln  
                  100                 105                 110  
Ser Arg Cys Ala Glu Glu Phe Lys Leu Arg Lys Lys Gln Asn Asp Val  
                 115                 120                 125  
Leu Lys Ala Asp Ala Lys Ala Arg Gly Glu Thr Ile Ser Thr Lys Arg  
130                 135                 140  
Gln Pro Lys Gly Pro Lys Pro Gly Phe Met Val Glu Gly Met Thr Leu  
145                 150                 155                 160  
Glu Thr Val Thr Pro Ile Pro Tyr Asp Val Val Asn Asp Leu Lys Gly  
                 165                 170                 175  
Gly Tyr

- (2) INFORMATION FOR SEQ ID NO:2364:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 164 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..164  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1572776  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

Met Pro Ala Gly His Gly Val Arg Ala Arg Thr Arg Asp Leu Phe Ala  
1                  5                  10                  15  
Arg Pro Phe Arg Lys Lys Gly Tyr Ile Pro Leu Ser Thr Tyr Leu Arg  
                  20                  25                  30  
Thr Phe Lys Val Gly Asp Tyr Val Asp Val Lys Val Asn Gly Ala Ile  
35                  40                  45  
His Lys Gly Met Pro His Lys Phe Tyr His Gly Arg Thr Gly Arg Ile  
50                  55                  60  
Trp Asn Val Thr Lys Arg Ala Val Gly Val Glu Val Asn Lys Gln Ile  
65                  70                  75                  80  
Gly Asn Arg Ile Ile Arg Lys Arg Ile His Val Arg Val Glu His Val  
                  85                  90                  95  
Gln Gln Ser Arg Cys Ala Glu Glu Phe Lys Leu Arg Lys Lys Gln Asn  
                 100                 105                 110  
Asp Val Leu Lys Ala Asp Ala Lys Ala Arg Gly Glu Thr Ile Ser Thr  
115                 120                 125  
Lys Arg Gln Pro Lys Gly Pro Lys Pro Gly Phe Met Val Glu Gly Met  
130                 135                 140  
Thr Leu Glu Thr Val Thr Pro Ile Pro Tyr Asp Val Val Asn Asp Leu

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145                                      150                                      155                                      160  
Lys Gly Gly Tyr

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met Pro His Lys Phe Tyr His Gly Arg Thr Gly Arg Ile Trp Asn Val  
1                                      5                                      10                                      15  
Thr Lys Arg Ala Val Gly Val Glu Val Asn Lys Gln Ile Gly Asn Arg  
20                                      25                                      30  
Ile Ile Arg Lys Arg Ile His Val Arg Val Glu His Val Gln Gln Ser  
35                                      40                                      45  
Arg Cys Ala Glu Glu Phe Lys Leu Arg Lys Lys Gln Asn Asp Val Leu  
50                                      55                                      60  
Lys Ala Asp Ala Lys Ala Arg Gly Glu Thr Ile Ser Thr Lys Arg Gln  
65                                      70                                      75                                      80  
Pro Lys Gly Pro Lys Pro Gly Phe Met Val Glu Gly Met Thr Leu Glu  
85                                      90                                      95  
Thr Val Thr Pro Ile Pro Tyr Asp Val Asn Asp Leu Lys Gly Gly  
100                                      105                                      110  
Tyr

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

aaaaaagtca atcatatcaa atcccaaata cccccagatg tttttatcat cttcttcttc 60  
ctgaagattt gatttcattt tctctcttt cagatcccta ttctcatggc ttctggatct 120  
tactggtgct atagttgtag ccgattcggt tgggtttcog attcaatctc ttgccctgat 180  
tgcgacggtg gtttcctcga actcatocaa gagcctctcg atttcacacc ttccgattcc 240  
ttcaccacca ccaccaccac tcaacatcgc agccccactc gcttccctcc tcttcttct 300  
tcttctctca ccccatccgc ttctatgcac gccgataaca gtcccaactc taccatcggt 360  
actcgtacac gaagcaatcg atctcctaata ccagttattg ttctccgtgg atctgctgct 420  
gctccttctt ctgatgttgt ttccgaagggt ttagatcgat ctgcttttca gatgtattac 480  
gatgatggta ctgattctgg tcttagacct ttaccaccga gtatgactga gtttttggtta 540  
ggttctggat ttgatcggtt gtttagatcag atctctcaga tcgagcttaa caccaatcgg 600  
aatcttctgt cttgtgaaca tccaccggct tctaaatcgg ccattgaagc tttgcctctg 660  
attgaaatcg atccgactca tctcttatcg gattctcaat ctattgogc tgtttgcaaa 720  
gagaatttctg ttttgaaatc atctgctcgc gagatgcctt gtaatcacat ctatcatcct 780  
gattgtattc ttccttggct tgcgattcgt aactcttgct cggtttgccg tcatgagcta 840  
ccggcggagg atctcaccga cgggaaccggt gctgctttga ctgctgttac cgctactgca 900  
gaggaagagg aagactcagc tgcgggggta acgatttgga ggttaccagg tggaggattc 960  
gctgtaggga gaatccctgg tggttggaga ggtggagata gaatgatgcc ggtggtttac 1020  
acggaggttg atggtggtag actcggatgat gagagacttc cgagaagagt agcttgggggt 1080



```
tgcgagaagag gtggaagaga tgggtggaggt agtagagagC agaggtggtg gcttttgcggg 1140
tcggatcatg aggccttttcg gatgttttag tggatcatct ggatccattg ctgctgctgc 1200
tgctgcatca tccgggtccg ggtccagaat tcgggttact cgtagaacca ggctcgttctc 1260
tatgttcagt acggcgctcgt cttcgtcaag gagacgaaat tggctagcgt gattactaga 1320
attaccaagc tctcttctca ggtgaaaact aaacacgaaa gaacacactc ttcttctggt 1380
taaatttttc ctatgttcct tattaagttt ttgtctattt cagtgtaatg attatatattca 1440
ttcctaaaaat ttgaatctat gcgagtaaat tg
```

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1572786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

```
Met Ala Ser Gly Ser Tyr Trp Cys Tyr Ser Cys Ser Arg Phe Val Trp
1 5 10 15
Val Ser Asp Ser Ile Ser Cys Pro Asp Cys Asp Gly Gly Phe Leu Glu
20 25 30
Leu Ile Gln Glu Pro Leu Asp Phe Thr Pro Ser Asp Ser Phe Thr Thr
35 40 45
Thr Thr Thr Thr Gln His Arg Ser Pro Thr Arg Phe Pro Pro Pro Ser
50 55 60
Ser Ser Ser Ser Thr Pro Ser Ala Ser Met His Ala Asp Asn Ser Pro
65 70 75 80
Thr Pro Thr Ile Val Thr Arg Thr Arg Ser Asn Arg Ser Pro Asn Pro
85 90 95
Val Ile Val Leu Arg Gly Ser Ala Ala Ala Pro Ser Ser Asp Val Val
100 105 110
Ser Glu Gly Leu Asp Arg Ser Ala Phe Gln Met Tyr Tyr Asp Asp Gly
115 120 125
Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro Ser Met Thr Glu Phe Leu
130 135 140
Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp Gln Ile Ser Gln Ile Glu
145 150 155 160
Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys Glu His Pro Pro Ala Ser
165 170 175
Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile Glu Ile Asp Pro Thr His
180 185 190
Leu Leu Ser Asp Ser Gln Ser His Cys Ala Val Cys Lys Glu Asn Phe
195 200 205
Val Leu Lys Ser Ser Ala Arg Glu Met Pro Cys Asn His Ile Tyr His
210 215 220
Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile Arg Asn Ser Cys Pro Val
225 230 235 240
Cys Arg His Glu Leu Pro Ala Glu Asp Leu Thr Asp Gly Thr Gly Ala
245 250 255
Ala Leu Thr Ala Val Thr Ala Thr Ala Glu Glu Glu Glu Asp Ser Ala
260 265 270
Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly Gly Gly Phe Ala Val Gly
275 280 285
Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp Arg Met Met Pro Val Val
290 295 300
Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly Asp Glu Arg Leu Pro Arg
305 310 315 320
Arg Val Ala Trp Gly Ser Arg Arg Gly Gly Arg Asp Gly Gly Gly Ser
325 330 335
```

Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser Asp His Glu Ala Phe Arg  
340 345 350  
Met Phe

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

Met His Ala Asp Asn Ser Pro Thr Pro Thr Ile Val Thr Arg Thr Arg  
1 5 10 15  
Ser Asn Arg Ser Pro Asn Pro Val Ile Val Leu Arg Gly Ser Ala Ala  
20 25 30  
Ala Pro Ser Ser Asp Val Val Ser Gly Leu Asp Arg Ser Ala Phe  
35 40 45  
Gln Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro  
50 55 60  
Pro Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu  
65 70 75 80  
Asp Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser  
85 90 95  
Cys Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu  
100 105 110  
Ile Glu Ile Asp Pro Thr His Leu Leu Ser Asp Ser Gln Ser His Cys  
115 120 125  
Ala Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met  
130 135 140  
Pro Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala  
145 150 155 160  
Ile Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp  
165 170 175  
Leu Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala  
180 185 190  
Glu Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro  
195 200 205  
Gly Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly  
210 215 220  
Asp Arg Met Met Pro Val Tyr Thr Glu Val Asp Gly Gly Arg Leu  
225 230 235 240  
Gly Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly  
245 250 255  
Gly Arg Asp Gly Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly  
260 265 270  
Ser Asp His Glu Ala Phe Arg Met Phe  
275 280

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1572788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Tyr | Asp | 5   | Gly | Thr | Asp | Ser | Gly | Leu | Arg | Pro | Leu | Pro | Pro |
| 1   |     |     |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Met | Thr | Glu | Phe | Leu | Leu | Gly | Ser | Gly | Phe | Asp | Arg | Leu | Leu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ile | Ser | Gln | Ile | Glu | Leu | Asn | Thr | Asn | Arg | Asn | Leu | Arg | Ser | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | His | Pro | Pro | Ala | Ser | Lys | Ser | Ala | Ile | Glu | Ala | Leu | Pro | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ile | Asp | Pro | Thr | His | Leu | Leu | Ser | Asp | Ser | Gln | Ser | His | Cys | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Cys | Lys | Glu | Asn | Phe | Val | Leu | Lys | Ser | Ser | Ala | Arg | Glu | Met | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Asn | His | Ile | Tyr | His | Pro | Asp | Cys | Ile | Leu | Pro | Trp | Leu | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Asn | Ser | Cys | Pro | Val | Cys | Arg | His | Glu | Leu | Pro | Ala | Glu | Asp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Thr | Asp | Gly | Thr | Gly | Ala | Ala | Leu | Thr | Ala | Val | Thr | Ala | Thr | Ala | Glu |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Glu | Glu | Glu | Asp | Ser | Ala | Ala | Gly | Leu | Thr | Ile | Trp | Arg | Leu | Pro | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Gly | Phe | Ala | Val | Gly | Arg | Ile | Pro | Gly | Gly | Trp | Arg | Gly | Gly | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Met | Met | Pro | Val | Val | Tyr | Thr | Glu | Val | Asp | Gly | Gly | Arg | Leu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Glu | Arg | Leu | Pro | Arg | Arg | Val | Ala | Trp | Gly | Ser | Arg | Arg | Gly | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Asp | Gly | Gly | Gly | Ser | Arg | Glu | Gln | Arg | Trp | Trp | Leu | Cys | Gly | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | His | Glu | Ala | Phe | Arg | Met | Phe |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..944

(D) OTHER INFORMATION: / Ceres Seq. ID 1572796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| acagtcgtca | ctcaccacct | caccgacctc | acogttcctt  | atccatttgg  | ctgacgcaaa  | 60  |
| atcgaatcgg | aaccctaaaa | tctctccgaa | agccatgtct  | cctcctcctg  | ctgtagtcac  | 120 |
| tgaatctgcc | gatggacaac | ctgagcaacc | acoggttacc  | gccattgctg  | aagagctgga  | 180 |
| gaaagcttca | gactgatgaa | cogattgtag | aagatgttaa  | agatgatgaa  | gacgatgatg  | 240 |
| atgatgacga | agaagaggaa | gacgacgatg | ctcaagggtgt | aagtggaagt  | tcaaagcaga  | 300 |
| gtagaagtga | aaagaagagt | aggaaggcga | tgttgaaagt  | cggtatgaaa  | cctgtcactg  | 360 |
| gtgtagtg   | agtaaccatc | aagagaacga | aaaacgttct  | cttctttatc  | tctaagcctg  | 420 |
| atgtctttaa | gagcccgcat | tcagaaacct | atgttatatt  | cggtgaggcc  | aagatcgagg  | 480 |
| atttgagctc | tcagcttcaa | acgcaagctg | ctcaacagtt  | taggatgcct  | gMaattggag  | 540 |
| ccacatctca | gagagcagag | gcacgcagac | ccactgtaga  | agcacagggtg | gaagaagatg  | 600 |
| aagaggaaat | cgatgagacc | ggtgtggagg | ctcgtgacat  | tgacttggtc  | atgactcagg  | 660 |
| ctggagtttc | gcgtagcaaa | gcggttaaag | cactcaagag  | tcacgatgga  | gacattgtaa  | 720 |
| gtgcaataat | ggaactcact | acttaagagt | taagagagat  | tgagtctcta  | tgctttattc  | 780 |
| acttgcagat | tgttttcaaa | tacttttgga | tttatcagga  | aattggatta  | ttgttgtcct  | 840 |
| tacgagtatc | taatctagtt | tgtttggtat | gatgcttatg  | cagtatctga  | gttggtactgt | 900 |
| gtttttcacg | acaatgtatt | ggagaaaata | catatcaaaa  | ttcg        |             |     |

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

Met Asp Asn Leu Ser Asn His Arg Leu Pro Pro Leu Leu Lys Ser Trp  
1 5 10 15  
Arg Lys Leu Gln Thr Asp Glu Pro Ile Val Glu Asp Val Lys Asp Asp  
20 25 30  
Glu Asp Asp Asp Asp Asp Asp Glu Glu Glu Asp Asp Asp Ala Gln  
35 40 45  
Gly Val Ser Gly Ser Ser Lys Gln Ser Arg Ser Glu Lys Lys Ser Arg  
50 55 60  
Lys Ala Met Leu Lys Leu Gly Met Lys Pro Val Thr Gly Val Ser Arg  
65 70 75 80  
Val Thr Ile Lys Arg Thr Lys Asn Val Leu Phe Phe Ile Ser Lys Pro  
85 90 95  
Asp Val Phe Lys Ser Pro His Ser Glu Thr Tyr Val Ile Phe Gly Glu  
100 105 110  
Ala Lys Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr Gln Ala Ala Gln  
115 120 125  
Gln Phe Arg Met Pro Xaa Ile Gly Ala Thr Ser Gln Arg Ala Glu Ala  
130 135 140  
Ser Thr Ala Thr Val Glu Ala Gln Val Glu Glu Asp Glu Glu Glu Ile  
145 150 155 160  
Asp Glu Thr Gly Val Glu Ala Arg Asp Ile Asp Leu Val Met Thr Gln  
165 170 175  
Ala Gly Val Ser Arg Ser Lys Ala Val Lys Ala Leu Lys Ser His Asp  
180 185 190  
Gly Asp Ile Val Ser Ala Ile Met Glu Leu Thr Thr  
195 200

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

Met Leu Lys Leu Gly Met Lys Pro Val Thr Gly Val Ser Arg Val Thr  
1 5 10 15  
Ile Lys Arg Thr Lys Asn Val Leu Phe Phe Ile Ser Lys Pro Asp Val  
20 25 30  
Phe Lys Ser Pro His Ser Glu Thr Tyr Val Ile Phe Gly Glu Ala Lys  
35 40 45  
Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr Gln Ala Ala Gln Gln Phe  
50 55 60  
Arg Met Pro Xaa Ile Gly Ala Thr Ser Gln Arg Ala Glu Ala Ser Thr  
65 70 75 80  
Ala Thr Val Glu Ala Gln Val Glu Glu Asp Glu Glu Glu Ile Asp Glu

85 90 95  
Thr Gly Val Glu Ala Arg Asp Ile Asp Leu Val Met Thr Gln Ala Gly  
100 105 110  
Val Ser Arg Ser Lys Ala Val Lys Ala Leu Lys Ser His Asp Gly Asp  
115 120 125  
Ile Val Ser Ala Ile Met Glu Leu Thr Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1572799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Met Lys Pro Val Thr Gly Val Ser Arg Val Thr Ile Lys Arg Thr Lys  
1 5 10 15  
Asn Val Leu Phe Phe Ile Ser Lys Pro Asp Val Phe Lys Ser Pro His  
20 25 30  
Ser Glu Thr Tyr Val Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser  
35 40 45  
Ser Gln Leu Gln Thr Gln Ala Ala Gln Gln Phe Arg Met Pro Xaa Ile  
50 55 60  
Gly Ala Thr Ser Gln Arg Ala Glu Ala Ser Thr Ala Thr Val Glu Ala  
65 70 75 80  
Gln Val Glu Glu Asp Glu Glu Glu Ile Asp Glu Thr Gly Val Glu Ala  
85 90 95  
Arg Asp Ile Asp Leu Val Met Thr Gln Ala Gly Val Ser Arg Ser Lys  
100 105 110  
Ala Val Lys Ala Leu Lys Ser His Asp Gly Asp Ile Val Ser Ala Ile  
115 120 125  
Met Glu Leu Thr Thr  
130

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1793

(D) OTHER INFORMATION: / Ceres Seq. ID 1572800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

ctctcggatt tttattttctt atatacaaat cctaaaaacc ctatagcctt ctttcttcat 60  
cacctactac taactccaag ctcaagcccc tctgtttctt ctgcttgttg ttaaaaaatca 120  
tttcagacac agtgcttttg atgactctct gcaacaaaca acagcagctg cagacaaagc 180  
ttatacgaag ctgtatctac tgactttgat ggtgaaatat caaaaaccct aaattaaatt 240  
aaaaaaaaa aacacatttt ttttcttctt ttggtttttc ctctgagggt attcatcatc 300  
aatgcttaca agtacagtgt ggtaaacaaa acaaaaacaa aaaaccatt ttttctcct 360  
tctttaaatc ccaaaccaac cctaaagtgt tgatttttaa ttttgggggt aacaaaaaaa 420  
aaacaaaacc ctaatttttt ttcttttagtg atgagattat tgggtgatgat gaaatgattg 480  
gagatctaata gaagaataac aacaatggcg acgttgtgga taacgaagt aacaaccggt 540  
taagccggtg gcatcacaat tcttcccgga taattagggt ttcacgagct tccggtggtg 600  
aagatcgaca cagcaaagtc ttgacttcta aaggaccacg tgaccgtcgt gtccggttat 660  
cagtctccac cgctcttcaa ttctatgatc ttcaagatcg gttagggttat gatcaacct 720

gcaaagctgt tgaatgggtta atcaaagctg ctgaagattc aatctbtgag cttccttcac 780  
tcaacaacac tcattttccg accgatgacg agaatcacca gaatcagaca ttaacaacag 840  
ttgctgctaa ttccctgtct aaatctgctt gtagtagcaa ttcagacacg agcaagaact 900  
ctttgggttKK YYtthatcaa gatcggagct tagagataaa gctagagaga gagctagaga 960  
gagaacagct aaagagacca aggagagaga tcataaccac acttcgttta ccgatttggt 1020  
aaattccggt tcagatccgg ttaactcaaa ccggcaatgg atggcttctg ctcccttctc 1080  
atctccaatg gagtatttta gttcgggttt aattctcggg tcgggtcaac aaacccattt 1140  
cccgatttgc acaaattctc atcctttctc atcaatctcc gatcatcatc atcctcatca 1200  
tcagcaccaa gagttttcat tcgttcccgga ccatttgata tcaccggcag aatccaacgg 1260  
cggagcattc aatcttgatt ttaatatgtc gacaccctcc ggccgccggag ctgccgtctc 1320  
cgccgcatcc ggtgggtgggt tcagtggttt caacaggggg acccttcagt ccaattcaac 1380  
aaatcagcat cagtcatttc tcgctaattc acagagggtt ccaacatcag aaagtggagg 1440  
aggtccacag ttcttatttc gtgcactgcc tgcagagaat caccaccaca atcaccagtt 1500  
tcagctttac tatgaaaatg gatgcagaaa ctcatcagac cataagggtta aaggcaagaa 1560  
ctgatgatat taattattgc atctttggtt ttgttcaaat cctcattttg tatgtttatc 1620  
tttggtttat ttcaaaaacaa atgttaattc cttttgttgt ctgatgtgtg ttagggtttt 1680  
gttctacata tgtattgagg gtctttggaa atctttttgc attgtgcttg taatgttgta 1740  
ttttgtgata atagcatttt gtttgtgagt ttataattca atttttgaat gtt

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1572801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

Met Ile Gly Asp Leu Met Lys Asn Asn Gly Asp Val Val Asp  
1 5 10 15  
Asn Glu Val Asn Asn Arg Leu Ser Arg Trp His His Asn Ser Ser Arg  
20 25 30  
Ile Ile Arg Val Ser Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys  
35 40 45  
Val Leu Thr Ser Lys Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val  
50 55 60  
Ser Thr Ala Leu Gln Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp  
65 70 75 80  
Gln Pro Ser Lys Ala Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser  
85 90 95  
Ile Xaa Glu Leu Pro Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp  
100 105 110  
Glu Asn His Gln Asn Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu  
115 120 125  
Ser Lys Ser Ala Cys Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Leu  
130 135 140  
Val Xaa Xaa Xaa Gln Asp Arg Ser Leu Glu Ile Lys Leu Glu Arg Glu  
145 150 155 160  
Leu Glu Arg Glu Gln Leu Lys Arg Pro Arg Arg Glu Ile Ile Thr Thr  
165 170 175  
Leu Arg Leu Pro Ile Cys  
180

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1572802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

Met Lys Asn Asn Asn Asn Gly Asp Val Val Asp Asn Glu Val Asn Asn  
1 5 10 15  
Arg Leu Ser Arg Trp His His Asn Ser Ser Arg Ile Ile Arg Val Ser  
20 25 30  
Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr Ser Lys  
35 40 45  
Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala Leu Gln  
50 55 60  
Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser Lys Ala  
65 70 75 80  
Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Xaa Glu Leu Pro  
85 90 95  
Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp Glu Asn His Gln Asn  
100 105 110  
Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser Ala Cys  
115 120 125  
Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Leu Val Xaa Xaa Xaa Gln  
130 135 140  
Asp Arg Ser Leu Glu Ile Lys Leu Glu Arg Glu Leu Glu Arg Glu Gln  
145 150 155 160  
Leu Lys Arg Pro Arg Arg Glu Ile Ile Thr Thr Leu Arg Leu Pro Ile  
165 170 175  
Cys

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1572803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

Met Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Ser Gly  
1 5 10 15  
Leu Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr Asn  
20 25 30  
Ser His Pro Phe Ser Ser Ile Ser Asp His His His Pro His His Gln  
35 40 45  
His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser Pro Ala Glu  
50 55 60  
Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser Thr Pro Ser  
65 70 75 80  
Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly Phe Ser Gly  
85 90 95  
Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln His Gln Ser  
100 105 110  
Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser Gly Gly Gly  
115 120 125  
Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His His His Asn  
130 135 140  
His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn Ser Ser Asp  
145 150 155 160

His Lys Gly Lys Gly Lys Asn  
165

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aagttacact | ataaactcaa | acacatctat | cggcaagtct | taacacacga  | agatttccaa | 60  |
| aatggctaag | gccgaagGtc | tttttcttct | tggtttagta | gttatttcaa  | gtttagttat | 120 |
| gttaaccgag | agccgactcg | caagaaaaga | cttggggatt | gacctagggtg | ggattggaat | 180 |
| cggtttgggc | gttggattgg | ggattggtct | tggcggcggg | tcgggctccg  | gtgctggtgc | 240 |
| aggttctgga | tcaggttcag | gttccagatc | atcatctagc | tccagctcat  | catcaagttc | 300 |
| gagttctagt | ggttcgggtg | gttcagctgg | ttcatctgcc | ggttcatttg  | ctggctctag | 360 |
| agctggatca | ggatctggta | actaaattat | aataattact | tttcgactta  | aagtgtgaaa | 420 |
| caataagtat | gttttatggt | tttggttcgt | cgtagttaat | atcgtatgta  | cggaatggaa | 480 |
| tgaataattt | gtt        |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Ala | Glu | Gly | Leu | Phe | Leu | Leu | Gly | Leu | Val | Val | Ile | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Val | Met | Leu | Thr | Glu | Ser | Arg | Leu | Ala | Arg | Lys | Asp | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asp | Leu | Gly | Gly | Ile | Gly | Ile | Gly | Leu | Gly | Val | Gly | Leu | Gly | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Gly | Gly | Gly | Ser | Gly | Ser | Gly | Ala | Gly | Ala | Gly | Ser | Gly | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Ser | Gly | Ser | Arg | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ser | Ser | Gly | Ser | Gly | Gly | Ser | Ala | Gly | Ser | Ser | Ala | Gly | Ser | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Gly | Ser | Arg | Ala | Gly | Ser | Gly | Ser | Gly | Asn |     |     |     |     |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

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Met Leu Thr Glu Ser Arg Leu Ala Arg Lys Asp Leu Gly Ile Asp Leu  
1 5 10 15  
Gly Gly Ile Gly Ile Gly Leu Gly Val Gly Leu Gly Ile Gly Leu Gly  
20 25 30  
Gly Gly Ser Gly Ser Gly Ala Gly Ala Gly Ser Gly Ser Gly Ser Gly  
35 40 45  
Ser Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser  
50 55 60  
Gly Ser Gly Gly Ser Ala Gly Ser Ser Ala Gly Ser Phe Ala Gly Ser  
65 70 75 80  
Arg Ala Gly Ser Gly Ser Gly Asn  
85

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| aattgtcaaa aactcacaag gcattatcat gtggacatgc aacctttttt ttctatacgc | 60   |
| attacagaaa tgaaaacaat gattaggatc gcatgcacgt caagaaaaca acctatagct | 120  |
| gtactttgat atactaaact aaatcatgtc ttggctcaag cacacaagct tctagctaga | 180  |
| tacaactgca aacatatatg atggctttgt ctaataagaa gacgacgact tgggcaccgc | 240  |
| tttgaccagt caatacacca aatctgtatg tatcatttat ataaatatta tctttccaca | 300  |
| gttggtgaag aatcacatag acagcacaca cggattccat ggagactaaa cagagtatcc | 360  |
| ctctcctcat gccctataag atgggaccct tcaatctttc tcacagggtt gttttggcgc | 420  |
| cattgactag atcgagatcg tatggtaaca ttctcagcc taatgccaaa ttatattaca  | 480  |
| ctcagagaac aacacctggt ggtctcttta ttccgaatc ctgtgtagtc tccgagacat  | 540  |
| cattgggcta tccgattta cctggattat ggaacagaga ccaagtggag gcatggaagc  | 600  |
| ccatcggtga tgcggttcat tcgaaaggcg gtatcttctt ctgccagatt tggcatggtg | 660  |
| gcagagtttt tcatcaagac cagccaaatg gggaagcacc cgtctcctct acagacaagc | 720  |
| cattgatgtg caagaacatg tatggaggtc agtttaagcc tccacggcgg ttaaggagcg | 780  |
| acgagcttcg cgccattgtc aacgacttta gaatcgctgc acgaaacgct atcgaagctg | 840  |
| gcttcgatgg agtggaggtt cacggcgcac atggttacct gatcgatcag ttcctgaaag | 900  |
| acaaagtga tgacagaagt gaccaatatg gtggGtcatt agagaaccgc tgtagatttg  | 960  |
| ctcttgaagt aatcgaagca gtggtgaacg agatcggttc agatcgtgtt ggaatcagac | 1020 |
| tctcgccatt tgcagattac atggagtcag gagactcgaa tccagaagca ttagggctct | 1080 |
| acctggtgca agctatgaac aagcatggca tggagtcgtc tacggtcaca tggttgaacc | 1140 |
| tagaatgaaa acccttgaag gaatcttcga atgcacggaa tcgcttacgc ccatgcgaaa | 1200 |
| agccttcaaa ggtacgttca tagtagcagg aggatattct agagaagacg ggaacaaggc | 1260 |
| ggtggaagag ggaagaaccg atcttgtggc ttatggacgg ccgttcttgg cgaatccgga | 1320 |
| tctgacgagg agattcgaac tcaatgagcc gttgaatagg tacgatagat caacgttcta | 1380 |
| cacttcagat cctgtagtgg gctatacaga ctaccctttc ctcgagacca cagatacaac | 1440 |
| aactgcttaa ggggtttatt cagatgcatt attagcaaaa catatttttc c          |      |

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

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```

Met Glu Thr Lys Gln Ser Ile Pro Leu Leu Met Pro Tyr Lys Met Gly
1 5 10 15
Pro Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu Thr Arg Ser
 20 25 30
Arg Ser Tyr Gly Asn Ile Pro Gln Pro Asn Ala Lys Leu Tyr Tyr Thr
 35 40 45
Gln Arg Thr Thr Pro Gly Gly Leu Leu Ile Ser Glu Ser Cys Val Val
 50 55 60
Ser Glu Thr Ser Leu Gly Tyr Pro Asp Leu Pro Gly Leu Trp Asn Arg
65 70 75 80
Asp Gln Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val His Ser Lys
 85 90 95
Gly Gly Ile Phe Phe Cys Gln Ile Trp His Gly Gly Arg Val Phe His
 100 105 110
Gln Asp Gln Pro Asn Gly Glu Ala Pro Val Ser Ser Thr Asp Lys Pro
 115 120 125
Leu Met Cys Lys Asn Met Tyr Gly Gly Gln Phe Lys Pro Pro Arg Arg
130 135 140
Leu Arg Ser Asp Glu Leu Pro Ala Ile Val Asn Asp Phe Arg Ile Ala
145 150 155 160
Ala Arg Asn Ala Ile Glu Ala Gly Phe Asp Gly Val Glu Val His Gly
 165 170 175
Ala His Gly Tyr Leu Ile Asp Gln Phe Leu Lys Asp Lys Val Asn Asp
 180 185 190
Arg Ser Asp Gln Tyr Gly Gly Ser Leu Glu Asn Arg Cys Arg Phe Ala
195 200 205
Leu Glu Val Ile Glu Ala Val Val Asn Glu Ile Gly Ser Asp Arg Val
210 215 220
Gly Ile Arg Leu Ser Pro Phe Ala Asp Tyr Met Glu Ser Gly Asp Ser
225 230 235 240
Asn Pro Glu Ala Leu Gly Leu Tyr Leu Val Gln Ala Met Asn Lys His
 245 250 255
Gly Met Glu Ser Ser Thr Val Thr Trp Leu Asn Leu Glu
 260 265

```

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1572809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

```

Met Pro Tyr Lys Met Gly Pro Phe Asn Leu Ser His Arg Val Val Leu
1 5 10 15
Ala Pro Leu Thr Arg Ser Arg Ser Tyr Gly Asn Ile Pro Gln Pro Asn
 20 25 30
Ala Lys Leu Tyr Tyr Thr Gln Arg Thr Thr Pro Gly Gly Leu Leu Ile
 35 40 45
Ser Glu Ser Cys Val Val Ser Glu Thr Ser Leu Gly Tyr Pro Asp Leu
 50 55 60
Pro Gly Leu Trp Asn Arg Asp Gln Val Glu Ala Trp Lys Pro Ile Val
65 70 75 80
Asp Ala Val His Ser Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His
 85 90 95
Gly Gly Arg Val Phe His Gln Asp Gln Pro Asn Gly Glu Ala Pro Val
 100 105 110
Ser Ser Thr Asp Lys Pro Leu Met Cys Lys Asn Met Tyr Gly Gly Gln

```

```
(2) INFORMATION FOR SEQ ID NO:2384:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..255
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572810
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Pro | Phe | Asn | Leu | Ser | His | Arg | Val | Val | Leu | Ala | Pro | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ser | Arg | Ser | Tyr | Gly | Asn | Ile | Pro | Gln | Pro | Asn | Ala | Lys | Leu | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Thr | Gln | Arg | Thr | Thr | Pro | Gly | Gly | Leu | Leu | Ile | Ser | Glu | Ser | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Ser | Glu | Thr | Ser | Leu | Gly | Tyr | Pro | Asp | Leu | Pro | Gly | Leu | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Arg | Asp | Gln | Val | Glu | Ala | Trp | Lys | Pro | Ile | Val | Asp | Ala | Val | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Lys | Gly | Gly | Ile | Phe | Phe | Cys | Gln | Ile | Trp | His | Gly | Gly | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | His | Gln | Asp | Gln | Pro | Asn | Gly | Glu | Ala | Pro | Val | Ser | Ser | Thr | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Pro | Leu | Met | Cys | Lys | Asn | Met | Tyr | Gly | Gly | Gln | Phe | Lys | Pro | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Arg | Leu | Arg | Ser | Asp | Glu | Leu | Pro | Ala | Ile | Val | Asn | Asp | Phe | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Ala | Ala | Arg | Asn | Ala | Ile | Glu | Ala | Gly | Phe | Asp | Gly | Val | Glu | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| His | Gly | Ala | His | Gly | Tyr | Leu | Ile | Asp | Gln | Phe | Leu | Lys | Asp | Lys | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Asp | Arg | Ser | Asp | Gln | Tyr | Gly | Gly | Ser | Leu | Glu | Asn | Arg | Cys | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Ala | Leu | Glu | Val | Ile | Glu | Ala | Val | Val | Asn | Glu | Ile | Gly | Ser | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Val | Gly | Ile | Arg | Leu | Ser | Pro | Phe | Ala | Asp | Tyr | Met | Glu | Ser | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Ser | Asn | Pro | Glu | Ala | Leu | Gly | Leu | Tyr | Leu | Val | Gln | Ala | Met | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Lys His Gly Met Glu Ser Ser Thr Val Thr Trp Leu Asn Leu Glu  
245 250 255

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aatgctattg ttgggttcca tggacgggta ggttcttgtg ttgatagtat cgggtgcatat | 60  |
| tacgctccgt tttctccttc tctccacct acagagaaac tagagggaca aggtgggtgat  | 120 |
| ggaggagatt cttgggacga tgggtgctttc ctaaagtata agaaagtata tgttggacaa | 180 |
| ggctcgaacg gtattgtcgc cgtaaagttt gagtacgaga acgacgctag tgagggttgtt | 240 |
| ggtggagatg aacatggaaa gactacattg cttggatacg aaKgTggtga tgactactcc  | 300 |
| ttactttaat tgtttaaagt ttcaaaacta tactatatat cg                     |     |

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asn Ala Ile Val Gly Phe His Gly Arg Val Gly Ser Cys Val Asp Ser |  |
| 1 5 10 15                                                       |  |
| Ile Gly Ala Tyr Tyr Ala Pro Phe Ser Pro Ser Pro Pro Thr Glu     |  |
| 20 25 30                                                        |  |
| Lys Leu Glu Gly Gln Gly Gly Asp Gly Gly Asp Ser Trp Asp Asp Gly |  |
| 35 40 45                                                        |  |
| Ala Phe Leu Asn Val Lys Lys Val Tyr Val Gly Gln Gly Ser Asn Gly |  |
| 50 55 60                                                        |  |
| Ile Val Ala Val Lys Phe Glu Tyr Glu Asn Asp Ala Ser Glu Val Val |  |
| 65 70 75 80                                                     |  |
| Val Gly Asp Glu His Gly Lys Thr Thr Leu Leu Gly Tyr Glu Xaa Gly |  |
| 85 90 95                                                        |  |
| Asp Asp Tyr Ser Leu Leu                                         |  |
| 100                                                             |  |

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Leu Asp Lys Ala Arg Thr Val Leu Ser Pro Leu Ser Leu Ser Thr |  |
| 1 5 10 15                                                       |  |
| Arg Thr Thr Leu Val Arg Leu Leu Leu Glu Met Asn Met Glu Arg Leu |  |

20 25 30  
His Cys Leu Asp Thr Xaa Val Val Met Thr Thr Pro Tyr Phe Asn Cys  
35 40 45  
Leu Lys Phe Gln Asn Tyr Thr Ile Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

cmcraracca ttmcctagam catcctaaat caaaagtttc tcaaaaatca aaatcccttc 60  
ctctctctct ctcaccgagc cggcgagccc gttctctcgg tgttttttaa gatgcttatg 120  
atgatgatgg ggagtaatat cagaaatcaa gctttttcac aatctcagaa attgtagtag 180  
agtttggcga ttttatcaac ctccggaaca agcttcttct tcttcgtttt actcttgta 240  
tccgtaaaKg ggttgtttcc attccacggc tgccagagaa tttcccgatc acgaaaaccc 300  
tgtgaagctt gcttctgaga ctgcttttag tgtagtgaa gttgaagcat tgtatgaatt 360  
gttcaagagc ataagcagct cggttgttga cgatggcttg ataaacaagg aagagtttca 420  
acttgctttg ttcaagaaca gaaagaaaga aaatttgttt gccaatagga tatttgattt 480  
atttgatgtt aaacgaaaag gcgtaattga ttttgagac tttgtgagat cactcaatgt 540  
tttccatcct aatgcttccc tagaggagaa aacagacttt accttaggc tttacgacat 600  
ggactgcaca ggcttcattg agcgccaaga ggtgaagcag atgttgattg cacttctctg 660  
cgaatctgaa atgaaactgg ctgatgatac aatagagatg atacttgatc agacatttga 720  
ggacgcagat gtggatcggg atggaaagat tgataagaca gaatggagca atttcgttat 780  
caaaaaccca tctttgctta aaatcatgac tcttccgtat ctacaggata taacgacgac 840  
atttccgagt ttcgtattta actcggaggt ggacgagatt gcgacgtgaa agagacaaga 900  
caagctgggt tatagagacc aagtcgtagg ctggaccaag aataaaaaag aagattgatt 960  
ccaacaatgt tatatagcag gatcgagctc tatttccttt ggaattttta gtctattgga 1020  
tttcaatttc atgtattgag attacttttg gctctcttcc tttaacagtt ttgaatactc 1080  
aagttgtagt tctacgaaaa gattaatata aaaccacaat ttctg

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..96  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

Met Asp Cys Thr Gly Phe Ile Glu Arg Gln Glu Val Lys Gln Met Leu  
1 5 10 15  
Ile Ala Leu Leu Cys Glu Ser Glu Met Lys Leu Ala Asp Asp Thr Ile  
20 25 30  
Glu Met Ile Leu Asp Gln Thr Phe Glu Asp Ala Asp Val Asp Arg Asp  
35 40 45  
Gly Lys Ile Asp Lys Thr Glu Trp Ser Asn Phe Val Ile Lys Asn Pro  
50 55 60  
Ser Leu Leu Lys Ile Met Thr Leu Pro Tyr Leu Arg Asp Ile Thr Thr  
65 70 75 80  
Thr Phe Pro Ser Phe Val Phe Asn Ser Glu Val Asp Glu Ile Ala Thr  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

```
Met Leu Ile Ala Leu Leu Cys Glu Ser Glu Met Lys Leu Ala Asp Asp
1 5 10 15
Thr Ile Glu Met Ile Leu Asp Gln Thr Phe Glu Asp Ala Asp Val Asp
 20 25 30
Arg Asp Gly Lys Ile Asp Lys Thr Glu Trp Ser Asn Phe Val Ile Lys
 35 40 45
Asn Pro Ser Leu Leu Lys Ile Met Thr Leu Pro Tyr Leu Arg Asp Ile
 50 55 60
Thr Thr Thr Phe Pro Ser Phe Val Phe Asn Ser Glu Val Asp Glu Ile
65 70 75 80
Ala Thr
```

(2) INFORMATION FOR SEQ ID NO:2391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

```
Met Lys Leu Ala Asp Thr Ile Glu Met Ile Leu Asp Gln Thr Phe
1 5 10 15
Glu Asp Ala Asp Val Asp Arg Asp Gly Lys Ile Asp Lys Thr Glu Trp
 20 25 30
Ser Asn Phe Val Ile Lys Asn Pro Ser Leu Leu Lys Ile Met Thr Leu
 35 40 45
Pro Tyr Leu Arg Asp Ile Thr Thr Thr Phe Pro Ser Phe Val Phe Asn
 50 55 60
Ser Glu Val Asp Glu Ile Ala Thr
65 70
```

(2) INFORMATION FOR SEQ ID NO:2392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..950
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

```
acatcaaaaa ctaaacaata aaccatatac cataaaaaaac atgaaaatcc tctcactttc 60
acttctcttg ctcttggccg ctacggtctc tgcattccatt ccagagctca tcgaactcgt 120
```

(2) INFORMATION FOR SEO ID NO:2393:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1572827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

[illegible]

275

(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1572828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

```
Met Lys Ile Leu Ser Leu Ser Leu Leu Leu Leu Ala Ala Thr Val
1 5 10 15
Ser Ala Ser Ile Pro Glu Leu Ile Glu Leu Val Asp Ser Asn Thr Ile
 20 25 30
Phe Thr Asn Glu Ala Glu Leu Leu Glu Lys Glu Lys Leu Ser Ile Asn
 35 40 45
Tyr Ala Asn Cys Arg Ser Trp His Leu Gly Val Glu Thr Ser Asn Ile
 50 55 60
Ile Asp Phe Asp Thr Val Pro Ala Asn Cys Lys Asp Tyr Val Glu Asp
 65 70 75 80
Tyr Leu Ile Thr Ser Lys Gln Tyr Gln Tyr Asp Ser Lys Thr Val Cys
 85 90 95
Lys Glu Ala Tyr Phe Tyr Ala Lys Gly Leu Ala Leu Lys Asn Asp Thr
 100 105 110
Val Asn Val Trp Ile Phe Asp Leu Asp Asp Thr Leu Leu Ser Ser Ile
 115 120 125
Pro Tyr Tyr Ala Lys Tyr Gly Tyr Gly Thr Glu Lys Thr Asp Pro Gly
 130 135 140
Ala Tyr Trp Leu Trp Leu Gly Thr Gly Ala Ser Thr Pro Gly Leu Pro
 145 150 155 160
Glu Ala Leu His Leu Tyr Gln Asn Ile Ile Glu Leu Gly Ile Glu Pro
 165 170 175
Ile Ile Leu Ser Asp Arg Trp Lys Leu Trp Lys Asn Val Thr Leu Asp
 180 185 190
Asn Leu Glu Ala Ala Gly Val Ala Tyr Trp Lys His Leu Ile Leu Lys
 195 200 205
Pro Asn Gly Ser Asn Leu Arg Gln Val Val Tyr Lys Ser Lys Val Arg
 210 215 220
Lys Ser Leu Val Lys Lys Gly Tyr Asn Ile Val Gly Asn Ile Gly Asp
 225 230 235 240
Gln Trp Ala Asp Leu Val Glu Asp Thr Pro Gly Arg Val Phe Lys Leu
 245 250 255
Pro Asn Pro Leu Tyr Tyr Val Pro Ser
 260 265
```

(2) INFORMATION FOR SEQ ID NO:2395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1005

(D) OTHER INFORMATION: / Ceres Seq. ID 1572833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

```
ctaccactta agaagcacag atggacataa tctcagggca agctctgtta ctctctttt 60
gcttttatctt atcatgtttt cttatcttca ccaccacaag atctggacga atctcccgcg 120
```



gggccaccgc gctgcctcca ggacctccac ggttaccgat catcggaat attcacctcg 180  
tcggaaaaaca tccacatcgc tcattogccg agctctcaaa aacttatgga ccagtcatga 240  
gtcttaagct tggaaagtta aatacagtggt ttatagcttc accagaagct gcgagagagg 300  
ttttacgaac acatgaccag attttgtctg cccgtagtcc cactaacgcg gtacggtCca 360  
tcaatcacca agacgcttct cttgtctggc ttcttctgtc gtccgctcgt tggaggctgt 420  
tgagaaggct gtcggtgact cagctcttgt caccacagcg tatcgaagcc acgaaagcct 480  
tgaggatgaa caaggtgaag gaacttgtga gcttcataag tgaaagcagc gatagggaag 540  
aatctGgttg atatttctcg tgtagccttc atcacaactc ttaatatcat atcgaacatt 600  
ctgttttccg tcgatctcgg tagctacaac gcgaaagcgt ctattaatgg ggttcaagac 660  
acggtgatta gtgttatgga tgctgccggg actccagacg ctgctaatta ctttccattt 720  
ctgaggtttc ttgatctgca aggtaatgtg aagactttta aggtttgcac ggagaggctg 780  
gtaagggttt tccgtgggtt cattgatgct aagattgcgg aaaaatcatc gcagaataac 840  
cctaaagatg tttcaaaaaa cgatttctgt gacaaccttc tcgattacaa aggagatgaa 900  
tcagaactct ccattagcga tattgaacac cttctcttgg taagtctgac cttactgcag 960  
ataatcatga tttataagat aatggaataa tcaattttgt ggatg

(2) INFORMATION FOR SEQ ID NO:2396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1572834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

Met Asp Ile Ile Ser Gly Gln Ala Leu Leu Leu Phe Cys Phe Ile  
1 5 10 15  
Leu Ser Cys Phe Leu Ile Phe Thr Thr Arg Ser Gly Arg Ile Ser  
20 25 30  
Arg Gly Ala Thr Ala Leu Pro Pro Gly Pro Pro Arg Leu Pro Ile Ile  
35 40 45  
Gly Asn Ile His Leu Val Gly Lys His Pro His Arg Ser Phe Ala Glu  
50 55 60  
Leu Ser Lys Thr Tyr Gly Pro Val Met Ser Leu Lys Leu Gly Ser Leu  
65 70 75 80  
Asn Thr Val Val Ile Ala Ser Pro Glu Ala Ala Arg Glu Val Leu Arg  
85 90 95  
Thr His Asp Gln Ile Leu Ser Ala Arg Ser Pro Thr Asn Ala Val Arg  
100 105 110  
Ser Ile Asn His Gln Asp Ala Ser Leu Val Trp Leu Pro Ser Ser Ser  
115 120 125  
Ala Arg Trp Arg Leu Leu Arg Leu Ser Val Thr Gln Leu Leu Ser  
130 135 140  
Pro Gln Arg Ile Glu Ala Thr Lys Ala Leu Arg Met Asn Lys Val Lys  
145 150 155 160  
Glu Leu Val Ser Phe Ile Ser Glu Ser Ser Asp Arg Glu Glu Ser Gly  
165 170 175

(2) INFORMATION FOR SEQ ID NO:2397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1572835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:

Met Ser Leu Lys Leu Gly Ser Leu Asn Thr Val Val Ile Ala Ser Pro  
1 5 10 15  
Glu Ala Ala Arg Glu Val Leu Arg Thr His Asp Gln Ile Leu Ser Ala  
20 25 30  
Arg Ser Pro Thr Asn Ala Val Arg Ser Ile Asn His Gln Asp Ala Ser  
35 40 45  
Leu Val Trp Leu Pro Ser Ser Ser Ala Arg Trp Arg Leu Leu Arg Arg  
50 55 60  
Leu Ser Val Thr Gln Leu Leu Ser Pro Gln Arg Ile Glu Ala Thr Lys  
65 70 75 80  
Ala Leu Arg Met Asn Lys Val Lys Glu Leu Val Ser Phe Ile Ser Glu  
85 90 95  
Ser Ser Asp Arg Glu Glu Ser Gly  
100

(2) INFORMATION FOR SEQ ID NO:2398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1572836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

Met Asp Ala Ala Gly Thr Pro Asp Ala Ala Asn Tyr Phe Pro Phe Leu  
1 5 10 15  
Arg Phe Leu Asp Leu Gln Gly Asn Val Lys Thr Phe Lys Val Cys Thr  
20 25 30  
Glu Arg Leu Val Arg Val Phe Arg Gly Phe Ile Asp Ala Lys Ile Ala  
35 40 45  
Glu Lys Ser Ser Gln Asn Asn Pro Lys Asp Val Ser Lys Asn Asp Phe  
50 55 60  
Val Asp Asn Leu Leu Asp Tyr Lys Gly Asp Glu Ser Glu Leu Ser Ile  
65 70 75 80  
Ser Asp Ile Glu His Leu Leu Leu Val Ser Leu Thr Leu Leu Gln Ile  
85 90 95  
Ile Met Ile Tyr Lys Ile Met Glu  
100

(2) INFORMATION FOR SEQ ID NO:2399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..907

(D) OTHER INFORMATION: / Ceres Seq. ID 1572837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aacacacata cataaaagta gtagaactaa aaaatggcaa acctcttggt ctctactttc  | 60  |
| atatttttccg cacttttgct catctccacc gcaacagccg ccacattcga aatcctaaac | 120 |
| caatgtagtt acaccgtgtg ggctgccgca agccctggag gtggccgacg tctagatgct  | 180 |
| ggccaatcat ggaggctaga tgtcgcggcg ggcactaaaa tggcacggat ttggggtagg  | 240 |
| accaattgta actttgactc ctcaggtcgt ggccgatgcc aaactgggtga ctgcagtggg | 300 |
| ggactccaat gtactggctg gggacaccca ccaaacacgt tggctgagta cgctttgaac  | 360 |
| caattcaaca acttagactt ctacgatatc tcacttgctg atggatttaa catacctatg  | 420 |

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| gagtttagcc caactagttc gaactgccat cggatactat gtaccgcaga cataaacgga   | 480 |
| caatgtccaa acgtgttgag agccccaggt ggatgcaaca acccgtgtac tgtatttcag   | 540 |
| acgaaccaat actgttgtac gaacggtcag ggatcatgta gcgatactga ctactcaaga   | 600 |
| ttctttaagc agagatgccc tgNacgctta cagctatcca caagatgacc cgactagcac   | 660 |
| tttactttgc accaactacta actacagggt cgtgttttgt ccaaggtcta ggctcgggtgc | 720 |
| tactggatcc caccagctcc cgatcaagat ggtcaccgag gagaattaat agactcgtat   | 780 |
| ctactgtatg tgtgtgtgtg tgagggtgta cgtagatatg cgtacgtgtg acgtgatcat   | 840 |
| atatacgtta ccataaacac ttaatggatt ataataaggc atgcaataat aattacgtta   | 900 |
| gtcgacc                                                             |     |

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Leu | Val | Ser | Thr | Phe | Ile | Phe | Ser | Ala | Leu | Leu | Leu |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Ile | Ser | Thr | Ala | Thr | Ala | Ala | Thr | Phe | Glu | Ile | Leu | Asn | Gln | Cys | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Tyr | Thr | Val | Trp | Ala | Ala | Ala | Ser | Pro | Gly | Gly | Gly | Arg | Arg | Leu | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Gln | Ser | Trp | Arg | Leu | Asp | Val | Ala | Ala | Gly | Thr | Lys | Met | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Trp | Gly | Arg | Thr | Asn | Cys | Asn | Phe | Asp | Ser | Ser | Gly | Arg | Gly |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Cys | Gln | Thr | Gly | Asp | Cys | Ser | Gly | Gly | Leu | Gln | Cys | Thr | Gly | Trp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | His | Pro | Pro | Asn | Thr | Leu | Ala | Glu | Tyr | Ala | Leu | Asn | Gln | Phe | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Asn | Leu | Asp | Phe | Tyr | Asp | Ile | Ser | Leu | Val | Asp | Gly | Phe | Asn | Ile | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Glu | Phe | Ser | Pro | Thr | Ser | Ser | Asn | Cys | His | Arg | Ile | Leu | Cys | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ala | Asp | Ile | Asn | Gly | Gln | Cys | Pro | Asn | Val | Leu | Arg | Ala | Pro | Gly | Gly |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Cys | Asn | Asn | Pro | Cys | Thr | Val | Phe | Gln | Thr | Asn | Gln | Tyr | Cys | Cys | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Gly | Gln | Gly | Ser | Cys | Ser | Asp | Thr | Asp | Tyr | Ser | Arg | Phe | Phe | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Arg | Cys | Pro | Xaa | Arg | Leu | Gln | Leu | Ser | Thr | Arg |     |     |     |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1572839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Ile | Trp | Gly | Arg | Thr | Asn | Cys | Asn | Phe | Asp | Ser | Ser | Gly |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |

Arg Gly Arg Cys Gln Thr Gly Asp Cys Ser Gly Gly Leu Gln Cys Thr  
20 25 30  
Gly Trp Gly His Pro Pro Asn Thr Leu Ala Glu Tyr Ala Leu Asn Gln  
35 40 45  
Phe Asn Asn Leu Asp Phe Tyr Asp Ile Ser Leu Val Asp Gly Phe Asn  
50 55 60  
Ile Pro Met Glu Phe Ser Pro Thr Ser Ser Asn Cys His Arg Ile Leu  
65 70 75 80  
Cys Thr Ala Asp Ile Asn Gly Gln Cys Pro Asn Val Leu Arg Ala Pro  
85 90 95  
Gly Gly Cys Asn Asn Pro Cys Thr Val Phe Gln Thr Asn Gln Tyr Cys  
100 105 110  
Cys Thr Asn Gly Gln Gly Ser Cys Ser Asp Thr Asp Tyr Ser Arg Phe  
115 120 125  
Phe Lys Gln Arg Cys Pro Xaa Arg Leu Gln Leu Ser Thr Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..703
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aaaaagagat  | ggttctgcta  | gagaagcttt | gggatgatgt | tgtggctgga | cctcagcctg | 60  |
| accgtggcct  | tggccgcctc  | cgtaagatca | ccaccaacc  | cattaatatc | cgagatatag | 120 |
| gagaagggag  | cagcagtaag  | gtggtgatgc | ataggtcggt | gaccatgccg | gcggcagtga | 180 |
| gccttggaaac | tccaacgact  | ccaaccactc | cgacgacgcc | acgtaaggat | aacgtgtgga | 240 |
| ggagcgtctt  | taatccggga  | agcaacctcg | ccactagagc | catcggtcc  | aacatctttg | 300 |
| ataaaccac   | ccatccaaat  | tctccctccg | tctacgactg | gttgtagcgc | ggtgactcaa | 360 |
| ggagtacgca  | ccgttaGgga  | tggtccgatg | gagtgtgaca | tgcgggtgat | gtaaatatgg | 420 |
| tgacctgatac | ttccgccacc  | ttactttggt | ttttttatat | tgtttttgtg | tactttatca | 480 |
| gagtggataa  | agtgaagggg  | aatgtttttc | ttttgtacaa | aaaactgtct | tcccacctaa | 540 |
| gcaatgtgtg  | ttagttttctg | ttttgggctg | tgttttgcaa | gtttttgtat | ttcagagttg | 600 |
| tagttagttt  | gcaagtggcg  | gttgatctt  | tcactatctt | gttgatttt  | gatgatggtt | 660 |
| gatgcttttg  | ctttaatggt  | aaataataaa | gcatactttt | gct        |            |     |

(2) INFORMATION FOR SEQ ID NO:2403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

Lys Glu Met Val Leu Leu Glu Lys Leu Trp Asp Asp Val Val Ala Gly  
1 5 10 15  
Pro Gln Pro Asp Arg Gly Leu Gly Arg Leu Arg Lys Ile Thr Thr Gln  
20 25 30  
Pro Ile Asn Ile Arg Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val  
35 40 45  
Met His Arg Ser Leu Thr Met Pro Ala Ala Val Ser Pro Gly Thr Pro  
50 55 60  
Thr Thr Pro Thr Thr Pro Thr Thr Pro Arg Lys Asp Asn Val Trp Arg

(2) INFORMATION FOR SEQ ID NO:2404:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1572842

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Leu | Glu | Lys | Leu | Trp | Asp | Asp | Val | Val | Ala | Gly | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Asp | Arg | Gly | Leu | Gly | Arg | Leu | Arg | Lys | Ile | Thr | Thr | Gln | Pro | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Arg | Asp | Ile | Gly | Glu | Gly | Ser | Ser | Ser | Lys | Val | Val | Met | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Ser | Leu | Thr | Met | Pro | Ala | Ala | Val | Ser | Pro | Gly | Thr | Pro | Thr | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Thr | Thr | Pro | Thr | Thr | Pro | Arg | Lys | Asp | Asn | Val | Trp | Arg | Ser | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Asn | Pro | Gly | Ser | Asn | Leu | Ala | Thr | Arg | Ala | Ile | Gly | Ser | Asn | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Asp | Lys | Pro | Thr | His | Pro | Asn | Ser | Pro | Ser | Val | Tyr | Asp | Trp | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Ser | Gly | Asp | Ser | Arg | Ser | Gln | His | Arg |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1572843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Arg | Ser | Leu | Thr | Met | Pro | Ala | Ala | Val | Ser | Pro | Gly | Thr | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Thr | Pro | Thr | Thr | Pro | Thr | Thr | Pro | Arg | Lys | Asp | Asn | Val | Trp | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Phe | Asn | Pro | Gly | Ser | Asn | Leu | Ala | Thr | Arg | Ala | Ile | Gly | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ile | Phe | Asp | Lys | Pro | Thr | His | Pro | Asn | Ser | Pro | Ser | Val | Tyr | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Leu | Tyr | Ser | Gly | Asp | Ser | Arg | Ser | Gln | His | Arg |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..597  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572844  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| tccttatata  | attaagtttc | accttcttcc | ttaatagctc | ttcaaaacac | ttttgttcaa  | 60  |
| actctctctt  | aNttaaatga | aggtctctcc | tcgtttgaag | tcagcccttc | tcctattgtt  | 120 |
| catgatcctt  | gccacagtga | tgggtccggt | cagggtagag | gcacggacgt | gtgaaacgag  | 180 |
| tagcaacttg  | ttcaatggac | catgtctgag | ctcaagcaat | tgcgctaata | tttgccacaa  | 240 |
| tgaagggttt  | tcagatggtg | actgccgtgg | attccgtcgt | cgctgtttgt | gcaccagacc  | 300 |
| ctgttgatag  | atgatctatt | tatatataat | gaatatatat | tatcaaaaac | taaatagatct | 360 |
| tttctatggt  | ttctatctct | ttgatcattt | tctgactttt | atcctatcgt | ttgcctttga  | 420 |
| aacaacgata  | aggagatcta | aaatctttta | gtccttttgg | cttgagcttt | ctattatcta  | 480 |
| ccaagggttaa | acaataatac | cttttatagt | taccattttc | aaatcttatg | actttttatg  | 540 |
| tatcaaaata  | gattggactt | acacatccaa | tctaaataaa | acatgattat | ccaatct     |     |

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572845  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Val | Ser | Pro | Arg | Leu | Lys | Ser | Ala | Leu | Leu | Leu | Phe | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Ala | Thr | Val | Met | Gly | Pro | Val | Arg | Val | Glu | Ala | Arg | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Cys |
| Glu | Thr | Ser | Ser | Asn | Leu | Phe | Asn | Gly | Pro | Cys | Leu | Ser | Ser | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  | Asn |
| Cys | Ala | Asn | Val | Cys | His | Asn | Glu | Gly | Phe | Ser | Asp | Gly | Asp | Cys |
|     |     |     | 50  |     |     |     |     | 55  |     |     | 60  |     |     | Arg |
| Gly | Phe | Arg | Arg | Arg | Cys | Leu | Cys | Thr | Arg | Pro | Cys |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 61 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..61  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572846  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Ala | Thr | Val | Met | Gly | Pro | Val | Arg | Val | Glu | Ala | Arg | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Cys | Glu | Thr | Ser | Ser | Asn | Leu | Phe | Asn | Gly | Pro | Cys | Leu | Ser | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Asn | Cys | Ala | Asn | Val | Cys | His | Asn | Glu | Gly | Phe | Ser | Asp | Gly | Asp | Cys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Arg | Gly | Phe | Arg | Arg | Arg | Cys | Leu | Cys | Thr | Arg | Pro | Cys |     |     |     |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2409:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 59 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..59  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572847  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

Met Ile Tyr Leu Tyr Ile Met Asn Ile Tyr Tyr Gln Lys Leu Asn Asp  
1                    5                    10                    15  
Leu Phe Tyr Val Phe Tyr Leu Phe Asp His Phe Leu Thr Phe Ile Leu  
                    20                    25                    30  
Ser Phe Ala Phe Glu Thr Thr Ile Arg Arg Ser Lys Ile Phe Lys Ser  
                    35                    40                    45  
Phe Trp Leu Glu Leu Ser Ile Ile Tyr Gln Gly  
50                    55

(2) INFORMATION FOR SEQ ID NO:2410:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1145 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1145  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

aaattttccc cattaatacaa aaaaaaatca aatctctctc tttctctctc taatggcggc 60  
gacattaggg agagaccagt atgtgtacat ggcgaagCtc gccgagcagg cggagcgtta 120  
cgaagagatg gttcaattca tggaacagct cgttacaggc gctactccag cggaagagct 180  
caccgttgaa gagaggaatc tcctctctgt tgcttacaaa aacgtgatcg gatctctacg 240  
cgccgcctgg aggatcttgt ctctgattga gcagaaggaa gagagtagga agaacgacga 300  
gcacgtgtcg cttgtcaagg attacatata taaagttgag tctgagcttt cttctgtttg 360  
ctctggaatc cttaagctcc ttgactcgca tctgatccca tctgctggag cgagtgaatc 420  
taaggtcttt tacttgaaaga tgaaagggtga ttatcatcgg tacatggctg agtttaagtc 480  
tggtgatgag aggaaaaactg ctgctgaaga taccatgctc gcttacaaaag cagctcagga 540  
tatcgagcgt gcggatatgg cacctactca tccgataagg cttgggtctgg ccctgaattt 600  
ctcagtggtc tactatgaga ttctcaattc ttccagacaaa gcttgtaaca tggccaaaca 660  
ggcttttgag gagggcatag ctgagcttga cactctggga gaggaatcct acaaagacag 720  
cactctcata atgcagttgc tgaggggacaa ttttaaccctt tggacctccg atatgcagga 780  
gcagatggac gaggcctgag gatctagatg aaggggggga ggggtgttac gcgatgtttc 840  
tgccacacaa tcgatctcaa aatccccata acctttgctc aaaaactgtg aaaaaagatt 900  
gaagtgttta tgatgattat gattgtgcac agcttgatga tttatctact ctactaaacc 960  
tctgtgctct taatatattat tgtctcgact ctgctcaagc cttaaaaaaca tctttctcct 1020  
taaggctcct ctggttaaat tatgatcctt ctactgtatc gtcaaaaatca agttggaacc 1080  
caaaattcgt ggattttttg tcggtgtgaa actgtgaata ataaaaaccg tcaatgttgt 1140  
tacgt

(2) INFORMATION FOR SEQ ID NO:2411:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 248 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..248

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(D) OTHER INFORMATION: / Ceres Seq. ID 1572853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

Met Ala Ala Thr Leu Gly Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu  
1 5 10 15  
Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln  
20 25 30  
Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr Val Glu Glu Arg  
35 40 45  
Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala  
50 55 60  
Ala Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys  
65 70 75 80  
Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Ile Ser Lys Val Glu  
85 90 95  
Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys Leu Leu Asp Ser  
100 105 110  
His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys Val Phe Tyr Leu  
115 120 125  
Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu Glu Phe Lys Ser Gly  
130 135 140  
Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu Ala Tyr Lys Ala  
145 150 155 160  
Ala Gln Asp Ile Ala Ala Ala Asp Met Ala Pro Thr His Pro Ile Arg  
165 170 175  
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn  
180 185 190  
Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala Phe Glu Glu Ala  
195 200 205  
Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr  
210 215 220  
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp  
225 230 235 240  
Met Gln Glu Gln Met Asp Glu Ala  
245

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1572854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln  
1 5 10 15  
Phe Met Glu Gln Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr  
20 25 30  
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly  
35 40 45  
Ser Leu Arg Ala Ala Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu  
50 55 60  
Glu Ser Arg Lys Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Ile  
65 70 75 80  
Ser Lys Val Glu Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys  
85 90 95  
Leu Leu Asp Ser His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys  
100 105 110  
Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 115                                                             | 120 | 125 |
| Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu |     |     |
| 130                                                             | 135 | 140 |
| Ala Tyr Lys Ala Ala Gln Asp Ile Ala Ala Ala Asp Met Ala Pro Thr |     |     |
| 145                                                             | 150 | 155 |
| His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr |     | 160 |
|                                                                 | 165 | 170 |
| Glu Ile Leu Asn Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala |     | 175 |
|                                                                 | 180 | 185 |
| Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr |     | 190 |
|                                                                 | 195 | 200 |
| Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu |     | 205 |
|                                                                 | 210 | 215 |
| Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala                 |     | 220 |
| 225                                                             | 230 | 235 |

(2) INFORMATION FOR SEQ ID NO:2413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1572855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Val Gln Phe Met Glu Gln Leu Val Thr Gly Ala Thr Pro Ala Glu |     |     |
| 1                                                               | 5   | 10  |
| Glu Leu Thr Val Glu Glu Arg Asn Leu Ser Val Ala Tyr Lys Asn     |     | 15  |
|                                                                 | 20  | 25  |
| Val Ile Gly Ser Leu Arg Ala Ala Trp Arg Ile Leu Ser Ser Ile Glu |     | 30  |
|                                                                 | 35  | 40  |
| Gln Lys Glu Glu Ser Arg Lys Asn Asp Glu His Val Ser Leu Val Lys |     | 45  |
|                                                                 | 50  | 55  |
| Asp Tyr Ile Ser Lys Val Glu Ser Glu Leu Ser Ser Val Cys Ser Gly |     | 60  |
| 65                                                              | 70  | 75  |
| Ile Leu Lys Leu Leu Asp Ser His Leu Ile Pro Ser Ala Gly Ala Ser |     | 80  |
|                                                                 | 85  | 90  |
| Glu Ser Lys Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr |     | 95  |
|                                                                 | 100 | 105 |
| Met Ala Glu Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp |     | 110 |
|                                                                 | 115 | 120 |
| Thr Met Leu Ala Tyr Lys Ala Ala Gln Asp Ile Ala Ala Ala Asp Met |     | 125 |
|                                                                 | 130 | 135 |
| Ala Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val |     | 140 |
| 145                                                             | 150 | 155 |
| Phe Tyr Tyr Glu Ile Leu Asn Ser Ser Asp Lys Ala Cys Asn Met Ala |     | 160 |
|                                                                 | 165 | 170 |
| Lys Gln Ala Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu |     | 175 |
|                                                                 | 180 | 185 |
| Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn |     | 190 |
|                                                                 | 195 | 200 |
| Leu Thr Leu Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala     |     | 205 |
|                                                                 | 210 | 215 |
|                                                                 |     | 220 |

(2) INFORMATION FOR SEQ ID NO:2414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1208 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1208  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572858  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

```
acaagcaaaa aaaattcact ttttgttttt gttaacactc acgtgaaagc ttcgtttcttc 60
ttcaaaccctt ttgaacaatt tctccgatgc cggtaaatac cgggttttacg tttagctacc 120
ggttactctt cctcatcttc cttttgagtt tcgaaacggc acagcgtttg gtcaccgggtg 180
acccaaacga cgaagcatgc ttgacgaatc tccgtcggag tttagaagat cccgcgaata 240
atctccgtaa ctggacaaaa tccttcttca taaatccttg ctccggcttc tcttcttata 300
ttcatggagt catttgcaac aatggcagaa tttacaaact ctcttaaca aatctctctc 360
tccgtggctc aatctctccg tttctctcta attgcacaaa tctccaatcc ctatgcttat 420
cttccaacca gatctccggc gagatccgcg cgcaattaca gtttctcgtt aacctagccg 480
ttcttaatat ctcttctaatt cgtctctccg gtcaaatctc accacaaaatc gctctctgcg 540
cttacttaaa cgtcatcgat cttcacgata accaactctc cggtcaaaatt ccgtttcagt 600
tcgggcttct cgctagatta acggcgtttg atgtctctaa taacaaatta tccggtcaga 660
ttccctcgaa tctggcgcgtg cgtaacggaa acttgccgag atttaacgcg agctcgttta 720
tagggaacaa gaaattgttc gggtatccgt tggaggagat gaagaacaaa ggattgtcga 780
taatggcgat tgttgggatt ggacttgcaa gtggaatcgc gagcttagtg attagcttca 840
ctggagtttg tatatggttg aagattacag agaagaagat ggaggaagaa gaaggaaaga 900
taagtcactc catgcctgtt tactaaacac aaacatttcg ttttttttct tcttaagtat 960
aattaacggt ttctttttatc acataattag tttttttttt ccattttgat caaaagcata 1020
cagcaatagg gagggttcaA ttaagcgaat ttagggttaa ttaatgcttt gatcatatat 1080
acatgtttct ttggttatct ttggatacat attaacaaaa atcacaaggt ttaagcatga 1140
ggtactaagt tattgttgta tagtttttgt agttatgaaa gtgtaattta tagtgacatc 1200
atttatgc
```

(2) INFORMATION FOR SEQ ID NO:2415:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 279 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..279  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

```
Met Pro Val Asn His Arg Phe Thr Phe Ser Tyr Arg Leu Leu Phe Leu
1 5 10 15
Ile Phe Leu Leu Ser Phe Glu Thr Ala Gln Arg Leu Val Thr Gly Asp
20 25 30
Pro Asn Asp Glu Ala Cys Leu Thr Asn Leu Arg Arg Ser Leu Glu Asp
35 40 45
Pro Ala Asn Asn Leu Arg Asn Trp Thr Lys Ser Phe Phe Ile Asn Pro
50 55 60
Cys Ser Gly Phe Ser Ser Tyr Leu His Gly Val Ile Cys Asn Asn Gly
65 70 75 80
Arg Ile Tyr Lys Leu Ser Leu Thr Asn Leu Ser Leu Arg Gly Ser Ile
85 90 95
Ser Pro Phe Leu Ser Asn Cys Thr Asn Leu Gln Ser Leu Asp Leu Ser
100 105 110
Ser Asn Gln Ile Ser Gly Glu Ile Pro Pro Gln Leu Gln Phe Leu Val
115 120 125
Asn Leu Ala Val Leu Asn Leu Ser Ser Asn Arg Leu Ser Gly Gln Ile
130 135 140
Ser Pro Gln Ile Ala Leu Cys Ala Tyr Leu Asn Val Ile Asp Leu His
145 150 155 160
Asp Asn Gln Leu Ser Gly Gln Ile Pro Phe Gln Phe Gly Leu Leu Ala
165 170 175
```

Arg Leu Thr Ala Phe Asp Val Ser Asn Asn Lys Leu Ser Gly Gln Ile  
180 185 190  
Pro Ser Asn Leu Ala Met Arg Asn Gly Asn Leu Pro Arg Phe Asn Ala  
195 200 205  
Ser Ser Phe Ile Gly Asn Lys Lys Leu Phe Gly Tyr Pro Leu Glu Glu  
210 215 220  
Met Lys Asn Lys Gly Leu Ser Ile Met Ala Ile Val Gly Ile Gly Leu  
225 230 235 240  
Gly Ser Gly Ile Ala Ser Leu Val Ile Ser Phe Thr Gly Val Cys Ile  
245 250 255  
Trp Leu Lys Ile Thr Glu Lys Lys Met Glu Glu Glu Glu Gly Lys Ile  
260 265 270  
Ser His Ser Met Pro Val Tyr  
275

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..989
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aagttgaatg tactgatcaa gataacaaat ttatcaaaaa taaatacatc atactggttt   | 60  |
| atgagcaaga aacattgctc agaattatta ccaaataaga tgtttagaaa ccaagactcg   | 120 |
| aaatacttga tcccggtgca gaaagaagcg ccaccggtga caactttacc gatgaaagct   | 180 |
| tcaacggtga aatctccaca caactgtgag gccattctca gagacgcaga tcctccgac    | 240 |
| tctctctcct ctgttaatct ctctgaacag ctacggctctg gtgttttctt gaaacccaag  | 300 |
| aaacagatca aatattgggt ggacgagaga aacagcaact gcttcattgct ctttgcaaaag | 360 |
| aacctctcta taacttggtc tgatgacgct aactattgga cttgggtttac cgaaaaagag  | 420 |
| tcaccaaacg agaatgtgga agctgtggga ttgaaaaacg tttgttggtc cgacatcacg   | 480 |
| ggaaaattcg acacgaggaa cctcactccg gggattgttt acgagggtgt cttcaagggtg  | 540 |
| aagctagagg atccggccta tggatgggac acgccggtga acctaaagct agtcttgCct   | 600 |
| aacggtaagg agacgccaca agagcaaaaag ttgagtttga gggaacttcc aaggtataaa  | 660 |
| tgggtcgatg tcagagttgg cgagttcgta cctgagaaat ccgctgcccg agagatcact   | 720 |
| ttctcaatgt atgagcatgt ggctggtgtt tgggaagaaag ggctctccct caaagggtgtt | 780 |
| gcaattcgct ccaaacagta ataattgtta tggcatagaa aaacataaat ctccatatgc   | 840 |
| accaatggac cttctcaaca tatatttcac atcatgtcat gtgtgtataa taaggttgtt   | 900 |
| ctatcgatatt tttagtttta ataataactt taatgttggt gttgaataaa ctcaaaacga  | 960 |
| gtgttttgaa gggtgttata ttcgaatcg                                     |     |

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

Lys Leu Asn Val Leu Ile Lys Ile Thr Asn Leu Ser Lys Ile Asn Thr  
1 5 10 15  
Ser Tyr Trp Phe Met Ser Lys Lys His Cys Ser Glu Leu Leu Pro Asn  
20 25 30  
Lys Met Phe Arg Asn Gln Asp Ser Lys Tyr Leu Ile Pro Val Gln Lys  
35 40 45

Glu Ala Pro Pro Val Thr Thr Leu Pro Met Lys Ala Ser Thr Val Lys  
50 55 60  
Ser Pro His Asn Cys Glu Ala Ile Leu Arg Asp Ala Asp Pro Pro Ile  
65 70 75 80  
Ser Leu Ser Ser Val Asn Leu Ser Glu Gln Leu Arg Ser Gly Val Phe  
85 90 95  
Leu Lys Pro Lys Lys Gln Ile Lys Tyr Trp Val Asp Glu Arg Asn Ser  
100 105 110  
Asn Cys Phe Met Leu Phe Ala Lys Asn Leu Ser Ile Thr Trp Ser Asp  
115 120 125  
Asp Val Asn Tyr Trp Thr Trp Phe Thr Glu Lys Glu Ser Pro Asn Glu  
130 135 140  
Asn Val Glu Ala Val Gly Leu Lys Asn Val Cys Trp Leu Asp Ile Thr  
145 150 155 160  
Gly Lys Phe Asp Thr Arg Asn Leu Thr Pro Gly Ile Val Tyr Glu Val  
165 170 175  
Val Phe Lys Val Lys Leu Glu Asp Pro Ala Tyr Gly Trp Asp Thr Pro  
180 185 190  
Val Asn Leu Lys Leu Val Leu Pro Asn Gly Lys Glu Thr Pro Gln Glu  
195 200 205  
Gln Lys Leu Ser Leu Arg Glu Leu Pro Arg Tyr Lys Trp Val Asp Val  
210 215 220  
Arg Val Gly Glu Phe Val Pro Glu Lys Ser Ala Ala Gly Glu Ile Thr  
225 230 235 240  
Phe Ser Met Tyr Glu His Val Ala Gly Val Trp Lys Lys Gly Leu Ser  
245 250 255  
Leu Lys Gly Val Ala Ile Arg Pro Lys Gln  
260 265

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1572862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

Met Ser Lys Lys His Cys Ser Glu Leu Leu Pro Asn Lys Met Phe Arg  
1 5 10 15  
Asn Gln Asp Ser Lys Tyr Leu Ile Pro Val Gln Lys Glu Ala Pro Pro  
20 25 30  
Val Thr Thr Leu Pro Met Lys Ala Ser Thr Val Lys Ser Pro His Asn  
35 40 45  
Cys Glu Ala Ile Leu Arg Asp Ala Asp Pro Pro Ile Ser Leu Ser Ser  
50 55 60  
Val Asn Leu Ser Glu Gln Leu Arg Ser Gly Val Phe Leu Lys Pro Lys  
65 70 75 80  
Lys Gln Ile Lys Tyr Trp Val Asp Glu Arg Asn Ser Asn Cys Phe Met  
85 90 95  
Leu Phe Ala Lys Asn Leu Ser Ile Thr Trp Ser Asp Asp Val Asn Tyr  
100 105 110  
Trp Thr Trp Phe Thr Glu Lys Glu Ser Pro Asn Glu Asn Val Glu Ala  
115 120 125  
Val Gly Leu Lys Asn Val Cys Trp Leu Asp Ile Thr Gly Lys Phe Asp  
130 135 140  
Thr Arg Asn Leu Thr Pro Gly Ile Val Tyr Glu Val Val Phe Lys Val  
145 150 155 160  
Lys Leu Glu Asp Pro Ala Tyr Gly Trp Asp Thr Pro Val Asn Leu Lys

165 170 175  
Leu Val Leu Pro Asn Gly Lys Glu Thr Pro Gln Glu Gln Lys Leu Ser  
180 185 190  
Leu Arg Glu Leu Pro Arg Tyr Lys Trp Val Asp Val Arg Val Gly Glu  
195 200 205  
Phe Val Pro Glu Lys Ser Ala Ala Gly Glu Ile Thr Phe Ser Met Tyr  
210 215 220  
Glu His Val Ala Gly Val Trp Lys Lys Gly Leu Ser Leu Lys Gly Val  
225 230 235 240  
Ala Ile Arg Pro Lys Gln  
245

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

Met Phe Arg Asn Gln Asp Ser Lys Tyr Leu Ile Pro Val Gln Lys Glu  
1 5 10 15  
Ala Pro Pro Val Thr Thr Leu Pro Met Lys Ala Ser Thr Val Lys Ser  
20 25 30  
Pro His Asn Cys Glu Ala Ile Leu Arg Asp Ala Asp Pro Pro Ile Ser  
35 40 45  
Leu Ser Ser Val Asn Leu Ser Glu Gln Leu Arg Ser Gly Val Phe Leu  
50 55 60  
Lys Pro Lys Lys Gln Ile Lys Tyr Trp Val Asp Glu Arg Asn Ser Asn  
65 70 75 80  
Cys Phe Met Leu Phe Ala Lys Asn Leu Ser Ile Thr Trp Ser Asp Asp  
85 90 95  
Val Asn Tyr Trp Thr Trp Phe Thr Glu Lys Glu Ser Pro Asn Glu Asn  
100 105 110  
Val Glu Ala Val Gly Leu Lys Asn Val Cys Trp Leu Asp Ile Thr Gly  
115 120 125  
Lys Phe Asp Thr Arg Asn Leu Thr Pro Gly Ile Val Tyr Glu Val Val  
130 135 140  
Phe Lys Val Lys Leu Glu Asp Pro Ala Tyr Gly Trp Asp Thr Pro Val  
145 150 155 160  
Asn Leu Lys Leu Val Leu Pro Asn Gly Lys Glu Thr Pro Gln Glu Gln  
165 170 175  
Lys Leu Ser Leu Arg Glu Leu Pro Arg Tyr Lys Trp Val Asp Val Arg  
180 185 190  
Val Gly Glu Phe Val Pro Glu Lys Ser Ala Ala Gly Glu Ile Thr Phe  
195 200 205  
Ser Met Tyr Glu His Val Ala Gly Val Trp Lys Lys Gly Leu Ser Leu  
210 215 220  
Lys Gly Val Ala Ile Arg Pro Lys Gln  
225 230

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..516

(D) OTHER INFORMATION: / Ceres Seq. ID 1572868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| aaaccctaga | ccctaaatct | tagcgaaatt  | aagcagagca | acatttttct  | aatccgatct  | 60  |
| ccgtcgctcg | cgtcgaatca | gataaaaaatg | gcgaaGcggt | tgatcccgcac | tctcaaccgt  | 120 |
| gtattgggtg | agaagattct | cccaccgtca  | aagaccgtct | ccggcattct  | cctaccggag  | 180 |
| aaatcatctc | agttgaattc | cgggagaggt  | atagcagttg | gtcctggagc  | tagagacaga  | 240 |
| gcagggaatc | taattccggt | ttcgggttaag | gaaggagaca | atgttctttt  | gcctgaattt  | 300 |
| ggtggtactc | aagttaagct | tggagagaaa  | gagttcctat | tgtataggga  | tgaagatatc  | 360 |
| atggctacac | ttcacgagtg | atgtgttaaa  | gagatagaat | ttatgattcc  | tctttgtttt  | 420 |
| gttgtctgca | attgtctgac | atttggtatca | attgttatga | ttgttcttca  | ctgttggtcaa | 480 |
| caagttctta | taattcaata | atctcttttg  | tttggc     |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1572869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Arg | Leu | Ile | Pro | Thr | Leu | Asn | Arg | Val | Leu | Val | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Pro | Pro | Ser | Lys | Thr | Val | Ser | Gly | Ile | Leu | Leu | Pro | Glu | Lys |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Ser | Gln | Leu | Asn | Ser | Gly | Arg | Val | Ile | Ala | Val | Gly | Pro | Gly | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asp | Arg | Ala | Gly | Asn | Leu | Ile | Pro | Val | Ser | Val | Lys | Glu | Gly | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Val | Leu | Leu | Pro | Glu | Phe | Gly | Gly | Thr | Gln | Val | Lys | Leu | Gly | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Glu | Phe | Leu | Leu | Tyr | Arg | Asp | Glu | Asp | Ile | Met | Ala | Thr | Leu | His |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..691

(D) OTHER INFORMATION: / Ceres Seq. ID 1572878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| atcagaaatc | gaaaaatcaa | agttctcaag | aagatatcaa | caaaaaaaaa | gtaaattctt  | 60  |
| taaaatgtcg | atgattccaa | gtttcttcaa | caacaacaga | cgaagcaaca | tctttgatcc  | 120 |
| attctctctt | gacgtatggg | atccattcaa | ggaactaaca | tcatcatcac | tttctcgtga  | 180 |
| gaactcagcg | atcgtgaacg | cacgtgtgga | ctggagagag | acgcctgagg | cgcacgtgtt  | 240 |
| taaagctgac | ttgcctggag | tgaagaagga | ggaagttaaa | gttgagattg | aggaggatag  | 300 |
| tgttttgaag | atcagtggag | agagacacgt | ggagaaagaa | gataagaatg | acacgtggca  | 360 |
| ccgtgtggag | agatcgagtg | gacagtttac | gaggagggtt | aggttgccgg | agaatgtgaa  | 420 |
| gatggatcag | gttaaggctg | cgatggagaa | tggtgtgttg | actgttacgg | tgccctaaggc | 480 |
| tgagRactaa | gaaggctgat | gttaagtcta | ttcagatctc | tggttgagta | atgggttcga  | 540 |
| gttttatcat | cggagttgct | tgtgtttttg | tcatggttat | ggttcattgt | ttacttgagt  | 600 |

gtgtgagtcc tctatctaaa ttataataat ctccgattga gctatgaatt atgatgtatc 660  
ggatacattt gatcctaag aagtatggaa t

(2) INFORMATION FOR SEQ ID NO:2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1572879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Ile | Glu | Lys | Ser | Lys | Phe | Ser | Arg | Arg | Tyr | Gln | Gln | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Lys | Phe | Phe | Lys | Met | Ser | Met | Ile | Pro | Ser | Phe | Phe | Asn | Asn | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Ser | Asn | Ile | Phe | Asp | Pro | Phe | Ser | Leu | Asp | Val | Trp | Asp | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Lys | Glu | Leu | Thr | Ser | Ser | Ser | Leu | Ser | Arg | Glu | Asn | Ser | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Asn | Ala | Arg | Val | Asp | Trp | Arg | Glu | Thr | Pro | Glu | Ala | His | Val | Phe |
| 65  |     |     |     |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |
| Lys | Ala | Asp | Leu | Pro | Gly | Leu | Lys | Lys | Glu | Glu | Val | Lys | Val | Glu | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Glu | Asp | Ser | Val | Leu | Lys | Ile | Ser | Gly | Glu | Arg | His | Val | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asp | Lys | Asn | Asp | Thr | Trp | His | Arg | Val | Glu | Arg | Ser | Ser | Gly | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Thr | Arg | Arg | Phe | Arg | Leu | Pro | Glu | Asn | Val | Lys | Met | Asp | Gln | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ala | Ala | Met | Glu | Asn | Gly | Val | Leu | Thr | Val | Thr | Val | Pro | Lys | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Glu | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1572880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Met | Ile | Pro | Ser | Phe | Phe | Asn | Asn | Arg | Arg | Ser | Asn | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Asp | Pro | Phe | Ser | Leu | Asp | Val | Trp | Asp | Pro | Phe | Lys | Glu | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Ser | Ser | Leu | Ser | Arg | Glu | Asn | Ser | Ala | Ile | Val | Asn | Ala | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Trp | Arg | Glu | Thr | Pro | Glu | Ala | His | Val | Phe | Lys | Ala | Asp | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Leu | Lys | Lys | Glu | Glu | Val | Lys | Val | Glu | Ile | Glu | Glu | Asp | Ser |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Lys | Ile | Ser | Gly | Glu | Arg | His | Val | Glu | Lys | Glu | Asp | Lys | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Thr | Trp | His | Arg | Val | Glu | Arg | Ser | Ser | Gly | Gln | Phe | Thr | Arg | Arg |

100 105 110  
Arg Leu Pro Glu Asn Val Lys Met Asp Gln Val Lys Ala Ala Met Glu  
115 120 125  
Asn Gly Val Leu Thr Val Thr Val Pro Lys Ala Glu Xaa  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1572881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

Met Ile Pro Ser Phe Phe Asn Asn Asn Arg Arg Ser Asn Ile Phe Asp  
1 5 10 15  
Pro Phe Ser Leu Asp Val Trp Asp Pro Phe Lys Glu Leu Thr Ser Ser  
20 25 30  
Ser Leu Ser Arg Glu Asn Ser Ala Ile Val Asn Ala Arg Val Asp Trp  
35 40 45  
Arg Glu Thr Pro Glu Ala His Val Phe Lys Ala Asp Leu Pro Gly Leu  
50 55 60  
Lys Lys Glu Glu Val Lys Val Glu Ile Glu Glu Asp Ser Val Leu Lys  
65 70 75 80  
Ile Ser Gly Glu Arg His Val Glu Lys Glu Asp Lys Asn Asp Thr Trp  
85 90 95  
His Arg Val Glu Arg Ser Ser Gly Gln Phe Thr Arg Arg Phe Arg Leu  
100 105 110  
Pro Glu Asn Val Lys Met Asp Gln Val Lys Ala Ala Met Glu Asn Gly  
115 120 125  
Val Leu Thr Val Thr Val Pro Lys Ala Glu Xaa  
130 135

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1524

(D) OTHER INFORMATION: / Ceres Seq. ID 1572886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

tttttctttc ttcttttctc tgggagtttg ggattttctt gaggggtcttt ttcaattttc 60  
gctccatttt gtacgcatag aactgggttt gtgttttacac acataaagct cttatctttt 120  
ttcttctttc aatcgagaag attatagagc tgagtgactg attggtggtt tcttgagatt 180  
ttaatgggag gttgtttcag caatcggatt aaaacagata ttgcttcacag tacatggcta 240  
agttcgaaat tcttgagtag agatggggagc aagggtcgt cgaccgcttc cttctcttat 300  
atgcctcgaa cagaaggcga gatcttgcaa aatgctaata tcaagaactt tagtctcagt 360  
gaactgaaat ctgcaactag gaatttccgg cctgatagtg tgggttggtga aggtggattt 420  
ggttcggttt tcaaaggctg gatcgatgag tcctctctcg ctcttcttaa accggggacc 480  
Gggattgtca ttgctgtgaa aagacttaac caagaagggt ttcaaggcca tcgagagtgg 540  
ctggctgaga tcaattattht aggccagctg gatcatccta accttggtgaa actgattgga 600  
tactgcttgg aagaggagca caggcttctt gtttacagat ttatgactcg tggtagtctt 660  
gagaatcact tattcagaag aggaacattc tatcagccac ttatcatggaa cacgcgggtt 720  
cgtatggctc ttggtgcagc tagaggactt gcttttcttc acaatgctca accgcaagtt 780  
atataccgag acttcaaaagc atctaacatc ttgctagatt cgaactacaa cgcaaagctt 840



tccgatttcg gtttggctag agatgggtcca atgggtgaca acagccatgt ttctaccaga 900  
gtcatgggaa ctcaggata cgctgctcca gaatatctag ctacaggtca tttatcgggtg 960  
aagagcgatg tatacagttt tgggggttggtg ttactggagt tggtatcagg aagacgagca 1020  
attgacaaga atcaaccagt aggagaacac aatctcgtgg attgggcaag accctactta 1080  
acaaacaaga gaagacttct gcgagtgatg gatcctcgtc tccaagggtca atactcacta 1140  
acccgagctt tgaaaattgc agttcttgca ctcgattgca tatctataga tgccaagagt 1200  
agaccgacca tgaacgaaat cgtcaagaca atggaagaac ttcatatcca gaaggaagca 1260  
tcaaaagagc agcagaatcc tcaaatcagc attgacaaca tcatcaacaa atctccacaa 1320  
gctgtgaatt atcctaggcc ttcaattatg taacaatcct aggcgagcta tttaccgagt 1380  
tttagagatg tatagactct ttaccttctg tctgtttaga tattatgttg tttggtagta 1440  
acaaaagagc tggcaatgta agggagagaa ggaaacttac tagttgtaaa cttaggttct 1500  
cttacaacgt tcacatgtta tccc

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1572887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

Met Gly Gly Cys Phe Ser Asn Arg Ile Lys Thr Asp Ile Ala Ser Ser  
1 5 10 15  
Thr Trp Leu Ser Ser Lys Phe Leu Ser Arg Asp Gly Ser Lys Gly Ser  
20 25 30  
Ser Thr Ala Ser Phe Ser Tyr Met Pro Arg Thr Glu Gly Glu Ile Leu  
35 40 45  
Gln Asn Ala Asn Leu Lys Asn Phe Ser Leu Ser Glu Leu Lys Ser Ala  
50 55 60  
Thr Arg Asn Phe Arg Pro Asp Ser Val Val Gly Glu Gly Gly Phe Gly  
65 70 75 80  
Cys Val Phe Lys Gly Trp Ile Asp Glu Ser Ser Leu Ala Pro Ser Lys  
85 90 95  
Pro Gly Thr Gly Ile Val Ile Ala Val Lys Arg Leu Asn Gln Glu Gly  
100 105 110  
Phe Gln Gly His Arg Glu Trp Leu Ala Glu Ile Asn Tyr Leu Gly Gln  
115 120 125  
Leu Asp His Pro Asn Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Glu  
130 135 140  
Glu His Arg Leu Leu Val Tyr Glu Phe Met Thr Arg Gly Ser Leu Glu  
145 150 155 160  
Asn His Leu Phe Arg Arg Gly Thr Phe Tyr Gln Pro Leu Ser Trp Asn  
165 170 175  
Thr Arg Val Arg Met Ala Leu Gly Ala Ala Arg Gly Leu Ala Phe Leu  
180 185 190  
His Asn Ala Gln Pro Gln Val Ile Tyr Arg Asp Phe Lys Ala Ser Asn  
195 200 205  
Ile Leu Leu Asp Ser Asn Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu  
210 215 220  
Ala Arg Asp Gly Pro Met Gly Asp Asn Ser His Val Ser Thr Arg Val  
225 230 235 240  
Met Gly Thr Gln Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His  
245 250 255  
Leu Ser Val Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu  
260 265 270  
Leu Leu Ser Gly Arg Arg Ala Ile Asp Lys Asn Gln Pro Val Gly Glu  
275 280 285  
His Asn Leu Val Asp Trp Ala Arg Pro Tyr Leu Thr Asn Lys Arg Arg

290 295 300  
Leu Leu Arg Val Met Asp Pro Arg Leu Gln Gly Gln Tyr Ser Leu Thr  
305 310 315 320  
Arg Ala Leu Lys Ile Ala Val Leu Ala Leu Asp Cys Ile Ser Ile Asp  
325 330 335  
Ala Lys Ser Arg Pro Thr Met Asn Glu Ile Val Lys Thr Met Glu Glu  
340 345 350  
Leu His Ile Gln Lys Glu Ala Ser Lys Glu Gln Gln Asn Pro Gln Ile  
355 360 365  
Ser Ile Asp Asn Ile Ile Asn Lys Ser Pro Gln Ala Val Asn Tyr Pro  
370 375 380  
Arg Pro Ser Ile Met  
385

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1572888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

Met Pro Arg Thr Glu Gly Glu Ile Leu Gln Asn Ala Asn Leu Lys Asn  
1 5 10 15  
Phe Ser Leu Ser Glu Leu Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp  
20 25 30  
Ser Val Val Gly Glu Gly Gly Phe Gly Cys Val Phe Lys Gly Trp Ile  
35 40 45  
Asp Glu Ser Ser Leu Ala Pro Ser Lys Pro Gly Thr Gly Ile Val Ile  
50 55 60  
Ala Val Lys Arg Leu Asn Gln Glu Gly Phe Gln Gly His Arg Glu Trp  
65 70 75 80  
Leu Ala Glu Ile Asn Tyr Leu Gly Gln Leu Asp His Pro Asn Leu Val  
85 90 95  
Lys Leu Ile Gly Tyr Cys Leu Glu Glu His Arg Leu Leu Val Tyr  
100 105 110  
Glu Phe Met Thr Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly  
115 120 125  
Thr Phe Tyr Gln Pro Leu Ser Trp Asn Thr Arg Val Arg Met Ala Leu  
130 135 140  
Gly Ala Ala Arg Gly Leu Ala Phe Leu His Asn Ala Gln Pro Gln Val  
145 150 155 160  
Ile Tyr Arg Asp Phe Lys Ala Ser Asn Ile Leu Leu Asp Ser Asn Tyr  
165 170 175  
Asn Ala Lys Leu Ser Asp Phe Gly Leu Ala Arg Asp Gly Pro Met Gly  
180 185 190  
Asp Asn Ser His Val Ser Thr Arg Val Met Gly Thr Gln Gly Tyr Ala  
195 200 205  
Ala Pro Glu Tyr Leu Ala Thr Gly His Leu Ser Val Lys Ser Asp Val  
210 215 220  
Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala  
225 230 235 240  
Ile Asp Lys Asn Gln Pro Val Gly Glu His Asn Leu Val Asp Trp Ala  
245 250 255  
Arg Pro Tyr Leu Thr Asn Lys Arg Arg Leu Leu Arg Val Met Asp Pro  
260 265 270  
Arg Leu Gln Gly Gln Tyr Ser Leu Thr Arg Ala Leu Lys Ile Ala Val  
275 280 285

Leu Ala Leu Asp Cys Ile Ser Ile Asp Ala Lys Ser Arg Pro Thr Met  
290 295 300  
Asn Glu Ile Val Lys Thr Met Glu Glu Leu His Ile Gln Lys Glu Ala  
305 310 315 320  
Ser Lys Glu Gln Gln Asn Pro Gln Ile Ser Ile Asp Asn Ile Ile Asn  
325 330 335  
Lys Ser Pro Gln Ala Val Asn Tyr Pro Arg Pro Ser Ile Met  
340 345 350

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1572889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Met Thr Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly Thr Phe  
1 5 10 15  
Tyr Gln Pro Leu Ser Trp Asn Thr Arg Val Arg Met Ala Leu Gly Ala  
20 25 30  
Ala Arg Gly Leu Ala Phe Leu His Asn Ala Gln Pro Gln Val Ile Tyr  
35 40 45  
Arg Asp Phe Lys Ala Ser Asn Ile Leu Leu Asp Ser Asn Tyr Asn Ala  
50 55 60  
Lys Leu Ser Asp Phe Gly Leu Ala Arg Asp Gly Pro Met Gly Asp Asn  
65 70 75 80  
Ser His Val Ser Thr Arg Val Met Gly Thr Gln Gly Tyr Ala Ala Pro  
85 90 95  
Glu Tyr Leu Ala Thr Gly His Leu Ser Val Lys Ser Asp Val Tyr Ser  
100 105 110  
Phe Gly Val Val Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Ile Asp  
115 120 125  
Lys Asn Gln Pro Val Gly Glu His Asn Leu Val Asp Trp Ala Arg Pro  
130 135 140  
Tyr Leu Thr Asn Lys Arg Arg Leu Leu Arg Val Met Asp Pro Arg Leu  
145 150 155 160  
Gln Gly Gln Tyr Ser Leu Thr Arg Ala Leu Lys Ile Ala Val Leu Ala  
165 170 175  
Leu Asp Cys Ile Ser Ile Asp Ala Lys Ser Arg Pro Thr Met Asn Glu  
180 185 190  
Ile Val Lys Thr Met Glu Glu Leu His Ile Gln Lys Glu Ala Ser Lys  
195 200 205  
Glu Gln Gln Asn Pro Gln Ile Ser Ile Asp Asn Ile Ile Asn Lys Ser  
210 215 220  
Pro Gln Ala Val Asn Tyr Pro Arg Pro Ser Ile Met  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..583

(D) OTHER INFORMATION: / Ceres Seq. ID 1572890

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aaaaacaaaa | ataaaaaaaa | catcgacaaa | gaaaataaaa | gatttgtaga  | atcaactaag | 60  |
| aaaatggcta | gcactatgat | gactacattg | cctcagttca | atgggtcttcg | agccaccaaa | 120 |
| atctctgcag | ctcctgtaca | aggcctggca | agtgttcagc | ccatgagacg  | caagggaat  | 180 |
| ggagctttgg | gtgcaaagtg | tgacttcac  | ggttcatcaa | caaattctgat | aatggtaacg | 240 |
| tcgacgaccc | tgattttgtt | cgcggggaga | ttcggacttg | cgccatcagc  | caataggaag | 300 |
| gcgacagctg | gacttaggtt | ggaggcacgt | gactcaggtc | tacaaacggg  | tgacccggcc | 360 |
| gggttcacgc | ttgcggacac | tttggcttgt | ggcaccgttg | gtcatatcat  | cggtgtagga | 420 |
| gttgtccttg | gccttaaaaa | cattggtgct | atttgaagtt | cctaaagctc  | ttttatttgt | 480 |
| atttgtaaaa | Atttgtagat | ttttataaca | atattctcat | gcacctgaac  | gagatcta   | 540 |
| ggattttaca | agtctttatg | tttatcttat | aatgttgtat | cgc         |            |     |

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Asn | Lys | Asn | Lys | Lys | Asn | Ile | Ala | Gln | Glu | Asn | Lys | Arg | Phe | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Ser | Thr | Lys | Lys | Met | Ala | Ser | Thr | Met | Met | Thr | Thr | Leu | Pro | Gln |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |  |
| Phe | Asn | Gly | Leu | Arg | Ala | Thr | Lys | Ile | Ser | Ala | Ala | Pro | Val | Gln | Gly |  |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Leu | Ala | Ser | Val | Gln | Pro | Met | Arg | Arg | Lys | Gly | Asn | Gly | Ala | Leu | Gly |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Lys | Cys | Asp | Phe | Ile | Gly | Ser | Ser | Thr | Asn | Leu | Ile | Met | Val | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Thr | Thr | Leu | Ile | Leu | Phe | Ala | Gly | Arg | Phe | Gly | Leu | Ala | Pro | Ser |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Asn | Arg | Lys | Ala | Thr | Ala | Gly | Leu | Arg | Leu | Glu | Ala | Arg | Asp | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Leu | Gln | Thr | Gly | Asp | Pro | Ala | Gly | Phe | Thr | Leu | Ala | Asp | Thr | Leu |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Ala | Cys | Gly | Thr | Val | Gly | His | Ile | Ile | Gly | Val | Gly | Val | Val | Leu | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Lys | Asn | Ile | Gly | Ala | Ile |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Thr | Met | Met | Thr | Thr | Leu | Pro | Gln | Phe | Asn | Gly | Leu | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Thr | Lys | Ile | Ser | Ala | Ala | Pro | Val | Gln | Gly | Leu | Ala | Ser | Val | Gln |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Met | Arg | Arg | Lys | Gly | Asn | Gly | Ala | Leu | Gly | Ala | Lys | Cys | Asp | Phe |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     |     | 45  |     |     |  |

Ile Gly Ser Ser Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile  
50 55 60  
Leu Phe Ala Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala  
65 70 75 80  
Thr Ala Gly Leu Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly  
85 90 95  
Asp Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val  
100 105 110  
Gly His Ile Ile Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly  
115 120 125  
Ala Ile  
130

(2) INFORMATION FOR SEQ ID NO:2433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile  
1 5 10 15  
Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg  
20 25 30  
Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser  
35 40 45  
Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile Leu Phe Ala Gly  
50 55 60  
Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu  
65 70 75 80  
Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly  
85 90 95  
Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val Gly His Ile Ile  
100 105 110  
Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly Ala Ile  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..661
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| attttcccgag | tgagaaatgg | cgacgaagga | accagaatct | gtttacgagt | taagcatcga  | 60  |
| ggatgcaaaa  | gggaacaact | tagcactcag | tcaatacaaa | gacaaagttc | ttttaattgt  | 120 |
| caatgttgct  | tccaaatgtg | ggatgacaaa | ctcaaactac | actgaattga | atgagcttta  | 180 |
| caacagggtat | aaagataaag | gtctggagat | tctagcattt | ccttgtaacc | agtttggtga  | 240 |
| cgaggaaccg  | ggaactaatg | accaaattac | tgactttgtt | tgtactcgct | tcaaactctga | 300 |
| attccccatt  | ttcaacaaga | ttgaagtaaa | cggagagaat | gcttctcctc | tgtataagtt  | 360 |
| cctgaagaaa  | ggcaaatggg | gaatcttcgg | cgatgacatt | caatggaact | ttgctaagtt  | 420 |
| tottgttgac  | aaaaacggtc | aagctgtaca | acgttattat | ccaactactt | ccctcttac   | 480 |
| acttgagcat  | gacataaaga | atcttctgaa | tatctcctga | atgatgaagc | tttgttgctg  | 540 |

aatcgtattg tatttgatta tgaacctctc tcattcaatA aagagCcatg acattgactt 600  
ggattgatta gttctgtttg agagccaaat cggttattta gataaaccag cattattatc 660  
c

(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Lys | Glu | Pro | Glu | Ser | Val | Tyr | Glu | Leu | Ser | Ile | Glu | Asp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Lys | Gly | Asn | Asn | Leu | Ala | Leu | Ser | Gln | Tyr | Lys | Asp | Lys | Val | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Ile | Val | Asn | Val | Ala | Ser | Lys | Cys | Gly | Met | Thr | Asn | Ser | Asn | Tyr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Glu | Leu | Asn | Glu | Leu | Tyr | Asn | Arg | Tyr | Lys | Asp | Lys | Gly | Leu | Glu |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Leu | Ala | Phe | Pro | Cys | Asn | Gln | Phe | Gly | Asp | Glu | Glu | Pro | Gly | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asn | Asp | Gln | Ile | Thr | Asp | Phe | Val | Cys | Thr | Arg | Phe | Lys | Ser | Glu | Phe |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Pro | Ile | Phe | Asn | Lys | Ile | Glu | Val | Asn | Gly | Glu | Asn | Ala | Ser | Pro | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Lys | Phe | Leu | Lys | Lys | Gly | Lys | Trp | Gly | Ile | Phe | Gly | Asp | Asp | Ile |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Gln | Trp | Asn | Phe | Ala | Lys | Phe | Leu | Val | Asp | Lys | Asn | Gly | Gln | Ala | Val |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gln | Arg | Tyr | Tyr | Pro | Thr | Thr | Ser | Pro | Leu | Thr | Leu | Glu | His | Asp | Ile |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Lys | Asn | Leu | Leu | Asn | Ile | Ser |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Asn | Ser | Asn | Tyr | Thr | Glu | Leu | Asn | Glu | Leu | Tyr | Asn | Arg | Tyr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Asp | Lys | Gly | Leu | Glu | Ile | Leu | Ala | Phe | Pro | Cys | Asn | Gln | Phe | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Glu | Glu | Pro | Gly | Thr | Asn | Asp | Gln | Ile | Thr | Asp | Phe | Val | Cys | Thr |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Arg | Phe | Lys | Ser | Glu | Phe | Pro | Ile | Phe | Asn | Lys | Ile | Glu | Val | Asn | Gly |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Asn | Ala | Ser | Pro | Leu | Tyr | Lys | Phe | Leu | Lys | Lys | Gly | Lys | Trp | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ile | Phe | Gly | Asp | Asp | Ile | Gln | Trp | Asn | Phe | Ala | Lys | Phe | Leu | Val | Asp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |

Lys Asn Gly Gln Ala Val Gln Arg Tyr Tyr Pro Thr Thr Ser Pro Leu  
100 105 110  
Thr Leu Glu His Asp Ile Lys Asn Leu Leu Asn Ile Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..879
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

gcaaacgcta gttaccggaa gacacgtctt gagttttogca gcatctctct cctctcctct 60  
gttcataatct ctcttttagaa atttctcaat gaacatactc aacagattgg gtttgggatac 120  
aagtgggcaa accaatatgg atccttctcc gatcgctcag ggaaatgacg atgacacacc 180  
ggcgccgggg aatcagtttg cccaattcgg agctggatgt ttctgggggtg tcgagctggc 240  
gtttcagaga gtcccagggt tgactcagac cgaggctgga tacaccaag ggaccgtaca 300  
caatccttca tacggagatg tttgttctgg taccacaggc cattcgaggg ttgttagggg 360  
tcaatatgat cttaacgatt gcacctatga gtctctgctt gatttggtct ggtctaggca 420  
tgatccacc actttgaatc gccagggaaa tgacgtggga aCccaataca gatctggaat 480  
atacttctac acaccgagc aggagaaact agcccgtag tcaattgaac gtcaccagca 540  
acaaatggag agaaagatca tgactgaaat cttgccagct aagaaattct acagagctga 600  
agagcatcat caacagtatc tgtcaaaagg tgggcgggtt ggccaagggc aatccactgc 660  
caaaggctgc aacgacccaa tccgtgttta cggttaataa gctgctttcc tctgtccctc 720  
tccgaaaaca gaggacttag catcaaagga cttgtgtgtc aaatagattg tgtaaaactt 780  
tgactaagtt gttcacacgc tatgtaaacta cttctttgga atttcattcg caatgttgta 840  
atattgatgt tatactctat aaacataaac caaataatc

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

Gln Thr Leu Val Thr Gly Arg His Val Leu Ser Phe Ala Ala Ser Leu  
1 5 10 15  
Ser Ser Pro Leu Phe Ile Ser Leu Phe Arg Asn Phe Ser Met Asn Ile  
20 25 30  
Leu Asn Arg Leu Gly Leu Gly Ser Ser Gly Gln Thr Asn Met Asp Pro  
35 40 45  
Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala Pro Gly Asn  
50 55 60  
Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val Glu Leu Ala  
65 70 75 80  
Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly Tyr Thr Gln  
85 90 95  
Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser Gly Thr Thr  
100 105 110  
Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn Asp Cys Thr  
115 120 125  
Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp Pro Thr Thr  
130 135 140

Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Ser Gly Ile  
145 150 155 160  
Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu Ser Leu Glu  
165 170 175  
Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu Ile Leu Pro  
180 185 190  
Ala Lys Lys Phe Tyr Arg Ala Glu Glu His His Gln Gln Tyr Leu Ser  
195 200 205  
Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys Gly Cys Asn  
210 215 220  
Asp Pro Ile Arg Cys Tyr Gly  
225 230

(2) INFORMATION FOR SEQ ID NO:2439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met Asn Ile Leu Asn Arg Leu Gly Leu Gly Ser Ser Gly Gln Thr Asn  
1 5 10 15  
Met Asp Pro Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala  
20 25 30  
Pro Gly Asn Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val  
35 40 45  
Glu Leu Ala Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly  
50 55 60  
Tyr Thr Gln Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser  
65 70 75 80  
Gly Thr Thr Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn  
85 90 95  
Asp Cys Thr Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp  
100 105 110  
Pro Thr Thr Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg  
115 120 125  
Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu  
130 135 140  
Ser Leu Glu Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu  
145 150 155 160  
Ile Leu Pro Ala Lys Lys Phe Tyr Arg Ala Glu Glu His His Gln Gln  
165 170 175  
Tyr Leu Ser Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys  
180 185 190  
Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly  
195 200

(2) INFORMATION FOR SEQ ID NO:2440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572900

2025 RELEASE UNDER E.O. 14176



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Pro | Ser | Pro | Ile | Ala | Gln | Gly | Asn | Asp | Asp | Asp | Thr | Pro | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Gly | Asn | Gln | Phe | Ala | Gln | Phe | Gly | Ala | Gly | Cys | Phe | Trp | Gly | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Ala | Phe | Gln | Arg | Val | Pro | Gly | Val | Thr | Gln | Thr | Glu | Ala | Gly |
|     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Tyr | Thr | Gln | Gly | Thr | Val | His | Asn | Pro | Ser | Tyr | Gly | Asp | Val | Cys | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Thr | Thr | Gly | His | Ser | Glu | Val | Val | Arg | Val | Gln | Tyr | Asp | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Cys | Thr | Tyr | Glu | Ser | Leu | Leu | Asp | Leu | Phe | Trp | Ser | Arg | His | Asp |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Pro | Thr | Thr | Leu | Asn | Arg | Gln | Gly | Asn | Asp | Val | Gly | Thr | Gln | Tyr | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly | Ile | Tyr | Phe | Tyr | Thr | Pro | Glu | Gln | Glu | Lys | Leu | Ala | Arg | Glu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Leu | Glu | Arg | His | Gln | Gln | Gln | Met | Glu | Arg | Lys | Ile | Met | Thr | Glu |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Leu | Pro | Ala | Lys | Lys | Phe | Tyr | Arg | Ala | Glu | Glu | His | His | Gln | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Leu | Ser | Lys | Gly | Arg | Phe | Gly | Gln | Gly | Gln | Ser | Thr | Ala | Lys |     |
|     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| Gly | Cys | Asn | Asp | Pro | Ile | Arg | Cys | Tyr | Gly |     |     |     |     |     |     |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| acatgttttg | ctctgcttct | ctctttatct | tcttcttcat | cttttgtcac  | tcttttcttc  | 60   |
| tgctctaaac | tttttctttt | cgctgcaaaa | aattttccca | ggaatatatt  | ttaaaagaaa  | 120  |
| tttcatccct | aaataagaaa | aaagcatctc | cttctttagt | gtcctccttc  | accaaactct  | 180  |
| tgattccata | agcatatatt | aaaaaagctc | tctgctttct | tcaactttcc  | cgggaaaatc  | 240  |
| ttcttggtac | aaagcatcaa | tctcttggtt | taccagtttt | ctctctttat  | tccttttttg  | 300  |
| ccctttactt | ttcctaactt | tgggtctttt | atataaacac | acgacacaaa  | gaagaacaca  | 360  |
| cataagttaa | aactattaca | acagttttta | agagagagat | ttaaaaaatg  | gagacagaga  | 420  |
| agaaagtttc | tctoccaa   | atcttaacga | tctctgttac | tgatccttac  | gcaacagatt  | 480  |
| cgtcaagcga | cgaagaagaa | gaagttgatt | ttgatgcatt | atctacaaaa  | cgacgtcgtg  | 540  |
| ttaagaagta | cgtgaaggaa | gtggtgcttg | attcgggtgg | ttctgataaa  | gagaagccga  | 600  |
| tgaagaagaa | gagaaagaag | cgcgttggtt | ctgttccagt | ggttggttac  | acagcgacga  | 660  |
| ggaagtctcg | tggagtga   | caaagacogt | ggggaaaatg | ggcggcgag   | attagagatc  | 720  |
| cgagtagacg | tgttagggtt | tggtagggtt | cttttgacac | ggcggaggaa  | gctgccattg  | 780  |
| tttacgataa | cgcagctatt | cagctacgtg | gtcctaacgc | agagcttaac  | ttccctctctg | 840  |
| ctccggtgac | ggagaatggt | gaagaagctt | cgacggaggt | gaaaggagtt  | tcggatttta  | 900  |
| tcattggcgg | tggagaatat | cttcgttcgc | cggtttctgt | tctcgaatct  | ccgttctccg  | 960  |
| gcgagcttac | tgcggtwaaa | gaggagtttg | tccgtgtatc | gacggcgag   | attgtggtta  | 1020 |
| aaaaggagcc | gtcttttaac | ggttcagatt | tctcggcgcc | gttggttctcg | gacgacgacg  | 1080 |
| tttttggttt | ctcgacgtcg | atgagtga   | gtttcggcgg | cgattttatt  | ggagataatc  | 1140 |
| tttttgcgga | tatgagtttt | ggatccgggt | ttggattcgg | gtctgggtct  | ggattctcca  | 1200 |
| gctggcacgt | tgaggaccaa | tHttcaagat | attggggatt | tattcgagtc  | ggatcctgtc  | 1260 |
| ttaaactgtt | aagaaataac | tggcgcgttt | acggcgttta | gtgaagtttt  | gttaccggcg  | 1320 |
| acggcgagga | ttaaaaaaa  | acggcgattt | attttttgaa | tgaagatttg  | ttaaatatat  | 1380 |
| taaacttttt | tgtaaactta | ttaatggtga | ttttattttt | aaataaaaact | aatggtaaat  | 1440 |

ggt

(2) INFORMATION FOR SEQ ID NO:2442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1572906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Thr | Glu | Lys | Lys | Val | Ser | Leu | Pro | Arg | Ile | Leu | Arg | Ile | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Thr | Asp | Pro | Tyr | Ala | Thr | Asp | Ser | Ser | Ser | Asp | Glu | Glu | Glu | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Asp | Phe | Asp | Ala | Leu | Ser | Thr | Lys | Arg | Arg | Arg | Val | Lys | Lys | Tyr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Lys | Glu | Val | Val | Leu | Asp | Ser | Val | Val | Ser | Asp | Lys | Glu | Lys | Pro |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Met | Lys | Lys | Lys | Arg | Lys | Lys | Arg | Val | Val | Thr | Val | Pro | Val | Val | Val |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |  |
| Thr | Thr | Ala | Thr | Arg | Lys | Phe | Arg | Gly | Val | Arg | Gln | Arg | Pro | Trp | Gly |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Lys | Trp | Ala | Ala | Glu | Ile | Arg | Asp | Pro | Ser | Arg | Arg | Val | Arg | Val | Trp |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Gly | Thr | Phe | Asp | Thr | Ala | Glu | Ala | Ala | Ile | Val | Tyr | Asp | Asn |     |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Ala | Ile | Gln | Leu | Arg | Gly | Pro | Asn | Ala | Glu | Leu | Asn | Phe | Pro | Pro |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Pro | Val | Thr | Glu | Asn | Val | Glu | Glu | Ala | Ser | Thr | Glu | Val | Lys | Gly |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Val | Ser | Asp | Phe | Ile | Ile | Gly | Gly | Gly | Glu | Tyr | Leu | Arg | Ser | Pro | Val |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ser | Val | Leu | Glu | Ser | Pro | Phe | Ser | Gly | Glu | Ser | Thr | Ala | Xaa | Lys | Glu |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Glu | Phe | Val | Gly | Val | Ser | Thr | Ala | Glu | Ile | Val | Val | Lys | Lys | Glu | Pro |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Ser | Phe | Asn | Gly | Ser | Asp | Phe | Ser | Ala | Pro | Leu | Phe | Ser | Asp | Asp | Asp |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Val | Phe | Gly | Phe | Ser | Thr | Ser | Met | Ser | Glu | Ser | Phe | Gly | Gly | Asp | Leu |  |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |  |
| Phe | Gly | Asp | Asn | Leu | Phe | Ala | Asp | Met | Ser | Phe | Gly | Ser | Gly | Phe | Gly |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Phe | Gly | Ser | Gly | Ser | Gly | Phe | Ser | Ser | Trp | His | Val | Glu | Asp | His | Xaa |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ser | Arg | Tyr | Trp | Gly | Phe | Ile | Arg | Val | Gly | Ser | Cys | Leu | Asn | Cys | Leu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |  |
| Arg | Asn | Asn | Trp | Pro | Phe | Asn | Gly | Val |     |     |     |     |     |     |     |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

Met Lys Lys Lys Arg Lys Lys Arg Val Val Thr Val Pro Val Val Val  
1 5 10 15  
Thr Thr Ala Thr Arg Lys Phe Arg Gly Val Arg Gln Arg Pro Trp Gly  
20 25 30  
Lys Trp Ala Ala Glu Ile Arg Asp Pro Ser Arg Arg Val Arg Val Trp  
35 40 45  
Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Val Tyr Asp Asn  
50 55 60  
Ala Ala Ile Gln Leu Arg Gly Pro Asn Ala Glu Leu Asn Phe Pro Pro  
65 70 75 80  
Ala Pro Val Thr Glu Asn Val Glu Glu Ala Ser Thr Glu Val Lys Gly  
85 90 95  
Val Ser Asp Phe Ile Ile Gly Gly Gly Glu Tyr Leu Arg Ser Pro Val  
100 105 110  
Ser Val Leu Glu Ser Pro Phe Ser Gly Glu Ser Thr Ala Xaa Lys Glu  
115 120 125  
Glu Phe Val Gly Val Ser Thr Ala Glu Ile Val Val Lys Lys Glu Pro  
130 135 140  
Ser Phe Asn Gly Ser Asp Phe Ser Ala Pro Leu Phe Ser Asp Asp Asp  
145 150 155 160  
Val Phe Gly Phe Ser Thr Ser Met Ser Glu Ser Phe Gly Gly Asp Leu  
165 170 175  
Phe Gly Asp Asn Leu Phe Ala Asp Met Ser Phe Gly Ser Gly Phe Gly  
180 185 190  
Phe Gly Ser Gly Ser Gly Phe Ser Ser Trp His Val Glu Asp His Xaa  
195 200 205  
Ser Arg Tyr Trp Gly Phe Ile Arg Val Gly Ser Cys Leu Asn Cys Leu  
210 215 220  
Arg Asn Asn Trp Pro Phe Asn Gly Val  
225 230

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1284

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

caagatgatac aagattctgt tagattattg gccgttgagg gttgtgctgc tcttgggaaa 60  
ttgttggagc ctcaggattg tgtccaacac attcttcccg tgattgttaa tttctcgag 120  
gataagtctt ggcgtgtgcg ctatatggtt gcaaatcaac tctacgagct ttgtgaagcc 180  
gtgggacctg agcctactag gacggagctg gtgcctgcat atgtgcgcct acttcgtgat 240  
aatgaagctg aagtacgcat agcagctgcc ggaaaagtta caaagttttg tcggattcta 300  
aaccctgaaa ttgctatcca gcacattctc ccctgtgtga aggagctatc atcagactct 360  
tctcagcatg tcagatctgc attggcctca gttataatgg gaatggctcc agtcttgggt 420  
aaggatgcaa caattgagca tctccttcca atctttcttt ctctattgaa agatgagttc 480  
cCggatgtac gcttgaacat tatcagcaaa cttgaccaag tgaatcagggt tattgggatt 540  
gatctactat cacaatcctt gttgccagct attgtagaAc ttgctgaaga tagacactgg 600  
agagtaagac ttgctataat cgagtataat cctttgttgg caagtcagtt aggtgttgGc 660  
ttcttTgacg ataagcttgg tgctcttTgc atgcaatggT Tacaagacaa ggttcactca 720  
atcCgcgatg ctgctgctaa caatctcaag cggcttgctg aggaatttgg tcctgaatgg 780  
gcaatgcaac atatagttcc tcaggttctt gagatgggta acaaccctca ctatctctac 840  
cgaatgacca ttttgcgctg ggtgtctctt cttgcacctg taatgggctc agagattaca 900  
tgctctaagc tcttacctgt agtaatgact gcattctaaag acagagttcc aaacatcaaa 960  
ttcaacgtcg ctaaagtact tcaatccctc attccaatag ttgatcaatc gggttggagg 1020

aagacgattc gtcctgggct tgtggagcta agcgaggatc cagatgttga tgtcaggttt 1080  
ttcgcaaac aagctctaca atctattgac aatgtgatga tgtctagcta aaaacattag 1140  
atcttgctc tctgcttata atcgttttct atttgattga aaaaaaaac aaatctcaag 1200  
acttttgtaa cgtagtagtg gattctcgtc ttgtgttttt tattacacgc aaactactag 1260  
agtgcctcgg tacgggtttt gtcc

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1572913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asp | Asp | Gln | Asp | Ser | Val | Arg | Leu | Leu | Ala | Val | Glu | Gly | Cys | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Gly | Lys | Leu | Leu | Glu | Pro | Gln | Asp | Cys | Val | Gln | His | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Val | Ile | Val | Asn | Phe | Ser | Gln | Asp | Lys | Ser | Trp | Arg | Val | Arg | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Val | Ala | Asn | Gln | Leu | Tyr | Glu | Leu | Cys | Glu | Ala | Val | Gly | Pro | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Thr | Arg | Thr | Glu | Leu | Val | Pro | Ala | Tyr | Val | Arg | Leu | Leu | Arg | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Glu | Ala | Glu | Val | Arg | Ile | Ala | Ala | Ala | Gly | Lys | Val | Thr | Lys | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Arg | Ile | Leu | Asn | Pro | Glu | Ile | Ala | Ile | Gln | His | Ile | Leu | Pro | Cys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Lys | Glu | Leu | Ser | Ser | Asp | Ser | Ser | Gln | His | Val | Arg | Ser | Ala | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ser | Val | Ile | Met | Gly | Met | Ala | Pro | Val | Leu | Gly | Lys | Asp | Ala | Thr |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Glu | His | Leu | Leu | Pro | Ile | Phe | Leu | Ser | Leu | Leu | Lys | Asp | Glu | Phe |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Pro | Asp | Val | Arg | Leu | Asn | Ile | Ile | Ser | Lys | Leu | Asp | Gln | Val | Asn | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Ile | Gly | Ile | Asp | Leu | Leu | Ser | Gln | Ser | Leu | Leu | Pro | Ala | Ile | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Glu | Leu | Ala | Glu | Asp | Arg | His | Trp | Arg | Val | Arg | Leu | Ala | Ile | Ile | Glu |
|     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Tyr | Ile | Pro | Leu | Leu | Ala | Ser | Gln | Leu | Gly | Val | Gly | Phe | Phe | Asp | Asp |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Lys | Leu | Gly | Ala | Leu | Cys | Met | Gln | Trp | Leu | Gln | Asp | Lys | Val | His | Ser |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Arg | Asp | Ala | Ala | Ala | Asn | Asn | Leu | Lys | Arg | Leu | Ala | Glu | Glu | Phe |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Gly | Pro | Glu | Trp | Ala | Met | Gln | His | Ile | Val | Pro | Gln | Val | Leu | Glu | Met |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Val | Asn | Asn | Pro | His | Tyr | Leu | Tyr | Arg | Met | Thr | Ile | Leu | Arg | Ala | Val |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Leu | Leu | Ala | Pro | Val | Met | Gly | Ser | Glu | Ile | Thr | Cys | Ser | Lys | Leu |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Leu | Pro | Val | Val | Met | Thr | Ala | Ser | Lys | Asp | Arg | Val | Pro | Asn | Ile | Lys |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Phe | Asn | Val | Ala | Lys | Val | Leu | Gln | Ser | Leu | Ile | Pro | Ile | Val | Asp | Gln |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ser | Val | Val | Glu | Lys | Thr | Ile | Arg | Pro | Gly | Leu | Val | Glu | Leu | Ser | Glu |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |

Asp Pro Asp Val Asp Val Arg Phe Phe Ala Asn Gln Ala Leu Gln Ser  
355 360 365  
Ile Asp Asn Val Met Met Ser Ser  
370 375

(2) INFORMATION FOR SEQ ID NO:2446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..328
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

Met Val Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu  
1 5 10 15  
Pro Thr Arg Thr Glu Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp  
20 25 30  
Asn Glu Ala Glu Val Arg Ile Ala Ala Gly Lys Val Thr Lys Phe  
35 40 45  
Cys Arg Ile Leu Asn Pro Glu Ile Ala Ile Gln His Ile Leu Pro Cys  
50 55 60  
Val Lys Glu Leu Ser Ser Asp Ser Ser Gln His Val Arg Ser Ala Leu  
65 70 75 80  
Ala Ser Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr  
85 90 95  
Ile Glu His Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe  
100 105 110  
Pro Asp Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln  
115 120 125  
Val Ile Gly Ile Asp Leu Leu Ser Gln Ser Leu Leu Pro Ala Ile Val  
130 135 140  
Glu Leu Ala Glu Asp Arg His Trp Arg Val Arg Leu Ala Ile Ile Glu  
145 150 155 160  
Tyr Ile Pro Leu Leu Ala Ser Gln Leu Gly Val Gly Phe Phe Asp Asp  
165 170 175  
Lys Leu Gly Ala Leu Cys Met Gln Trp Leu Gln Asp Lys Val His Ser  
180 185 190  
Ile Arg Asp Ala Ala Ala Asn Asn Leu Lys Arg Leu Ala Glu Glu Phe  
195 200 205  
Gly Pro Glu Trp Ala Met Gln His Ile Val Pro Gln Val Leu Glu Met  
210 215 220  
Val Asn Asn Pro His Tyr Leu Tyr Arg Met Thr Ile Leu Arg Ala Val  
225 230 235 240  
Ser Leu Leu Ala Pro Val Met Gly Ser Glu Ile Thr Cys Ser Lys Leu  
245 250 255  
Leu Pro Val Val Met Thr Ala Ser Lys Asp Arg Val Pro Asn Ile Lys  
260 265 270  
Phe Asn Val Ala Lys Val Leu Gln Ser Leu Ile Pro Ile Val Asp Gln  
275 280 285  
Ser Val Val Glu Lys Thr Ile Arg Pro Gly Leu Val Glu Leu Ser Glu  
290 295 300  
Asp Pro Asp Val Asp Val Arg Phe Phe Ala Asn Gln Ala Leu Gln Ser  
305 310 315 320  
Ile Asp Asn Val Met Met Ser Ser  
325

(2) INFORMATION FOR SEQ ID NO:2447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..244  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572915  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr Ile Glu His Leu  
1 5 10 15  
Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe Pro Asp Val Arg  
20 25 30  
Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln Val Ile Gly Ile  
35 40 45  
Asp Leu Leu Ser Gln Ser Leu Leu Pro Ala Ile Val Glu Leu Ala Glu  
50 55 60  
Asp Arg His Trp Arg Val Arg Leu Ala Ile Ile Glu Tyr Ile Pro Leu  
65 70 75 80  
Leu Ala Ser Gln Leu Gly Val Gly Phe Phe Asp Asp Lys Leu Gly Ala  
85 90 95  
Leu Cys Met Gln Trp Leu Gln Asp Lys Val His Ser Ile Arg Asp Ala  
100 105 110  
Ala Ala Asn Asn Leu Lys Arg Leu Ala Glu Glu Phe Gly Pro Glu Trp  
115 120 125  
Ala Met Gln His Ile Val Pro Gln Val Leu Glu Met Val Asn Asn Pro  
130 135 140  
His Tyr Leu Tyr Arg Met Thr Ile Leu Arg Ala Val Ser Leu Leu Ala  
145 150 155 160  
Pro Val Met Gly Ser Glu Ile Thr Cys Ser Lys Leu Leu Pro Val Val  
165 170 175  
Met Thr Ala Ser Lys Asp Arg Val Pro Asn Ile Lys Phe Asn Val Ala  
180 185 190  
Lys Val Leu Gln Ser Leu Ile Pro Ile Val Asp Gln Ser Val Val Glu  
195 200 205  
Lys Thr Ile Arg Pro Gly Leu Val Glu Leu Ser Glu Asp Pro Asp Val  
210 215 220  
Asp Val Arg Phe Phe Ala Asn Gln Ala Leu Gln Ser Ile Asp Asn Val  
225 230 235 240  
Met Met Ser Ser

(2) INFORMATION FOR SEQ ID NO:2448:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 578 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..578  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572916  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

aaaaagaaaa aggttccttt ttttgacttt gtatccgtag atcatcttct Atctttcttct 60  
tccagagttt tatccttata cgttccatca aattctctct ctaagcaaag atgaataaag 120  
gaagcatctt taagatggac aacgatttcg aaaagagaaa aggaagaaga agaaggagaa 180  
gaagaagcca actactgaag ttgaggtaaa ggaggaagag aagaaaagggt ttatggagaa 240  
gttgaaagag aagcttcctg gacacaagaa acctgaagac ggttcagccg tcgctgcggc 300  
accggtgggt gttcctcctc ctgtgagaga agcgcattcca gtggagaaga aagggattct 360  
tgagaagatt aaggagaagc ttccaggata ccaccctaag accaccgtag aggaggagaa 420  
gaaagataaa gaataagaag attatcatta aagatattaa gaataatgat ggttgatttg 480

ctttgttttt atttttttta ttgtgatgat tgatcatctt ttgcttttgt gatgtgtaag 540

tttgttggt tttttgttga ttacaatttc ttattttc

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1572917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

Lys Lys Lys Lys Val Pro Phe Phe Asp Phe Val Ser Val Asp His Leu  
1 5 10 15  
Leu Ser Ser Ser Ser Arg Val Leu Ser Leu Ser Val Pro Ser Asn Ser  
20 25 30  
Leu Ser Lys Gln Arg  
35

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1572918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

Met Glu Lys Leu Lys Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp  
1 5 10 15  
Gly Ser Ala Val Ala Ala Ala Pro Val Val Val Pro Pro Pro Val Arg  
20 25 30  
Glu Ala His Pro Val Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu  
35 40 45  
Lys Leu Pro Gly Tyr His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys  
50 55 60  
Asp Lys Glu  
65

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1572927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

avaGWacaac aacaacaaac aagaactcaa acacttcata actaaacat cctttaagc 60  
cttttcaaaa actcaatcat gtcaagcaac tgcggaagct gcgactgtgc tgacaagacc 120  
cagtgcgtaa agaagggaac cagctacacc ttcgacatcg tcgagactca ggagagctac 180  
aaggaggcca tgatcatgga cgttggtgcc gaggagaaca acgcaaattg caagtgaag 240  
tgcggctcct cttgcagctg cgtaactgc acttgctgcc ccaactaatg aagcttcttt 300  
aatcaaaatg taatatgaat aaaagttgat gtttgattt ttgtttgttt ctgtatgatt 360  
agttgctttg taacaaaata atccaatcta aatgtgtttc ttgagc

(2) INFORMATION FOR SEQ ID NO:2452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

Xaa Xaa Asn Asn Asn Lys Gln Glu Leu Lys His Phe Ile Thr Lys Thr  
1 5 10 15  
Ser Phe Lys Ala Phe Ser Lys Thr Gln Ser Cys Gln Ala Thr Ala Glu  
20 25 30  
Ala Ala Thr Val Leu Thr Arg Pro Ser Ala  
35 40

(2) INFORMATION FOR SEQ ID NO:2453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

Met Ser Ser Asn Cys Gly Ser Cys Asp Cys Ala Asp Lys Thr Gln Cys  
1 5 10 15  
Val Lys Lys Gly Thr Ser Tyr Thr Phe Asp Ile Val Glu Thr Gln Glu  
20 25 30  
Ser Tyr Lys Glu Ala Met Ile Met Asp Val Gly Ala Glu Asn Asn  
35 40 45  
Ala Asn Cys Lys Cys Lys Cys Gly Ser Ser Cys Ser Cys Val Asn Cys  
50 55 60  
Thr Cys Cys Pro Asn  
65

(2) INFORMATION FOR SEQ ID NO:2454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..615
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

aacgaaagct agggtttttt ctctgtgaaa tcgctcgccg gcataaaaga gagtcagaag 60  
aggaagaaga gagttacaag gattgaaaaat gaaggacgt caaggagaga gagttagatt 120  
gtatgttcgt ggaacagtc tcggttacaa gaggtccaag tcgaaccaat accctaacac 180  
ttctctcgtc cagattgaag gtgtgaacac tcaagaggag gttaattggt acaagggtaa 240  
gcgtttggt tacatctaca aggcaaagac aaagaagaac ggttctcact accgttgcac 300  
ttggggcaaa gtcactaggc ctcatggtta cagtgtgtt gtccgttcta agttcacttc 360  
aaacctacca cccaagtcaa tgggagctag agtcagagtc ttcattgtacc ctagcaacat 420  
atgaggaggc tagatttcaa caagtatcgg aaggaatcgc cattatcatt tctcaggagc 480  
tgtagtttta tctattcact tttattctag actctctgtt gggttttgatt ttatcttgag 540



acgaagTaaa acattttttt tcttgagatc atatactatc gagtattaat ggaacttgag 600  
aaaagctatg atccc

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gly | Arg | Gln | Gly | Glu | Arg | Val | Arg | Leu | Tyr | Val | Arg | Gly | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Leu | Gly | Tyr | Lys | Arg | Ser | Lys | Ser | Asn | Gln | Tyr | Pro | Asn | Thr | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Val | Gln | Ile | Glu | Gly | Val | Asn | Thr | Gln | Glu | Glu | Val | Asn | Trp | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Gly | Lys | Arg | Leu | Ala | Tyr | Ile | Tyr | Lys | Ala | Lys | Thr | Lys | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Ser | His | Tyr | Arg | Cys | Ile | Trp | Gly | Lys | Val | Thr | Arg | Pro | His | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Asn | Ser | Gly | Val | Val | Arg | Ser | Lys | Phe | Thr | Ser | Asn | Leu | Pro | Pro | Lys |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Ser | Met | Gly | Ala | Arg | Val | Arg | Val | Phe | Met | Tyr | Pro | Ser | Asn | Ile |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1803
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| acacaccatt  | ttcacaacat  | cgtacttata | gccttctctt  | ctctctcaat  | acctctctca  | 60   |
| atttctggat  | ccaccatgca  | agctcttcaa | tcttcatctc  | tccgtgcttc  | tcctccaaac  | 120  |
| ccacttgcgt  | taccatcaaa  | togtcaatca | catcagctaa  | ttaccaatgc  | gagaccttg   | 180  |
| cgaagacaac  | aacgttccct  | catctccgca | tcagcatcca  | ctgtctccgc  | tcctaaacgc  | 240  |
| gaaacagatc  | cgaagaaacg  | agttgtcatt | actggtatgg  | gtctcgtctc  | tgtgtttggt  | 300  |
| aacgatgttg  | atgcttacta  | cgagaaattg | ttgtctggtg  | agagtggaaat | cagtttgatt  | 360  |
| gatcgtttcg  | atgcttccaa  | gttccctact | cgattcgggtg | gtcagatccg  | tgggttttagc | 420  |
| tctgaagggtt | atattgatgg  | caagaatgag | cgtaggcttg  | atgattgttt  | gaaatattgc  | 480  |
| attgttgctg  | gtaaaaaagc  | tcttgaaagt | gccaatcttg  | gtggtgataa  | gcttaacacg  | 540  |
| attgataaga  | ggaaagctgg  | agtactagtt | gggactggaa  | tgggaggttt  | aactgtgttt  | 600  |
| tcagaagggtg | ttcagaatct  | gattgagaag | ggatcatagga | ggattagtcc  | atcttttata  | 660  |
| ccttatgcta  | taacaaatat  | gggttctgct | ttgttggcga  | ttgatcttgg  | tcttatgggt  | 720  |
| cctaactatt  | cgatttcaac  | tgcttgtgct | acttogaatt  | actgctttta  | cgctgctgcg  | 780  |
| aatcacattc  | gtcgtgggtg  | agctgatatg | atgattgtctg | gtgggactga  | ggctgctatt  | 840  |
| attcctattg  | ggttgggagg  | ttttgttgct | tgtaggccat  | tgtcccagag  | aaatgatgac  | 900  |
| cctcaaaactg | cttccaggcc  | gtgggataaa | gcaagagatg  | ggtttgttat  | gggtgaagga  | 960  |
| gctggtgttc  | tgggtgatga  | aagcttggaa | catgcAaatg  | aaacgtggtg  | ctccaattgt  | 1020 |
| agcagaatat  | cttggagggtg | ctgttaattg | tgatgctcac  | catatgactg  | atccaagagc  | 1080 |
| tgatggtctt  | gggtttctt   | catgcattga | aagatgcctg  | gaagatgctg  | gtgtatcacc  | 1140 |
| tgaggaggta  | aattacatca  | atgcacatgc | aacttccact  | cttgctggtg  | atcttgctga  | 1200 |
| gattaatgcc  | attaaaaagg  | tattcaagag | cacttcaggg  | atcaaaatca  | acgccacca   | 1260 |

```
gtctatgata ggtcactgcc tcggtgcagc tggaggtcta gaagccatcg ccaccgtgaa 1320
ggctatcaac actggatggc tgcctccttc catcaaccaa tttaaccag aacaagctgt 1380
ggactttgac acggtcccaa acgagaagaa gcaacacgag gttgatgttg ccatatcaaa 1440
ctcgttcggg ttcggtggac acaactcggt agtcgccttc tctgccttca aaccttgatt 1500
tcttcatacc ttttagattc tctgccttat cggttactat catcatccat catccatcac 1560
caccacttgc agcttcttgg ttcacaagtt ggagctcttc ctctggcctt ttgcagttct 1620
ttcattcccc gtttcttacg gttgctgaga tttcagattt tgtttggtct ctctctgtgc 1680
tgcggaatgt tgtgtatctt agttcggtcc atatttgcgt aatttataaa aacagaaact 1740
gagagaatct tgtagtaacg gtgttattgt cagaataatc caattagggg attctcatct 1800
ttt
```

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1572937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

```
Thr His His Phe His Asn Ile Val Leu Ile Ala Phe Leu Ser Leu Ser
1 5 10 15
Ile Pro Leu Ser Ile Ser Gly Ser Thr Met Gln Ala Leu Gln Ser Ser
20 25 30
Ser Leu Arg Ala Ser Pro Pro Asn Pro Leu Arg Leu Pro Ser Asn Arg
35 40 45
Gln Ser His Gln Leu Ile Thr Asn Ala Arg Pro Leu Arg Arg Gln Gln
50 55 60
Arg Ser Phe Ile Ser Ala Ser Ala Ser Thr Val Ser Ala Pro Lys Arg
65 70 75 80
Glu Thr Asp Pro Lys Lys Arg Val Val Ile Thr Gly Met Gly Leu Val
85 90 95
Ser Val Phe Gly Asn Asp Val Asp Ala Tyr Tyr Glu Lys Leu Leu Ser
100 105 110
Gly Glu Ser Gly Ile Ser Leu Ile Asp Arg Phe Asp Ala Ser Lys Phe
115 120 125
Pro Thr Arg Phe Gly Gly Gln Ile Arg Gly Phe Ser Ser Glu Gly Tyr
130 135 140
Ile Asp Gly Lys Asn Glu Arg Arg Leu Asp Asp Cys Leu Lys Tyr Cys
145 150 155 160
Ile Val Ala Gly Lys Lys Ala Leu Glu Ser Ala Asn Leu Gly Gly Asp
165 170 175
Lys Leu Asn Thr Ile Asp Lys Arg Lys Ala Gly Val Leu Val Gly Thr
180 185 190
Gly Met Gly Gly Leu Thr Val Phe Ser Glu Gly Val Gln Asn Leu Ile
195 200 205
Glu Lys Gly His Arg Arg Ile Ser Pro Phe Phe Ile Pro Tyr Ala Ile
210 215 220
Thr Asn Met Gly Ser Ala Leu Leu Ala Ile Asp Leu Gly Leu Met Gly
225 230 235 240
Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ser Asn Tyr Cys Phe
245 250 255
Tyr Ala Ala Ala Asn His Ile Arg Arg Gly Glu Ala Asp Met Met Ile
260 265 270
Ala Gly Gly Thr Glu Ala Ala Ile Ile Pro Ile Gly Leu Gly Gly Phe
275 280 285
Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Asp Asp Pro Gln Thr Ala
290 295 300
Ser Arg Pro Trp Asp Lys Ala Arg Asp Gly Phe Val Met Gly Glu Gly
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..256
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572939
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Leu | Val | Ser | Val | Phe | Gly | Asn | Asp | Val | Asp | Ala | Tyr | Tyr | Glu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Lys | Leu | Leu | Ser | Gly | Glu | Ser | Gly | Ile | Ser | Leu | Ile | Asp | Arg | Phe | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Ser | Lys | Phe | Pro | Thr | Arg | Phe | Gly | Gly | Gln | Ile | Arg | Gly | Phe | Ser |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Ser | Glu | Gly | Tyr | Ile | Asp | Gly | Lys | Asn | Glu | Arg | Arg | Leu | Asp | Asp | Cys |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Leu | Lys | Tyr | Cys | Ile | Val | Ala | Gly | Lys | Lys | Ala | Leu | Glu | Ser | Ala | Asn |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Gly | Gly | Asp | Lys | Leu | Asn | Thr | Ile | Asp | Lys | Arg | Lys | Ala | Gly | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Val | Gly | Thr | Gly | Met | Gly | Gly | Leu | Thr | Val | Phe | Ser | Glu | Gly | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Gln | Asn | Leu | Ile | Glu | Lys | Gly | His | Arg | Arg | Ile | Ser | Pro | Phe | Phe | Ile |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Pro | Tyr | Ala | Ile | Thr | Asn | Met | Gly | Ser | Ala | Leu | Leu | Ala | Ile | Asp | Leu |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Gly | Leu | Met | Gly | Pro | Asn | Tyr | Ser | Ile | Ser | Thr | Ala | Cys | Ala | Thr | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Asn | Tyr | Cys | Phe | Tyr | Ala | Ala | Ala | Asn | His | Ile | Arg | Arg | Gly | Glu | Ala |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asp | Met | Met | Ile | Ala | Gly | Gly | Thr | Glu | Ala | Ala | Ile | Ile | Pro | Ile | Gly |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Gly | Gly | Phe | Val | Ala | Cys | Arg | Ala | Leu | Ser | Gln | Arg | Asn | Asp | Asp |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Pro | Gln | Thr | Ala | Ser | Arg | Pro | Trp | Asp | Lys | Ala | Arg | Asp | Gly | Phe | Val |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |  |
| Met | Gly | Glu | Gly | Ala | Gly | Val | Leu | Val | Met | Glu | Ser | Leu | Glu | His | Ala |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Asn | Glu | Thr | Trp | Cys | Ser | Asn | Cys | Ser | Arg | Ile | Ser | Trp | Arg | Cys | Cys |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |

(2) INFORMATION FOR SEQ ID NO:2460:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1719 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..1719
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1572944
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atTTTTtctca | gccacaaac  | actagtctct | tctgatttgt | accctaacgt | ttactcgact | 60  |
| tatctaaagc  | cgtgaacctc | gccggaattc | ttaaagtcgc | gatttttctt | taacgccgtt | 120 |
| tgattccctt  | acggcctttg | aggtccagga | gatagcaaat | ttgttggtga | gtactgaaaa | 180 |
| atggaggaag  | agaacgaagt | agtgaagacg | tttgacagac | ttggtgtgcg | tgaggagctt | 240 |
| gttaaagctt  | gcgagagatt | gggatggaag | aacccttcca | aaattcaagc | cgaagccctt | 300 |

ccttttgctc ttgaaggga agatgtaatt ggacttgccg aaaccgggtc tggtaaaacc 360  
ggagcttttg caattcctat attgcaagca ctacttgagt atgtttatga ttctgagcct 420  
aagaaaggac gtagaccgga tcctgctttc ttgctgtgtg ttttatctcc aactcgagaa 480  
cttgcaatcc agattgctga acagtttgaa gctcttggtg ctgatataag tcttaggtgt 540  
gctgtgcttt ttggaggtat agacaggatg caacaaacta ttgctcttgg gaaacggcct 600  
catgtttattg ttgcaaccac tggctgctct tgggatcata tgtctgatac aaaaggcttt 660  
tctctgaaat cattgaaata tcYtggttct tgatgaagca gatagactgt tgaatgaaga 720  
ttttgagaaa tctcttaacc agattttgga agagatccct cgtgagcgga aaacatttct 780  
tttttcagcg actatgacta aaaagggttcg aaaacttcaa agggcatgtt tgaggaatcc 840  
tgtgaagatt gaagctgcct ccaaattatc cactgtcgat actcttaagc agcagtatcg 900  
gtttgttgcc gctaaataca aggattgcta tctggtatac attctgagtg aaatgcctga 960  
atcaacatct atgattttca cccgaacatg tgatggtact cgttttctgg ctttgggtgct 1020  
tcggagcctt ggttttagag ctattcctat cagtggctca atgactcagt caaagagact 1080  
gggagcttta aataagttca aagcagggga atgtaatac ttggtttgta ccgatgtggc 1140  
tagtagaggg ctcgatatcc catcagttga tgtggttata aattatgata ttcccacaaa 1200  
ttcaaaggat tacatccata gtagtaggaag aaccgctcgt gctggacgtt ctgggtgttg 1260  
gatatcactt gtaaaccagt atgagctcga atggtatata caaatagaaa aactcattgg 1320  
caagaaacta cctgaatac cgcctgagga agatgaagtc ttgtcattgt tggagagagt 1380  
tgcagaagcg aaaaagctat ctgcaatgaa tatgaaagaa tcaggaggta ggaagagaag 1440  
gggagaagat gatgaagaaa gtgagagggt cttgggaggt aacaaggaca gaggcaacaa 1500  
ggaaagaggt ggtaacaaag acaagaagtc ttctaagaag ttcaaacgat aaaatagctc 1560  
tgtttttact gttttccgat aactcaccaa agttttgaat tgaagttttc catatgaact 1620  
agggaaattt aatccatttt gtactcgtaa tttgtatgtt cttttctttt tgctttgttt 1680  
ctcaatgaca gattatacaa tttaagttga aagatgttt

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1572945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Lys | Val | Arg | Lys | Leu | Gln | Arg | Ala | Cys | Leu | Arg | Asn | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Ile | Glu | Ala | Ala | Ser | Lys | Tyr | Ser | Thr | Val | Asp | Thr | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Tyr | Arg | Phe | Val | Ala | Ala | Lys | Tyr | Lys | Asp | Cys | Tyr | Leu | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ile | Leu | Ser | Glu | Met | Pro | Glu | Ser | Thr | Ser | Met | Ile | Phe | Thr | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Cys | Asp | Gly | Thr | Arg | Phe | Leu | Ala | Leu | Val | Leu | Arg | Ser | Leu | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Arg | Ala | Ile | Pro | Ile | Ser | Gly | Gln | Met | Thr | Gln | Ser | Lys | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Ala | Leu | Asn | Lys | Phe | Lys | Ala | Gly | Glu | Cys | Asn | Ile | Leu | Val | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Asp | Val | Ala | Ser | Arg | Gly | Leu | Asp | Ile | Pro | Ser | Val | Asp | Val | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Asn | Tyr | Asp | Ile | Pro | Thr | Asn | Ser | Lys | Asp | Tyr | Ile | His | Arg | Val |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Arg | Thr | Ala | Arg | Ala | Gly | Arg | Ser | Gly | Val | Gly | Ile | Ser | Leu | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Gln | Tyr | Glu | Leu | Glu | Trp | Tyr | Ile | Gln | Ile | Glu | Lys | Leu | Ile | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Lys | Leu | Pro | Glu | Tyr | Pro | Ala | Glu | Glu | Asp | Glu | Val | Leu | Ser | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Glu | Arg | Val | Ala | Glu | Ala | Lys | Lys | Leu | Ser | Ala | Met | Asn | Met | Lys |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 195                                                             | 200 | 205 |
| Glu Ser Gly Gly Arg Lys Arg Arg Gly Glu Asp Asp Glu Glu Ser Glu |     |     |
| 210                                                             | 215 | 220 |
| Arg Phe Leu Gly Gly Asn Lys Asp Arg Gly Asn Lys Glu Arg Gly Gly |     |     |
| 225                                                             | 230 | 235 |
| Asn Lys Asp Lys Lys Ser Ser Lys Lys Phe Lys Arg                 |     | 240 |
| 245                                                             | 250 |     |

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1572946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Glu | Ser | Thr | Ser | Met | Ile | Phe | Thr | Arg | Thr | Cys | Asp | Gly | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Phe | Leu | Ala | Leu | Val | Leu | Arg | Ser | Leu | Gly | Phe | Arg | Ala | Ile | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Ser | Gly | Gln | Met | Thr | Gln | Ser | Lys | Arg | Leu | Gly | Ala | Leu | Asn | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Lys | Ala | Gly | Glu | Cys | Asn | Ile | Leu | Val | Cys | Thr | Asp | Val | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Leu | Asp | Ile | Pro | Ser | Val | Asp | Val | Val | Ile | Asn | Tyr | Asp | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Thr | Asn | Ser | Lys | Asp | Tyr | Ile | His | Arg | Val | Gly | Arg | Thr | Ala | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Gly | Arg | Ser | Gly | Val | Gly | Ile | Ser | Leu | Val | Asn | Gln | Tyr | Glu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Trp | Tyr | Ile | Gln | Ile | Glu | Lys | Leu | Ile | Gly | Lys | Lys | Leu | Pro | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Tyr | Pro | Ala | Glu | Glu | Asp | Glu | Val | Leu | Ser | Leu | Leu | Glu | Arg | Val | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Lys | Lys | Leu | Ser | Ala | Met | Asn | Met | Lys | Glu | Ser | Gly | Gly | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Arg | Arg | Gly | Glu | Asp | Asp | Glu | Glu | Ser | Glu | Arg | Phe | Leu | Gly | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Lys | Asp | Arg | Gly | Asn | Lys | Glu | Arg | Gly | Gly | Asn | Lys | Asp | Lys | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ser | Ser | Lys | Lys | Phe | Lys | Arg |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1572947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Phe | Thr | Arg | Thr | Cys | Asp | Gly | Thr | Arg | Phe | Leu | Ala | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Ser | Leu | Gly | Phe | Arg | Ala | Ile | Pro | Ile | Ser | Gly | Gln | Met | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Gln Ser Lys Arg Leu Gly Ala Leu Asn Lys Phe Lys Ala Gly Glu Cys  
35 40 45  
Asn Ile Leu Val Cys Thr Asp Val Ala Ser Arg Gly Leu Asp Ile Pro  
50 55 60  
Ser Val Asp Val Val Ile Asn Tyr Asp Ile Pro Thr Asn Ser Lys Asp  
65 70 75 80  
Tyr Ile His Arg Val Gly Arg Thr Ala Arg Ala Gly Arg Ser Gly Val  
85 90 95  
Gly Ile Ser Leu Val Asn Gln Tyr Glu Leu Glu Trp Tyr Ile Gln Ile  
100 105 110  
Glu Lys Leu Ile Gly Lys Lys Leu Pro Glu Tyr Pro Ala Glu Glu Asp  
115 120 125  
Glu Val Leu Ser Leu Leu Glu Arg Val Ala Glu Ala Lys Lys Leu Ser  
130 135 140  
Ala Met Asn Met Lys Glu Ser Gly Gly Arg Lys Arg Arg Gly Glu Asp  
145 150 155 160  
Asp Glu Glu Ser Glu Arg Phe Leu Gly Gly Asn Lys Asp Arg Gly Asn  
165 170 175  
Lys Glu Arg Gly Gly Asn Lys Asp Lys Lys Ser Ser Lys Lys Phe Lys  
180 185 190  
Arg

(2) INFORMATION FOR SEQ ID NO:2464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gaagattaat tgaatcacac aaagtcgaat ccaaagtttt tgatcttaac caagtcgcat  | 60  |
| aatccagaga ggaatcaaaa gaagatgagt aacgtcagct tcaggcagga tcatgatttc  | 120 |
| gagaagagga aagctgaggc tttaaggatc agagagaagt attctgacag agtccgggtt  | 180 |
| attgtggaga agtcagagaa aagtgatata ccaaaccattg acaagaagaa ataccttgtc | 240 |
| ccagctgata taacggtagg ccagtttggtg tatgtgattc gtaagagaat ccaacttagt | 300 |
| gcagagaaaag ctatcttcat ctttggtgat aatgttcttc ctcccaccgg agcgatgatg | 360 |
| tcaaccattt acgatgagaa taaggaagaa gacggcttct tgtatgttac ctacagtggg  | 420 |
| gaaaacactt ttgatcgctc aatgacttaa tttggtgttc ttgcttttaa ttgaatgtaa  | 480 |
| atattccatt ttcttttctt gtccgtgaac ttgcttagat gcggatatga ttattatggc  | 540 |
| ttatgtaggc acaaccAatc ggtttgcaaa caaagtgttg gtttttttat cc          |     |

(2) INFORMATION FOR SEQ ID NO:2465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

Met Ser Asn Val Ser Phe Arg Gln Asp His Asp Phe Glu Lys Arg Lys  
1 5 10 15  
Ala Glu Ala Leu Arg Ile Arg Glu Lys Tyr Ser Asp Arg Val Pro Val  
20 25 30  
Ile Val Glu Lys Ser Glu Lys Ser Asp Ile Pro Asn Ile Asp Lys Lys

35 40 45  
Lys Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val  
50 55 60  
Ile Arg Lys Arg Ile Gln Leu Ser Ala Glu Lys Ala Ile Phe Ile Phe  
65 70 75 80  
Val Asp Asn Val Leu Pro Pro Thr Gly Ala Met Met Ser Thr Ile Tyr  
85 90 95  
Asp Glu Asn Lys Glu Glu Asp Gly Phe Leu Tyr Val Thr Tyr Ser Gly  
100 105 110  
Glu Asn Thr Phe Gly Ser Ser Met Thr  
115 120

(2) INFORMATION FOR SEQ ID NO:2466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

gtttcatctg ttgttccctg tgaccatggc tactccactc tcaatctcat caaatcctct 60  
cacctcccg c attgttacc gtctccactt atcttctact tcattcaagg taatctctca 120  
ttcttctaca aatgtcaatt ttgaatgaat ccataaaatt ggaatttgaa atgtgtacag 180  
ggaaatgtaa gtgttttggg ggcaaaccca agtcagattc tatctctgaa actcaaccaa 240  
acccttaaaa cgagaaacca acagcaattt gcgagacccc ttgttgtggg tagccaaacg 300  
gcggctacgt cgtcggcagt tgtagctccg gagagattcc gtttggataa tcttggacca 360  
cagccagggt cgaggaagaa gcagaagaga aaaggtagag gtatctctgc aggacaagga 420  
gcaagttgtg gttttggtat gagagggtcag aaatcaagat cgggtcctgg gattatgaga 480  
ggctttgaag gtggtcaaac tgctctttat cgtcgtcttc ccaaacttag aggaatcgct 540  
ggaggatagc gttcaggatt acctaaatac ttaccggtta atatcaaaga catagaaacc 600  
gctgggtttc aagagggaga tgaagtgtca ttggagacat tgaagcaaaa gggtttgatt 660  
aatccttcag ggagagaaag gaaactccct cttaagattc tgggtacagg agaactaagc 720  
atgaagctca ccttcaaagc tcgtgccttc tcaacacaag caaaagagaa gcttgaagct 780  
tcaggttgta cactcactgt gttgccggga agaaagaaat gggttaagcc atctgttgca 840  
aagaaccaag cagagcaga tgaatacttt gccaaagaag gagctgcagc agcagaagca 900  
gcaacttcag agccagcagc ctctgcttaa attacttcag ttccaagctc tttttagtgt 960  
tgtaaagctg cagagaagat aattgtctat gacaaatggt aattacaatt cctttgtctt 1020  
tttgtatggt gaagagattt acattttgtt gtttgaagag tcattatcaa aaagatatgt 1080  
aaacggtaat gaaatattga acattttgtt Tc

(2) INFORMATION FOR SEQ ID NO:2467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

Met Arg Gly Gln Lys Ser Arg Ser Gly Pro Gly Ile Met Arg Gly Phe  
1 5 10 15  
Glu Gly Gly Gln Thr Ala Leu Tyr Arg Arg Leu Pro Lys Leu Arg Gly  
20 25 30  
Ile Ala Gly Gly Met Arg Ser Gly Leu Pro Lys Tyr Leu Pro Val Asn  
35 40 45  
Ile Lys Asp Ile Glu Thr Ala Gly Phe Gln Glu Gly Asp Glu Val Ser



50 55 60  
Leu Glu Thr Leu Lys Gln Lys Gly Leu Ile Asn Pro Ser Gly Arg Glu  
65 70 75 80  
Arg Lys Leu Pro Leu Lys Ile Leu Gly Thr Gly Glu Leu Ser Met Lys  
85 90 95  
Leu Thr Phe Lys Ala Arg Ala Phe Ser Thr Gln Ala Lys Glu Lys Leu  
100 105 110  
Glu Ala Ser Gly Cys Thr Leu Thr Val Leu Pro Gly Arg Lys Lys Trp  
115 120 125  
Val Lys Pro Ser Val Ala Lys Asn Gln Ala Arg Ala Asp Glu Tyr Phe  
130 135 140  
Ala Lys Lys Arg Ala Ala Ala Glu Ala Ala Thr Ser Glu Pro Ala  
145 150 155 160  
Ala Ser Ala

(2) INFORMATION FOR SEQ ID NO:2468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1572964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

Met Arg Gly Phe Glu Gly Gly Gln Thr Ala Leu Tyr Arg Arg Leu Pro  
1 5 10 15  
Lys Leu Arg Gly Ile Ala Gly Gly Met Arg Ser Gly Leu Pro Lys Tyr  
20 25 30  
Leu Pro Val Asn Ile Lys Asp Ile Glu Thr Ala Gly Phe Gln Glu Gly  
35 40 45  
Asp Glu Val Ser Leu Glu Thr Leu Lys Gln Lys Gly Leu Ile Asn Pro  
50 55 60  
Ser Gly Arg Glu Arg Lys Leu Pro Leu Lys Ile Leu Gly Thr Gly Glu  
65 70 75 80  
Leu Ser Met Lys Leu Thr Phe Lys Ala Arg Ala Phe Ser Thr Gln Ala  
85 90 95  
Lys Glu Lys Leu Glu Ala Ser Gly Cys Thr Leu Thr Val Leu Pro Gly  
100 105 110  
Arg Lys Lys Trp Val Lys Pro Ser Val Ala Lys Asn Gln Ala Arg Ala  
115 120 125  
Asp Glu Tyr Phe Ala Lys Lys Arg Ala Ala Ala Ala Glu Ala Ala Thr  
130 135 140  
Ser Glu Pro Ala Ala Ser Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1572965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

Met Arg Ser Gly Leu Pro Lys Tyr Leu Pro Val Asn Ile Lys Asp Ile  
1 5 10 15

Glu Thr Ala Gly Phe Gln Glu Gly Asp Glu Val Ser Leu Glu Thr Leu  
20 25 30  
Lys Gln Lys Gly Leu Ile Asn Pro Ser Gly Arg Glu Arg Lys Leu Pro  
35 40 45  
Leu Lys Ile Leu Gly Thr Gly Glu Leu Ser Met Lys Leu Thr Phe Lys  
50 55 60  
Ala Arg Ala Phe Ser Thr Gln Ala Lys Glu Lys Leu Glu Ala Ser Gly  
65 70 75 80  
Cys Thr Leu Thr Val Leu Pro Gly Arg Lys Lys Trp Val Lys Pro Ser  
85 90 95  
Val Ala Lys Asn Gln Ala Arg Ala Asp Glu Tyr Phe Ala Lys Lys Arg  
100 105 110  
Ala Ala Ala Ala Glu Ala Ala Thr Ser Glu Pro Ala Ala Ser Ala  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..740
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| gaattttttt | aaagaaaata | aaaatcaagt | ctttctcttc | gtctatctct  | ctctctgctc | 60  |
| agactctctg | gtgttgaaga | ctaactactg | aagcagatct | attatacggg  | ggacgaagaa | 120 |
| gatgtatgag | cagcagcaac | atttcattga | tttgcaaagc | gattctgggt  | ttRgggacga | 180 |
| tagctccttg | ctcgccggcg | atgacgatct | tcgtctctct | cctcaaccaat | ctgccgcggg | 240 |
| tacgaactcc | ggcaatgaga | atctagatcg | tcgtctctta | aaagatctcg  | ttgagatggg | 300 |
| tccccttata | gagcattaca | tggacataa  | agaaaggagt | tcgtttaagc  | ggcgtgggtc | 360 |
| catgatctac | actaagatgc | cttcaaaa   | atccttgtcc | cgaaggGGaa  | gaaatgcttc | 420 |
| tcaaacagtc | ccaggaagaa | agaagagaga | ccaagaggga | aatgacgatg  | ttatgaacaa | 480 |
| ttctagggaa | gatgatgaaa | acgcaaaggc | tttggctggg | gcagaaaagg  | aagaaatgag | 540 |
| tagactaaga | gcaagtgaat | gacttgcaga | caaaattatc | ggagaaagaa  | gagggtttta | 600 |
| agtcaatgga | gatgtcaaag | aatcaggtaa | acgagataca | agaaaagcct  | gaagcaacaa | 660 |
| atcgattggg | tgctgagaag | gatatgttga | tcaagtctat | gcagttacaa  | ttatcggaca | 720 |
| caaagatcaa | acttgctgac |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

Met Tyr Glu Gln Gln Gln His Phe Met Asp Leu Gln Ser Asp Ser Gly  
1 5 10 15  
Phe Xaa Asp Asp Ser Ser Trp Leu Ala Gly Asp Asp Asp Leu Arg Leu  
20 25 30  
Ser Pro His Gln Ser Ala Ala Gly Thr Asn Ser Gly Asn Glu Asn Leu  
35 40 45  
Asp Arg Arg Leu Leu Lys Asp Leu Val Glu Met Val Pro Leu Ile Glu  
50 55 60  
His Tyr Met Glu His Lys Glu Arg Ser Ser Phe Lys Arg Arg Gly Ser  
65 70 75 80

Met Ile Tyr Thr Lys Met Pro Ser Lys Glu Ser Leu Ser Arg Arg Gly  
85 90 95  
Arg Asn Ala Ser Gln Thr Val Pro Gly Arg Lys Lys Arg Asp Gln Glu  
100 105 110  
Gly Asn Asp Asp Val Met Asn Asn Ser Arg Glu Asp Asp Glu Asn Ala  
115 120 125  
Lys Ala Leu Ala Gly Ala Glu Lys Glu Glu Met Ser Arg Leu Arg Ala  
130 135 140  
Ser Glu  
145

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1572968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Asp Leu Gln Ser Asp Ser Gly Phe Xaa Asp Asp Ser Ser Trp Leu  
1 5 10 15  
Ala Gly Asp Asp Asp Leu Arg Leu Ser Pro His Gln Ser Ala Ala Gly  
20 25 30  
Thr Asn Ser Gly Asn Glu Asn Leu Asp Arg Arg Leu Leu Lys Asp Leu  
35 40 45  
Val Glu Met Val Pro Leu Ile Glu His Tyr Met Glu His Lys Glu Arg  
50 55 60  
Ser Ser Phe Lys Arg Arg Gly Ser Met Ile Tyr Thr Lys Met Pro Ser  
65 70 75 80  
Lys Glu Ser Leu Ser Arg Arg Gly Arg Asn Ala Ser Gln Thr Val Pro  
85 90 95  
Gly Arg Lys Lys Arg Asp Gln Glu Gly Asn Asp Asp Val Met Asn Asn  
100 105 110  
Ser Arg Glu Asp Asp Glu Asn Ala Lys Ala Leu Ala Gly Ala Glu Lys  
115 120 125  
Glu Glu Met Ser Arg Leu Arg Ala Ser Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1572969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Val Pro Leu Ile Glu His Tyr Met Glu His Lys Glu Arg Ser Ser  
1 5 10 15  
Phe Lys Arg Arg Gly Ser Met Ile Tyr Thr Lys Met Pro Ser Lys Glu  
20 25 30  
Ser Leu Ser Arg Arg Gly Arg Asn Ala Ser Gln Thr Val Pro Gly Arg  
35 40 45  
Lys Lys Arg Asp Gln Glu Gly Asn Asp Asp Val Met Asn Asn Ser Arg  
50 55 60  
Glu Asp Asp Glu Asn Ala Lys Ala Leu Ala Gly Ala Glu Lys Glu Glu

80

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1450

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572970

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

| (A1) SEQUENCE ALIGNMENT |             |             |            |             |             |      |
|-------------------------|-------------|-------------|------------|-------------|-------------|------|
| agggggcttt              | tgtgttgacg  | gtggtgggaa  | caaaggaaca | tctgatccat  | tctgtccggg  | 60   |
| aaaRcacagc              | aatgttcatt  | tccgacaaat  | ctcgtcctac | tgattttctac | aaagacgatac | 120  |
| atcacaaatc              | ctccaccacc  | agcaccacac  | gcgatatgat | gatcgatgta  | ctcaccacta  | 180  |
| ccaacgaatc              | agtagatcta  | caatctcacc  | accaccacaa | tcacaatcac  | cacaatcatc  | 240  |
| atctcaacca              | atctcagcca  | caacaacaga  | ttctcctcgg | agaaagcagt  | ggagaagatc  | 300  |
| acgaagttaa              | agcaccaaaag | aaacgagcgg  | agacatgggt | tcaagacgaa  | actcgtagct  | 360  |
| taatcatgtt              | ccgttagagg  | atggatgggt  | tattcaatac | atccaaatct  | ataaacaatc  | 420  |
| tctgggaaca              | gatttcgtct  | aagatgagag  | aaaaagggtt | tgatcgatct  | ccgactatgt  | 480  |
| gtactgataa              | atggagggaat | ctgttgaaag  | agtttaagaa | agctaagcat  | catgatagag  | 540  |
| gaaatggatc              | ggcgaagatg  | tctgtattaca | aagagattga | agatattctt  | agagagagga  | 600  |
| gcaaaaaagt              | gacaccacca  | cagtataata  | agagccctaa | tacaccacct  | acatcagcca  | 660  |
| aagttgattc              | ctttatgcaa  | tttactgata  | aaggttttga | tgatacgagc  | atttcttttg  | 720  |
| gatccgttga              | agctaattggc | aggccagcct  | taaaccttga | aaggcgtctt  | gatcatgatg  | 780  |
| gtcatcctct              | tgcaatcaact | acagcagttg  | atgctgtttg | agcaaattgga | gttactcctt  | 840  |
| ggaattggag              | agagactcct  | ggaaacgggt  | atgatagtca | tggtcagcct  | tttgggtgta  | 900  |
| gggtcataac              | agtgaatttt  | ggtagactata | caagaagaat | cggttgtgat  | ggtagtgcag  | 960  |
| aagcaatcaa              | agaggttaatc | agactctgct  | ttgggttaag | aactcgaagg  | gctttttggt  | 1020 |
| tagaagatga              | agatcagatt  | attcgtctgtc | ttgaccgaga | catgccctta  | gggaactatc  | 1080 |
| tactccgtct              | ggatgatgga  | ctggccatta  | gggtttgcc  | ttatgatgaa  | tccaaccaat  | 1140 |
| taccagtcca              | ttcagaagag  | aaaatottct  | acactgaaga | agactaccgc  | gagttttctgg | 1200 |
| ctcgacgggg              | atggtcatgc  | ctgcaagttg  | atggttttag | gaacatagaa  | aacatggatg  | 1260 |
| atcttcaacc              | tggtgctgtg  | tatcgagggtg | tgagatgagg | aaatgagatc  | acaaaacttc  | 1320 |
| ttctccaatt              | ctatcaacag  | ttatcttgatc | agaaaacagt | cccctgtaga  | tatgatctca  | 1380 |
| tctctcttat              | acatttcttc  | tttttttcat  | gtacttgctc | aaatatgaaa  | tatcataact  | 1440 |
| ggcatttacc              |             |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2475:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids

- (B) TYPE: amino acid

- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..431

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572971

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

|       |     |        |        |       |     |        |     |        |     |     |        |        |     |        |     |
|-------|-----|--------|--------|-------|-----|--------|-----|--------|-----|-----|--------|--------|-----|--------|-----|
| Gly 1 | Ala | Phe    | Val    | Leu 5 | Thr | Val    | Val | Gly 10 | Thr | Lys | Glu    | His    | Arg | Ile 15 | His |
| Ser   | Val | Arg    | Glu 20 | Xaa   | Thr | Ala    | Met | Phe 25 | Ile | Ser | Asp    | Lys    | Ser | Arg 30 | Pro |
| Thr   | Asp | Phe 35 | Tyr    | Lys   | Asp | Asp 40 | His | His    | Asn | Ser | Ser    | Thr 45 | Thr | Ser    | Thr |
| Thr   | Arg | Asp 50 | Met    | Met   | Ile | Asp 55 | Val | Leu    | Thr | Thr | Thr 60 | Asn    | Glu | Ser    | Val |
| Asp   | Leu | Gln    | Ser    | His   | His | His    | His | Asn    | His | Asn | His    | His    | Asn | His    | His |

65 70 75 80  
Leu His Gln Ser Gln Pro Gln Gln Gln Ile Leu Leu Gly Glu Ser Ser  
85 90 95  
Gly Glu Asp His Glu Val Lys Ala Pro Lys Lys Arg Ala Glu Thr Trp  
100 105 110  
Val Gln Asp Glu Thr Arg Ser Leu Ile Met Phe Arg Arg Gly Met Asp  
115 120 125  
Gly Leu Phe Asn Thr Ser Lys Ser Asn Lys His Leu Trp Glu Gln Ile  
130 135 140  
Ser Ser Lys Met Arg Glu Lys Gly Phe Asp Arg Ser Pro Thr Met Cys  
145 150 155 160  
Thr Asp Lys Trp Arg Asn Leu Leu Lys Glu Phe Lys Lys Ala Lys His  
165 170 175  
His Asp Arg Gly Asn Gly Ser Ala Lys Met Ser Tyr Tyr Lys Glu Ile  
180 185 190  
Glu Asp Ile Leu Arg Glu Arg Ser Lys Lys Val Thr Pro Pro Gln Tyr  
195 200 205  
Asn Lys Ser Pro Asn Thr Pro Pro Thr Ser Ala Lys Val Asp Ser Phe  
210 215 220  
Met Gln Phe Thr Asp Lys Gly Phe Asp Asp Thr Ser Ile Ser Phe Gly  
225 230 235 240  
Ser Val Glu Ala Asn Gly Arg Pro Ala Leu Asn Leu Glu Arg Arg Leu  
245 250 255  
Asp His Asp Gly His Pro Leu Ala Ile Thr Thr Ala Val Asp Ala Val  
260 265 270  
Ala Ala Asn Gly Val Thr Pro Trp Asn Trp Arg Glu Thr Pro Gly Asn  
275 280 285  
Gly Asp Asp Ser His Gly Gln Pro Phe Gly Gly Arg Val Ile Thr Val  
290 295 300  
Lys Phe Gly Asp Tyr Thr Arg Arg Ile Gly Val Asp Gly Ser Ala Glu  
305 310 315 320  
Ala Ile Lys Glu Val Ile Arg Ser Ala Phe Gly Leu Arg Thr Arg Arg  
325 330 335  
Ala Phe Trp Leu Glu Asp Glu Asp Gln Ile Ile Arg Cys Leu Asp Arg  
340 345 350  
Asp Met Pro Leu Gly Asn Tyr Leu Leu Arg Leu Asp Asp Gly Leu Ala  
355 360 365  
Ile Arg Val Cys His Tyr Asp Glu Ser Asn Gln Leu Pro Val His Ser  
370 375 380  
Glu Glu Lys Ile Phe Tyr Thr Glu Glu Asp Tyr Arg Glu Phe Leu Ala  
385 390 395 400  
Arg Arg Gly Trp Ser Cys Leu Gln Val Asp Gly Phe Arg Asn Ile Glu  
405 410 415  
Asn Met Asp Asp Leu Gln Pro Gly Ala Val Tyr Arg Gly Val Arg  
420 425 430

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..408

(D) OTHER INFORMATION: / Ceres Seq. ID 1572972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

Met Phe Ile Ser Asp Lys Ser Arg Pro Thr Asp Phe Tyr Lys Asp Asp  
1 5 10 15  
His His Asn Ser Ser Thr Thr Ser Thr Thr Arg Asp Met Met Ile Asp  
20 25 30

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1572973

Met Ile Asp Val Leu Thr Thr Thr Asn Glu Ser Val Asp Leu Gln

Met Met Ile Asp Val Leu Thr Thr Thr Asn Glu Ser Val Asp Leu Gln

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2262 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

FEATURE:

(A) NAM

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2478:

ttcatct tcttcttctt cttcatcggt ttcgatttgt tgctccgata atgtcgtttc

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| tataacccga  | agatcatcaa  | cgaagaaagc | gaaataaacc  | tcaaaaatca  | cagagattat  | 180  |
| tacaaatggc  | ggctactgat  | tttttcttcg | ctttcgtctt  | ctctttcact  | cttatcttcg  | 240  |
| gtttctcttt  | cgctgggtgat | ccttacgtct | cttacgattt  | cactctctcc  | tacatcactg  | 300  |
| cttctcctct  | cgggtgttcct | caacaggtca | tagcagtcaa  | tgggaaattt  | ccagggtcctg | 360  |
| tgattaacgc  | tacgacaaac  | tacaatgttc | atgttaacgt  | actcaatcat  | ttggatgagc  | 420  |
| ctcttttact  | tacttggcct  | ggtgttcaga | tgaggcgtaa  | ctcgtggcaa  | gacggtgttc  | 480  |
| ttggaacaaa  | ctgtccaatt  | ccaccgaatt | ggaacttcac  | ttatgatttt  | cagttgaaag  | 540  |
| atcagattgg  | aagttatttc  | tactctcctt | cacttaactt  | tcagagagcc  | tctggttggtt | 600  |
| ttggtgcact  | cataatcaat  | aacagagacc | ttgttcctat  | tccgttcact  | gagcctgatg  | 660  |
| gtgaaattat  | ctttattatt  | ggtgattggt | atactcagaa  | ccatacagct  | ttaaggagga  | 720  |
| tacttgactc  | tggtaaagaa  | cttgggatgc | ccgatggagt  | actcatcaat  | gggaaagggtc | 780  |
| ctttcaagta  | caatagcagt  | gtacctgatg | gaattgaaca  | tgaaaccgtt  | aatgttgatc  | 840  |
| cagggaanaac | atacaggatc  | cgtgttcaca | atgttggtat  | ctcgacaagc  | ttgaacttca  | 900  |
| ggattccagaa | ccacaaattg  | ctcttgattg | agactgaggg  | tcgctacacc  | tcccaaataga | 960  |
| acttcaccga  | ttttgatatt  | catgtgggac | agtcttatcc  | tttcttggtg  | accatggacc  | 1020 |
| aaaacgccac  | aagtgactac  | tacattgtgg | cgagtgcctg  | atttggtta   | gaaacagtg   | 1080 |
| ggcaaagagt  | tacagggtgt  | ggcattctcc | attattccaa  | ttccaaagga  | cctgcttctg  | 1140 |
| gtcctttgcc  | agtttcagca  | actgatgtta | atcacccctg  | gtctgcaatg  | aaccaaccga  | 1200 |
| gagccataaa  | gcaaaacaca  | tctgcaagt  | gagctcgtcc  | aaatccgcag  | ggatcatttc  | 1260 |
| actacggaca  | gatcaacatt  | acaagaacat | acatcttgag  | gagtttgcct  | ccaacaaaaa  | 1320 |
| tcaatgggaa  | acttcgtgct  | acacttaatt | gaatttcatt  | tgtcaatcca  | agcaccacca  | 1380 |
| tgaggcttcc  | ggatgacct   | aaagtgaag  | gagattatat  | gttagatttt  | ccagacagac  | 1440 |
| cacttgatga  | aaaacttcca  | cgtttgtcca | gctctatcat  | caacgcaaca  | tacaagggtc  | 1500 |
| ttatacaagt  | tatcttcag   | aacaatgaca | ccaaaatcca  | gagcttccat  | attgatggat  | 1560 |
| atgcatttta  | cgtggttgcg  | atggactttg | gtatatggtc  | agaagacaga  | aacggttcat  | 1620 |
| ataacaactg  | ggatgcagta  | gcacgaagca | cgggtggaggt | ctatccagga  | gcattggactg | 1680 |
| ctgtacttat  | ttctctcgat  | Gaatgttgga | gtttggaata  | tccgggttga  | gaatcttgac  | 1740 |
| agatggtatc  | ttggccaaga  | aacatacatg | cgaattataa  | accctgagga  | aaacggaagt  | 1800 |
| acggaaatgg  | atccgcctga  | aaatgttatg | tactgtggtg  | ctcttcaggc  | catgcaaaag  | 1860 |
| gaacaacatc  | acagctcggc  | cacaaaatca | atgacaaatg  | gacagttgat  | actaattttc  | 1920 |
| agcatgatga  | tggttttgct  | ctcctcgttt | tgcctctttt  | gctgagtcctg | ttccatcatt  | 1980 |
| tacgaatcta  | ctctggtttg  | gtattctgat | ctcccattag  | ggctgtagat  | ggagaatgta  | 2040 |
| taactacaaa  | cagctgtttg  | gttcgttctg | ttctctctcat | atttcattga  | ttgttaggta  | 2100 |
| ctcatatctt  | ctatctctcat | gattctaaac | aacgttagtt  | cgtgagggtt  | tgtgtttaga  | 2160 |
| gctttgttct  | tctagttct   | aggtcatttg | gagttcaaaa  | ctttggcaac  | gactgtaact  | 2220 |
| aaagttctca  | ttgttggttc  | ttctacatta | atttctacta  | tt          |             |      |

(2) INFORMATION FOR SEQ ID NO:2479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1572975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Thr | Asp | Phe | Phe | Phe | Ala | Phe | Val | Phe | Ser | Phe | Thr | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Phe | Gly | Phe | Ser | Phe | Ala | Gly | Asp | Pro | Tyr | Val | Ser | Tyr | Asp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Thr | Leu | Ser | Tyr | Ile | Thr | Ala | Ser | Pro | Leu | Gly | Val | Pro | Gln | Gln | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ile | Ala | Val | Asn | Gly | Lys | Phe | Pro | Gly | Pro | Val | Ile | Asn | Ala | Thr | Thr |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Asn | Tyr | Asn | Val | His | Val | Asn | Val | Leu | Asn | His | Leu | Asp | Glu | Pro | Leu |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  | 80  |
| Leu | Leu | Thr | Trp | Pro | Gly | Val | Gln | Met | Arg | Arg | Asn | Ser | Trp | Gln | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Val | Leu | Gly | Thr | Asn | Cys | Pro | Ile | Pro | Pro | Asn | Trp | Asn | Phe | Thr |



[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) LENGTH: 327 amino acids

[illegible]

```
(2) INFORMATION FOR SEQ ID NO:2482:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 737 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..737
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1573108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| agaaaaatcg  | caagttgaat  | gaccttcttg  | atgcgttgga  | cttcaatcaa  | gttggtcattt | 60  |
| ttgtgaagag  | cgtgagCagg  | gctgcggaGc  | tgaacaagtt  | actgggtggaa | tgcaatttcc  | 120 |
| cctcaatatg  | catacactct  | ggcatgtctc  | aagaagagag  | gttgactcga  | tacaaaagtt  | 180 |
| tcaaggaagg  | gcacaagagg  | atccttgtgg  | cgactgactt  | ggtaggaaga  | gggattgaca  | 240 |
| tagagcgtgt  | caacattgtt  | atcaactatg  | acatgccaga  | ttctgcggat  | acctatcttc  | 300 |
| atagggttgg  | gagagctggg  | agatttgga   | ccaaggggtct | tgcaatcaca  | tttggttgc   | 360 |
| ctgcttcaga  | ttcagagggtc | cttaatcagg  | ttcaagagag  | gtttgagggtc | gatataaagg  | 420 |
| agcttcctga  | gcagattgat  | acatcgactt  | acatgccgtc  | ttaaacaagt  | agcatcatct  | 480 |
| ctgaggaacg  | aacctcttca  | gatttcaacc  | ttttagggtgt | tcaaaggggt  | catggagggtc | 540 |
| cacaactatc  | tctcacaccg  | tttggtgtctt | cgctatttta  | gacttttctc  | tgaggacaag  | 600 |
| tttttccata  | tatttagacc  | gttttgaac   | tcttgaaaaa  | tgagattgag  | ctactctcca  | 660 |
| aatcgcgcac  | agttgagagc  | tctcctgttt  | tttgtagtag  | tgatgggttat | ctttaaaata  | 720 |
| tttaagatttc | aggatct     |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1573109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Arg | Lys | Leu | Asn | Asp | Leu | Leu | Asp | Ala | Leu | Asp | Phe | Asn | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Ile | Phe | Val | Lys | Ser | Val | Ser | Arg | Ala | Ala | Glu | Leu | Asn | Lys |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Leu | Leu | Val | Glu | Cys | Asn | Phe | Pro | Ser | Ile | Cys | Ile | His | Ser | Gly | Met |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |
| Ser | Gln | Glu | Glu | Arg | Leu | Thr | Arg | Tyr | Lys | Ser | Phe | Lys | Glu | Gly | His |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Ile | Leu | Val | Ala | Thr | Asp | Leu | Val | Gly | Arg | Gly | Ile | Asp | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Arg | Val | Asn | Ile | Val | Ile | Asn | Tyr | Asp | Met | Pro | Asp | Ser | Ala | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Thr | Tyr | Leu | His | Arg | Val | Gly | Arg | Ala | Gly | Arg | Phe | Gly | Thr | Lys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Leu | Ala | Ile | Thr | Phe | Val | Ala | Ser | Ala | Ser | Asp | Ser | Glu | Val | Leu | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Val | Gln | Glu | Arg | Phe | Glu | Val | Asp | Ile | Lys | Glu | Leu | Pro | Glu | Gln |
| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Ile | Asp | Thr | Ser | Thr | Tyr | Met | Pro | Ser |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1573110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Glu | Glu | Arg | Leu | Thr | Arg | Tyr | Lys | Ser | Phe | Lys | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

His Lys Arg Ile Leu Val Ala Thr Asp Leu Val Gly Arg Gly Ile Asp  
20 25 30  
Ile Glu Arg Val Asn Ile Val Ile Asn Tyr Asp Met Pro Asp Ser Ala  
35 40 45  
Asp Thr Tyr Leu His Arg Val Gly Arg Ala Gly Arg Phe Gly Thr Lys  
50 55 60  
Gly Leu Ala Ile Thr Phe Val Ala Ser Ala Ser Asp Ser Glu Val Leu  
65 70 75 80  
Asn Gln Val Gln Glu Arg Phe Glu Val Asp Ile Lys Glu Leu Pro Glu  
85 90 95  
Gln Ile Asp Thr Ser Thr Tyr Met Pro Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| atgcaatatac | acggacctcc  | acaagtgatg  | cttgatact  | taaaatacca | atgggtcactt | 60   |
| ggagaggaac  | gtaagcgcaa  | agaggcattt  | accaagctgc | agattctaac | gagagagctc  | 120  |
| tcaagtgtgc  | cacattctca  | atctgacata  | ctggctagca | tggtatctag | caaggcgcca  | 180  |
| aatgttccac  | ttcttgacag  | tgtaaatctc  | aaactgggaa | cgtggcagt  | ggcactttct  | 240  |
| tccggtttga  | atgatgggtc  | tattcaagaa  | attcgtgatg | cgtttgacaa | atctacttgc  | 300  |
| tatgctccta  | aatgggctaa  | agcatggcac  | acatgggcat | tattcaatac | agcagtgatg  | 360  |
| tgcattaca   | tttcaagagg  | tcaaattgct  | tcccagtagc | ttgtttctgc | agtcactgga  | 420  |
| tattttttatt | ctatagcatg  | tgcagcaaat  | gccaaaggag | ttgatgatag | tttacaggac  | 480  |
| atactgcgtc  | ttctgacatt  | gtggttcaac  | catggagcta | cagctgatgt | ccaaaccgca  | 540  |
| ttgaagacag  | gattcagtoa  | tgtcaacatt  | aacacatggc | ttgtttgtgt | acctcaaatc  | 600  |
| attgctagga  | tacattctaa  | taatcgtgct  | gtcaggggaa | tgattcagtc | tcttctcatc  | 660  |
| cgcataggcg  | aaaaccaccc  | acaggctctg  | atgtatcccc | ttctcgttgc | atgtaaatca  | 720  |
| ataagcaatc  | ttcggagagc  | tgcggctcaa  | gaggttggtg | ataaagttcg | ccagcacagt  | 780  |
| ggtgcactcg  | tggatcaggc  | gcaacttgta  | tcacatgaac | ttatcagggt | tgccatactt  | 840  |
| tggcatgaaa  | tgtggcatga  | agcactagaa  | gaagctagtc | gcttgtattt | tggtgaacat  | 900  |
| aacattgaa   | gcatgctgaa  | agtacttgaa  | cccttacatg | acatgctcga | cgaaggtgta  | 960  |
| aaaaaggaca  | gtacgaccat  | acaggaaaga  | gcatttatag | aggcataccg | tcacgaacta  | 1020 |
| aaagaggcac  | atgaatgctg  | ttgcaattac  | aagataactg | ggaaagatgc | tgaacttaca  | 1080 |
| caggcttggg  | atctttacta  | tcacgttttc  | aaacggattg | acaaacagct | agccagctctc | 1140 |
| acgacattgg  | atttggaaatc | tgtttctcct  | gagttgctgc | tgtgccgtga | cttgagacta  | 1200 |
| gcagttcctg  | gaacatatcg  | tgcagatgcc  | cccgtcgtga | ctatatcatc | tttttcacgc  | 1260 |
| caacttggtg  | ttataacctc  | taaacaaaga  | ccaaggaaat | tgactattca | cggaaatgac  | 1320 |
| ggtgaggact  | acgccttctt  | gttgaaggga  | catgaagatt | taaggcaaga | tgagcgtggt  | 1380 |
| atgcagcttt  | ttggtttggt  | gaacactttg  | cttgagaatt | ccagaaaaac | agccgaaaaa  | 1440 |
| gatctttcca  | ttcaacgcta  | ttctgttaata | ccactatctc | ccaatagtgg | actcatcgga  | 1500 |
| tgggttccga  | actgcgatac  | ccttcaccat  | cttattcgag | agcgcagaga | tgcaagaaa   | 1560 |
| atcattctta  | atcaagaaaa  | taagcatatg  | ttgagttttg | ctocagacta | tgacaatcta  | 1620 |
| ccgcttatag  | caaaggttga  | agtattttgag | tatgctctag | aaaacacaga | gggaaatgat  | 1680 |
| ctatccaggg  | ttctctgggt  | aaaaagtgcg  | tcgtcagaag | tttggctaga | aagaagaaca  | 1740 |
| aactatacta  | gaagtttagc  | agttatgagt  | atggttggtt | atattcttgg | gttaggtgat  | 1800 |
| cgacacccaa  | gtaaccttat  | gcttcataga  | tacagaatgc | ttgtcaaagc | aatggaagtc  | 1860 |
| agtggcattg  | aaggaaaactt | ccgctcaacc  | tgcgaaaacg | ttatgcaagt | tctcagaacc  | 1920 |
| aataaagata  | gtgtaatggc  | aatgatggaa  | gcgtttgtac | atgatccttt | aatcaattgg  | 1980 |
| cgtcttttca  | atttcaatga  | agtcccccaa  | ttagcactgc | tcggttaaaa | caaccccaat  | 2040 |
| gctcctgctg  | atgttgagcc  | tgacgaagaa  | gatgaagatc | ccgctgatat | agatcttctt  | 2100 |
| cagcctcaaa  | ggagtactcg  | agagaaggag  | attcttcagg | ctgtaaatat | gcttggagat  | 2160 |
| gctaataaag  | ttttaaatga  | gcgtgcccga  | gttggttatg | cacgtatgag | tcataagctt  | 2220 |

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(2) INFORMATION FOR SEQ ID NO:2486:

(A) LENGTH: 803 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..803

(D) OTHER INFORMATION: / Ceres Seq. ID 1573152

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Tyr | His | Gly | Pro | Pro | Gln | Val | Met | Leu | Gly | Tyr | Leu | Lys | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Trp | Ser | Leu | Gly | Glu | Glu | Arg | Lys | Arg | Lys | Glu | Ala | Phe | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Ile | Leu | Thr | Arg | Glu | Leu | Ser | Ser | Val | Pro | His | Ser | Gln | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ile | Leu | Ala | Ser | Met | Val | Ser | Ser | Lys | Gly | Ala | Asn | Val | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Arg | Val | Asn | Leu | Lys | Leu | Gly | Thr | Trp | Gln | Trp | Ala | Leu | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gly | Leu | Asn | Asp | Gly | Ser | Ile | Gln | Glu | Ile | Arg | Asp | Ala | Phe | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ser | Thr | Cys | Tyr | Ala | Pro | Lys | Trp | Ala | Lys | Ala | Trp | His | Thr | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Phe | Asn | Thr | Ala | Val | Met | Ser | His | Tyr | Ile | Ser | Arg | Gly | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Ser | Gln | Tyr | Val | Val | Ser | Ala | Val | Thr | Gly | Tyr | Phe | Tyr | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Ala | Cys | Ala | Ala | Asn | Ala | Lys | Gly | Val | Asp | Asp | Ser | Leu | Gln | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Leu | Arg | Leu | Leu | Thr | Leu | Trp | Phe | Asn | His | Gly | Ala | Thr | Ala | Asp |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Gln | Thr | Ala | Leu | Lys | Thr | Gly | Phe | Ser | His | Val | Asn | Ile | Asn | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Trp | Leu | Val | Val | Leu | Pro | Gln | Ile | Ile | Ala | Arg | Ile | His | Ser | Asn | Asn |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Ala | Val | Arg | Glu | Leu | Ile | Gln | Ser | Leu | Leu | Ile | Arg | Ile | Gly | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | His | Pro | Gln | Ala | Leu | Met | Tyr | Pro | Leu | Leu | Val | Ala | Cys | Lys | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Ser | Asn | Leu | Arg | Arg | Ala | Ala | Ala | Gln | Glu | Val | Val | Asp | Lys | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Gln | His | Ser | Gly | Ala | Leu | Val | Asp | Gln | Ala | Gln | Leu | Val | Ser | His |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Leu | Ile | Arg | Val | Ala | Ile | Leu | Trp | His | Glu | Met | Trp | His | Glu | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Glu | Ala | Ser | Arg | Leu | Tyr | Phe | Gly | Glu | His | Asn | Ile | Glu | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Leu | Lys | Val | Leu | Glu | Pro | Leu | His | Asp | Met | Leu | Asp | Glu | Gly | Val |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Lys | Lys | Asp | Ser | Thr | Thr | Ile | Gln | Glu | Arg | Ala | Phe | Ile | Glu | Ala | Tyr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | His | Glu | Leu | Lys | Glu | Ala | His | Glu | Cys | Cys | Cys | Asn | Tyr | Lys | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Gly | Lys | Asp |     |     |     |     |     |     |     |     |     |     |     |     |

|                         |                     |                         |
|-------------------------|---------------------|-------------------------|
| 355                     | 360                 | 365                     |
| Val Phe Lys Arg Ile Asp | Lys Gln Leu Ala Ser | Leu Thr Thr Leu Asp     |
| 370                     | 375                 | 380                     |
| Leu Glu Ser Val Ser Pro | Glu Leu Leu Leu Cys | Arg Asp Leu Glu Leu     |
| 385                     | 390                 | 395                     |
| Ala Val Pro Gly Thr Tyr | Arg Ala Asp Ala Pro | Val Val Thr Ile Ser     |
| 405                     | 410                 | 415                     |
| Ser Phe Ser Arg Gln Leu | Val Val Ile Thr Ser | Lys Gln Arg Pro Arg     |
| 420                     | 425                 | 430                     |
| Lys Leu Thr Ile His Gly | Asn Asp Gly Glu Asp | Tyr Ala Phe Leu Leu     |
| 435                     | 440                 | 445                     |
| Lys Gly His Glu Asp Leu | Arg Gln Asp Glu Arg | Val Met Gln Leu Phe     |
| 450                     | 455                 | 460                     |
| Gly Leu Val Asn Thr Leu | Leu Glu Asn Ser Arg | Lys Thr Ala Glu Lys     |
| 465                     | 470                 | 475                     |
| Asp Leu Ser Ile Gln Arg | Tyr Ser Val Ile Pro | Leu Ser Pro Asn Ser     |
| 485                     | 490                 | 495                     |
| Gly Leu Ile Gly Trp Val | Pro Asn Cys Asp Thr | Leu His His Leu Ile     |
| 500                     | 505                 | 510                     |
| Arg Glu Xaa Arg Asp Ala | Arg Lys Ile Ile Leu | Asn Gln Glu Asn Lys     |
| 515                     | 520                 | 525                     |
| His Met Leu Ser Phe Ala | Pro Asp Tyr Asp Asn | Leu Pro Leu Ile Ala     |
| 530                     | 535                 | 540                     |
| Lys Val Glu Val Phe Glu | Tyr Ala Leu Glu Asn | Thr Glu Gly Asn Asp     |
| 545                     | 550                 | 555                     |
| Leu Ser Arg Val Leu Trp | Leu Lys Ser Arg Ser | Ser Ser Glu Val Trp Leu |
| 565                     | 570                 | 575                     |
| Glu Arg Arg Thr Asn Tyr | Thr Arg Ser Leu Ala | Val Met Ser Met Val     |
| 580                     | 585                 | 590                     |
| Gly Tyr Ile Leu Gly Leu | Gly Asp Arg His Pro | Ser Asn Leu Met Leu     |
| 595                     | 600                 | 605                     |
| His Arg Tyr Arg Met Leu | Val Lys Ala Met Glu | Val Ser Gly Ile Glu     |
| 610                     | 615                 | 620                     |
| Gly Asn Phe Arg Ser Thr | Cys Glu Asn Val Met | Gln Val Leu Arg Thr     |
| 625                     | 630                 | 635                     |
| Asn Lys Asp Ser Val Met | Ala Met Met Glu Ala | Phe Val His Asp Pro     |
| 645                     | 650                 | 655                     |
| Leu Ile Asn Trp Arg Leu | Phe Asn Phe Asn Glu | Val Pro Gln Leu Ala     |
| 660                     | 665                 | 670                     |
| Leu Leu Gly Asn Asn Asn | Pro Asn Ala Pro Ala | Asp Val Glu Pro Asp     |
| 675                     | 680                 | 685                     |
| Glu Glu Asp Glu Asp Pro | Ala Asp Ile Asp Leu | Pro Gln Pro Gln Arg     |
| 690                     | 695                 | 700                     |
| Ser Thr Arg Glu Lys Glu | Ile Leu Gln Ala Val | Asn Met Leu Gly Asp     |
| 705                     | 710                 | 715                     |
| Ala Asn Glu Val Leu Asn | Glu Arg Ala Val Val | Met Ala Arg Met         |
| 725                     | 730                 | 735                     |
| Ser His Lys Leu Thr Gly | Arg Asp Phe Ser Ser | Ala Ile Pro Ser         |
| 740                     | 745                 | 750                     |
| Asn Pro Ile Ala Asp His | Asn Asn Leu Leu Gly | Gly Asp Ser His Glu     |
| 755                     | 760                 | 765                     |
| Val Glu His Gly Leu Ser | Val Lys Val Gln Val | Gln Lys Leu Ile Asn     |
| 770                     | 775                 | 780                     |
| Gln Ala Thr Ser His Glu | Asn Leu Cys Gln Asn | Tyr Val Gly Trp Cys     |
| 785                     | 790                 | 795                     |
| Pro Phe Trp             |                     |                         |

(2) INFORMATION FOR SEQ ID NO:2487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..794  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573154  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Tyr | Leu | Lys | Tyr | Gln | Trp | Ser | Leu | Gly | Glu | Glu | Arg | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Lys | Glu | Ala | Phe | Thr | Lys | Leu | Gln | Ile | Leu | Thr | Arg | Glu | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | Pro | His | Ser | Gln | Ser | Asp | Ile | Leu | Ala | Ser | Met | Val | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gly | Ala | Asn | Val | Pro | Leu | Leu | Ala | Arg | Val | Asn | Leu | Lys | Leu | Gly |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Trp | Gln | Trp | Ala | Leu | Ser | Ser | Gly | Leu | Asn | Asp | Gly | Ser | Ile | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ile | Arg | Asp | Ala | Phe | Asp | Lys | Ser | Thr | Cys | Tyr | Ala | Pro | Lys | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Ala | Trp | His | Thr | Trp | Ala | Leu | Phe | Asn | Thr | Ala | Val | Met | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Tyr | Ile | Ser | Arg | Gly | Gln | Ile | Ala | Ser | Gln | Tyr | Val | Val | Ser | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Thr | Gly | Tyr | Phe | Tyr | Ser | Ile | Ala | Cys | Ala | Ala | Asn | Ala | Lys | Gly |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Val | Asp | Asp | Ser | Leu | Gln | Asp | Ile | Leu | Arg | Leu | Leu | Thr | Leu | Trp | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | His | Gly | Ala | Thr | Ala | Asp | Val | Gln | Thr | Ala | Leu | Lys | Thr | Gly | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | His | Val | Asn | Ile | Asn | Thr | Trp | Leu | Val | Val | Leu | Pro | Gln | Ile | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Arg | Ile | His | Ser | Asn | Asn | Arg | Ala | Val | Arg | Glu | Leu | Ile | Gln | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Ile | Arg | Ile | Gly | Glu | Asn | His | Pro | Gln | Ala | Leu | Met | Tyr | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Leu | Val | Ala | Cys | Lys | Ser | Ile | Ser | Asn | Leu | Arg | Arg | Ala | Ala | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Glu | Val | Val | Asp | Lys | Val | Arg | Gln | His | Ser | Gly | Ala | Leu | Val | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Ala | Gln | Leu | Val | Ser | His | Glu | Leu | Ile | Arg | Val | Ala | Ile | Leu | Trp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Glu | Met | Trp | His | Glu | Ala | Leu | Glu | Glu | Ala | Ser | Arg | Leu | Tyr | Phe |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Glu | His | Asn | Ile | Glu | Gly | Met | Leu | Lys | Val | Leu | Glu | Pro | Leu | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Met | Leu | Asp | Glu | Gly | Val | Lys | Lys | Asp | Ser | Thr | Thr | Ile | Gln | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Ala | Phe | Ile | Glu | Ala | Tyr | Arg | His | Glu | Leu | Lys | Glu | Ala | His | Glu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Cys | Cys | Cys | Asn | Tyr | Lys | Ile | Thr | Gly | Lys | Asp | Ala | Glu | Leu | Thr | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Trp | Asp | Leu | Tyr | Tyr | His | Val | Phe | Lys | Arg | Ile | Asp | Lys | Gln | Leu |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Ser | Leu | Thr | Thr | Leu | Asp | Leu | Glu | Ser | Val | Ser | Pro | Glu | Leu | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Leu | Cys | Arg | Asp | Leu | Glu | Leu | Ala | Val | Pro | Gly | Thr | Tyr | Arg | Ala | Asp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ala | Pro | Val | Val | Thr | Ile | Ser | Ser | Phe | Ser | Arg | Gln | Leu | Val | Val | Ile |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Thr | Ser | Lys | Gln | Arg | Pro | Arg | Lys | Leu | Thr | Ile | His | Gly | Asn | Asp | Gly |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 420 |     |     |     |     |     |     |     |     |     | 425 |     |     |     | 430 |     |  |  |
| Glu | Asp | Tyr | Ala | Phe | Leu | Leu | Lys | Gly | His | Glu | Asp | Leu | Arg | Gln | Asp |  |  |
| 435 |     |     |     |     |     |     |     |     |     | 440 |     |     |     | 445 |     |  |  |
| Glu | Arg | Val | Met | Gln | Leu | Phe | Gly | Leu | Val | Asn | Thr | Leu | Leu | Glu | Asn |  |  |
| 450 |     |     |     |     |     |     |     |     |     | 455 |     |     |     | 460 |     |  |  |
| Ser | Arg | Lys | Thr | Ala | Glu | Lys | Asp | Leu | Ser | Ile | Gln | Arg | Tyr | Ser | Val |  |  |
| 465 |     |     |     |     |     |     |     |     |     | 470 |     |     |     | 475 |     |  |  |
| Ile | Pro | Leu | Ser | Pro | Asn | Ser | Gly | Leu | Ile | Gly | Trp | Val | Pro | Asn | Cys |  |  |
| 485 |     |     |     |     |     |     |     |     |     | 490 |     |     |     | 495 |     |  |  |
| Asp | Thr | Leu | His | His | Leu | Ile | Arg | Glu | Xaa | Arg | Asp | Ala | Arg | Lys | Ile |  |  |
| 500 |     |     |     |     |     |     |     |     |     | 505 |     |     |     | 510 |     |  |  |
| Ile | Leu | Asn | Gln | Glu | Asn | Lys | His | Met | Leu | Ser | Phe | Ala | Pro | Asp | Tyr |  |  |
| 515 |     |     |     |     |     |     |     |     |     | 520 |     |     |     | 525 |     |  |  |
| Asp | Asn | Leu | Pro | Leu | Ile | Ala | Lys | Val | Glu | Val | Phe | Glu | Tyr | Ala | Leu |  |  |
| 530 |     |     |     |     |     |     |     |     |     | 535 |     |     |     | 540 |     |  |  |
| Glu | Asn | Thr | Glu | Gly | Asn | Asp | Leu | Ser | Arg | Val | Leu | Trp | Leu | Lys | Ser |  |  |
| 545 |     |     |     |     |     |     |     |     |     | 550 |     |     |     | 555 |     |  |  |
| Arg | Ser | Ser | Glu | Val | Trp | Leu | Glu | Arg | Arg | Thr | Asn | Tyr | Thr | Arg | Ser |  |  |
| 565 |     |     |     |     |     |     |     |     |     | 570 |     |     |     | 575 |     |  |  |
| Leu | Ala | Val | Met | Ser | Met | Val | Gly | Tyr | Ile | Leu | Gly | Leu | Gly | Asp | Arg |  |  |
| 580 |     |     |     |     |     |     |     |     |     | 585 |     |     |     | 590 |     |  |  |
| His | Pro | Ser | Asn | Leu | Met | Leu | His | Arg | Tyr | Arg | Met | Leu | Val | Lys | Ala |  |  |
| 595 |     |     |     |     |     |     |     |     |     | 600 |     |     |     | 605 |     |  |  |
| Met | Glu | Val | Ser | Gly | Ile | Glu | Gly | Asn | Phe | Arg | Ser | Thr | Cys | Glu | Asn |  |  |
| 610 |     |     |     |     |     |     |     |     |     | 615 |     |     |     | 620 |     |  |  |
| Val | Met | Gln | Val | Leu | Arg | Thr | Asn | Lys | Asp | Ser | Val | Met | Ala | Met | Met |  |  |
| 625 |     |     |     |     |     |     |     |     |     | 630 |     |     |     | 635 |     |  |  |
| Glu | Ala | Phe | Val | His | Asp | Pro | Leu | Ile | Asn | Trp | Arg | Leu | Phe | Asn | Phe |  |  |
| 645 |     |     |     |     |     |     |     |     |     | 650 |     |     |     | 655 |     |  |  |
| Asn | Glu | Val | Pro | Gln | Leu | Ala | Leu | Leu | Gly | Asn | Asn | Asn | Pro | Asn | Ala |  |  |
| 660 |     |     |     |     |     |     |     |     |     | 665 |     |     |     | 670 |     |  |  |
| Pro | Ala | Asp | Val | Glu | Pro | Asp | Glu | Glu | Asp | Glu | Asp | Pro | Ala | Asp | Ile |  |  |
| 675 |     |     |     |     |     |     |     |     |     | 680 |     |     |     | 685 |     |  |  |
| Asp | Leu | Pro | Gln | Pro | Gln | Arg | Ser | Thr | Arg | Glu | Lys | Glu | Ile | Leu | Gln |  |  |
| 690 |     |     |     |     |     |     |     |     |     | 695 |     |     |     | 700 |     |  |  |
| Ala | Val | Asn | Met | Leu | Gly | Asp | Ala | Asn | Glu | Val | Leu | Asn | Glu | Arg | Ala |  |  |
| 705 |     |     |     |     |     |     |     |     |     | 710 |     |     |     | 715 |     |  |  |
| Val | Val | Val | Met | Ala | Arg | Met | Ser | His | Lys | Leu | Thr | Gly | Arg | Asp | Phe |  |  |
| 725 |     |     |     |     |     |     |     |     |     | 730 |     |     |     | 735 |     |  |  |
| Ser | Ser | Ser | Ala | Ile | Pro | Ser | Asn | Pro | Ile | Ala | Asp | His | Asn | Asn | Leu |  |  |
| 740 |     |     |     |     |     |     |     |     |     | 745 |     |     |     | 750 |     |  |  |
| Leu | Gly | Gly | Asp | Ser | His | Glu | Val | Glu | His | Gly | Leu | Ser | Val | Lys | Val |  |  |
| 755 |     |     |     |     |     |     |     |     |     | 760 |     |     |     | 765 |     |  |  |
| Gln | Val | Gln | Lys | Leu | Ile | Asn | Gln | Ala | Thr | Ser | His | Glu | Asn | Leu | Cys |  |  |
| 770 |     |     |     |     |     |     |     |     |     | 775 |     |     |     | 780 |     |  |  |
| Gln | Asn | Tyr | Val | Gly | Trp | Cys | Pro | Phe | Trp |     |     |     |     |     |     |  |  |
| 785 |     |     |     |     |     |     |     |     |     | 790 |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..837
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

atggcggaag aagcaaatc caaaggaaac gcagctttct cttccggcga ttacgccacc  
gcaataaccc atttcacaga agcaatcaac ctttcatcaa ccaatcacat cctctactca

60  
120

SEQUENCE LISTING

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| aacagatccg | cttcttacgc  | ttctctccac | cgttacgaag  | aagctttatc | agaagcgaag | 180 |
| aagactatag | agcttaaacc  | tgattggtct | aaaggatata  | gccgattagg | tgctgcgttt | 240 |
| attggattgt | ccaagtttga  | tgaagcggtt | gattcgtata  | agaaaggatt | agagattgat | 300 |
| ccgagtaatg | agatgcttaa  | atcgggatta | gctgatgctt  | cgagatctag | ggtttcgtca | 360 |
| aagtcgaatc | cttttggtga  | tgcgtttcaa | gggaaggaga  | tgtgggagaa | ggtgacggcg | 420 |
| gatccgggga | ctaggggttta | tttggagcag | gatgattttg  | ttaagacgat | gaaggagatt | 480 |
| cagaggaacc | ctaataatct  | taatttgtat | atgaaggata  | agagagttat | gaaggcttta | 540 |
| ggggttttgt | tgaatgtgaa  | gtttggtgga | tctagtgggtg | aagatactga | gatgaaggag | 600 |
| gctgatgaga | ggaaagagcc  | tgaaccggag | atggaacccta | tggagttgac | ggaggaggag | 660 |
| aggcagaaga | aggagagaaa  | ggagaaggct | ttgaaggaga  | aaggggaagg | aatgttgct  | 720 |
| tataagaaga | aggattttga  | gagagctggt | gaacattata  | ctaaggccat | ggagctcgat | 780 |
| gatgaggata | tttcgtatgt  | gacgaatcgt | gctgctgttt  | atcttgagat | ggggaag    |     |

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1573309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Glu | Ala | Lys | Ser | Lys | Gly | Asn | Ala | Ala | Phe | Ser | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Tyr | Ala | Thr | Ala | Ile | Thr | His | Phe | Thr | Glu | Ala | Ile | Asn | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Asn | His | Ile | Leu | Tyr | Ser | Asn | Arg | Ser | Ala | Ser | Tyr | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | His | Arg | Tyr | Glu | Glu | Ala | Leu | Ser | Asp | Ala | Lys | Lys | Thr | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Lys | Pro | Asp | Trp | Ser | Lys | Gly | Tyr | Ser | Arg | Leu | Gly | Ala | Ala | Phe |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Gly | Leu | Ser | Lys | Phe | Asp | Glu | Ala | Val | Asp | Ser | Tyr | Lys | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Leu | Glu | Ile | Asp | Pro | Ser | Asn | Glu | Met | Leu | Lys | Ser | Gly | Leu | Ala | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Arg | Ser | Arg | Val | Ser | Ser | Lys | Ser | Asn | Pro | Phe | Val | Asp | Ala |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Phe | Gln | Gly | Lys | Glu | Met | Trp | Glu | Lys | Leu | Thr | Ala | Asp | Pro | Gly | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Val | Tyr | Leu | Glu | Gln | Asp | Asp | Phe | Val | Lys | Thr | Met | Lys | Glu | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Arg | Asn | Pro | Asn | Asn | Leu | Asn | Leu | Tyr | Met | Lys | Asp | Lys | Arg | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Lys | Ala | Leu | Gly | Val | Leu | Leu | Asn | Val | Lys | Phe | Gly | Gly | Ser | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Asp | Thr | Glu | Met | Lys | Glu | Ala | Asp | Glu | Arg | Lys | Glu | Pro | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Glu | Met | Glu | Pro | Met | Glu | Leu | Thr | Glu | Glu | Glu | Arg | Gln | Lys | Lys |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Glu | Arg | Lys | Glu | Lys | Ala | Leu | Lys | Glu | Lys | Gly | Glu | Gly | Asn | Val | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Tyr | Lys | Lys | Lys | Asp | Phe | Glu | Arg | Ala | Val | Glu | His | Tyr | Thr | Lys | Ala |
|     |     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |
| Met | Glu | Leu | Asp | Asp | Glu | Asp | Ile | Ser | Tyr | Leu | Thr | Asn | Arg | Ala | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Tyr | Leu | Glu | Met | Gly | Lys |     |     |     |     |     |     |     |     |     |
|     |     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2490:

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(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 175 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..175  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573311  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:  
Met Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser  
1                  5                  10                  15  
Lys Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu  
                  20                  25                  30  
Lys Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp  
                  35                  40                  45  
Phe Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn  
50                  55                  60  
Leu Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu  
65                  70                  75                  80  
Asn Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu  
                  85                  90                  95  
Ala Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu  
                  100                 105                 110  
Thr Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys  
                 115                 120                 125  
Glu Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Glu Arg  
130                 135                 140  
Ala Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile  
145                 150                 155                 160  
Ser Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
                 165                 170                 175

(2) INFORMATION FOR SEQ ID NO:2491:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1573315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

acttacacca cgacaaaaag ggaatgtgtt cacgtgtgtc ttcgtttttt tgatcgctat 60  
cggattcgct gcagttatcg tttatgtctg ctttgcatac gcacgagaaa cacgtgaaaa 120  
acggcgtgaa gaacaac

(2) INFORMATION FOR SEQ ID NO:2492:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 38 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1573316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

Thr Tyr Thr Thr Thr Lys Arg Glu Cys Val His Val Cys Leu Arg Phe

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..114  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573401  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:  
atggatgaag aaggtcacat tatacacatt gatttcgggt ttatgctttc aaattctcct 60  
ggtggcgtga accttgagag tgccccatctt aagctaactc gggaacttct tgag  
(2) INFORMATION FOR SEQ ID NO:2497:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 38 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..38  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573402  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:  
Met Asp Glu Glu Gly His Ile Ile His Ile Asp Phe Gly Phe Met Leu  
1                  5                  10                  15  
Ser Asn Ser Pro Gly Gly Val Asn Phe Glu Ser Ala Pro Phe Lys Leu  
                  20                  25                  30  
Thr Arg Glu Leu Leu Glu  
                  35  
(2) INFORMATION FOR SEQ ID NO:2498:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 178 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..178  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573446  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:  
atgtatgaaa acaagagtga tgggccaagc tggcgagtac caacgggtcg taaagacggg 60  
agactctcgt tggcaactaa agcatogaat ctaccttctc cacttgactc tgttgctgtt 120  
caaaagcaaa agtttcaaga taaaggattg gatactcatg atcttggtac tctactag  
(2) INFORMATION FOR SEQ ID NO:2499:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 59 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..59  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573447  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:  
Met Tyr Glu Asn Lys Ser Asp Gly Pro Ser Trp Arg Val Pro Thr Gly  
1                  5                  10                  15  
Arg Lys Asp Gly Arg Leu Ser Leu Ala Thr Lys Ala Ser Asn Leu Pro  
                  20                  25                  30  
Ser Pro Leu Asp Ser Val Ala Val Gln Lys Gln Lys Phe Gln Asp Lys  
                  35                  40                  45  
Gly Leu Asp Thr His Asp Leu Val Thr Leu Leu  
                  50                  55

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(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Cys Met Lys Thr Arg Val Met Gly Gln Ala Gly Glu Tyr Gln Arg Val  
1 5 10 15  
Val Lys Thr Gly Asp Ser Arg Trp Gln Leu Lys His Arg Ile Tyr Leu  
20 25 30  
Leu His Leu Thr Leu Leu Leu Phe Lys Ser Lys Ser Phe Lys Ile Lys  
35 40 45  
Asp Trp Ile Leu Met Ile Leu Leu Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..759
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

atgcaaaactc gatccaaagg ttctgcacac ctactaccat tcagagacgg aatagataga 60  
atagctcgtg agttacaaga aaccaaagca aaggcaacct gtgatcagca aagaccagct 120  
gctatggatc aacagaacat accagttgat gttcaagacc cacctaattg tgatcaacca 180  
agaaacattg gtgctggtga tgccccaagg aatcatcacc aaagacaagg gatagtgcct 240  
ccaccagttc agaacaacaa ctttgaaatc aagagtggtc tcatctccat gatccaagga 300  
aacaagtttc atggtttacc tatggaagat cccctggacc atcttgacag ctttgatagg 360  
ctctgtggcc ttaccaagat caatgggtgc actgaagata tgtttaagct cagactatct 420  
cccttctctt tgggaaacaa ggcacaccac tgggagaaga ctctgcccc agactccatc 480  
aactcatggg acgattataa gaaagctttt cttgtcaagt tctactctaa cgctcgacc 540  
gctagattga ggaacgagat cccaggcttc acacagaaaa acaatgaaac tttctgtgaa 600  
gcttgggaaa ggtttcaaga aggcttcatt attgagcaca ctctaccaag gagctttacc 660  
aaatatcaga atgctactcg acaccgcgct caatggaaac ttctgaact aggatgtaga 720  
agaaggctag gagttagtcg aaaatctagc acaatctaa

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

Met Gln Thr Arg Ser Lys Gly Ser Ala His Leu Leu Pro Phe Arg Asp  
1 5 10 15  
Gly Ile Asp Arg Ile Ala Arg Glu Leu Gln Glu Thr Lys Ala Lys Ala  
20 25 30

Thr Cys Asp Gln Gln Arg Pro Ala Ala Met Asp Gln Gln Asn Ile Pro  
35 40 45  
Val Asp Val Gln Asp Pro Pro Asn Val Asp Gln Pro Arg Asn Ile Gly  
50 55 60  
Ala Gly Asp Ala Pro Arg Asn His His Gln Arg Gln Gly Ile Val Pro  
65 70 75 80  
Pro Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ser  
85 90 95  
Met Ile Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu  
100 105 110  
Asp His Leu Asp Ser Phe Asp Arg Leu Cys Gly Leu Thr Lys Ile Asn  
115 120 125  
Gly Val Thr Glu Asp Met Phe Lys Leu Arg Leu Phe Pro Phe Ser Leu  
130 135 140  
Gly Asn Lys Ala His His Trp Glu Lys Thr Leu Pro Pro Asp Ser Ile  
145 150 155 160  
Asn Ser Trp Asp Asp Tyr Lys Lys Ala Phe Leu Val Lys Phe Tyr Ser  
165 170 175  
Asn Ala Arg Thr Ala Arg Leu Arg Asn Glu Ile Pro Gly Phe Thr Gln  
180 185 190  
Lys Asn Asn Glu Thr Phe Cys Glu Ala Trp Glu Arg Phe Gln Glu Gly  
195 200 205  
Phe Ile Ile Glu His Thr Leu Pro Arg Ser Phe Thr Lys Tyr Gln Asn  
210 215 220  
Ala Thr Arg His Arg Val Gln Trp Lys Leu Pro Glu Leu Gly Cys Arg  
225 230 235 240  
Arg Arg Leu Gly Val Ser Arg Lys Ser Ser Thr Ile  
245 250

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

Met Asp Gln Gln Asn Ile Pro Val Asp Val Gln Asp Pro Pro Asn Val  
1 5 10 15  
Asp Gln Pro Arg Asn Ile Gly Ala Gly Asp Ala Pro Arg Asn His His  
20 25 30  
Gln Arg Gln Gly Ile Val Pro Pro Val Gln Asn Asn Phe Glu  
35 40 45  
Ile Lys Ser Gly Leu Ile Ser Met Ile Gln Gly Asn Lys Phe His Gly  
50 55 60  
Leu Pro Met Glu Asp Pro Leu Asp His Leu Asp Ser Phe Asp Arg Leu  
65 70 75 80  
Cys Gly Leu Thr Lys Ile Asn Gly Val Thr Glu Asp Met Phe Lys Leu  
85 90 95  
Arg Leu Phe Pro Phe Ser Leu Gly Asn Lys Ala His His Trp Glu Lys  
100 105 110  
Thr Leu Pro Pro Asp Ser Ile Asn Ser Trp Asp Asp Tyr Lys Lys Ala  
115 120 125  
Phe Leu Val Lys Phe Tyr Ser Asn Ala Arg Thr Ala Arg Leu Arg Asn  
130 135 140  
Glu Ile Pro Gly Phe Thr Gln Lys Asn Asn Glu Thr Phe Cys Glu Ala  
145 150 155 160  
Trp Glu Arg Phe Gln Glu Gly Phe Ile Ile Glu His Thr Leu Pro Arg

(2) INFORMATION FOR SEQ ID NO:2504:

(A) LENGTH: 566 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..566  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573558

| (X1) SEQUENCE ALIGNMENT: SEQ ID NO: 1 |            |            |            |             |            |     |
|---------------------------------------|------------|------------|------------|-------------|------------|-----|
| atcgtcaaag                            | caaccaaac  | cataaaagag | agatttaata | caaaaagaaag | agaaaaaaga | 60  |
| aagatatagg                            | aggactcatc | aacaagatcg | gagacgcact | ccacattgga  | ggaggcaaca | 120 |
| aggaaggtga                            | gcacaagaag | gaagaggaac | acaagaaaca | cgttgacgag  | cacaagagtg | 180 |
| gtgagcacia                            | agaaggtatt | gttgacaaga | tcaaagacaa | gatccacggt  | ggtgaaggta | 240 |
| aaagccacga                            | cggagaaggc | aaaagccacg | acggtgagaa | gaaaaagaag  | aaggacaaga | 300 |
| aggagaagaa                            | acatcatgat | gatggtcacc | acagcagcag | cagtgcacgc  | gacagcattt | 360 |
| aaggtgagga                            | agtgaggagg | atcgtcttga | taaaacagat | ctggttcttg  | ctattattaa | 420 |
| ttaatgttgc                            | tgtatgttct | tatcatctta | gagagaggtt | aagacagga   | gaaccgtgca | 480 |
| tctatctttg                            | Ytgtttatgt | ttctgttttc | ttgtcatgaa | aattatgctc  | atgtatctta | 540 |
| tctaatacaa                            | aaataataat | ttgatg     |            |             |            |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573559

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Lys | Ala | Thr | Lys | His | Ile | Lys | Glu | Arg | Phe | Asn | Thr | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | Lys | Arg | Lys | Ile | Trp | Gln | Asp | Ser | Ser | Thr | Arg | Ser | Glu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ser | Thr | Leu | Glu | Glu | Ala | Thr | Arg | Lys | Val | Ser | Thr | Arg | Arg | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asn | Thr | Arg | Asn | Thr | Leu | Thr | Ser | Thr | Arg | Val | Val | Ser | Thr | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Val | Leu | Leu | Thr | Arg | Ser | Lys | Thr | Arg | Ser | Thr | Val | Val | Lys | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Ala | Thr | Thr | Glu | Lys | Ala | Lys | Ala | Thr | Thr | Val | Arg | Arg | Lys | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Arg | Thr | Arg | Arg | Arg | Arg | Asn | Ile | Met | Met | Met | Val | Thr | Thr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ala | Val | Thr | Ala | Thr | Ala | Phe | Lys | Val | Arg | Lys |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: amino acid



[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1363

(D) OTHER INFORMATION: / Ceres Seq. ID 1573561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

| (X1) SEQUENCE | DESCRIPTION | SIZE (bp)   |             |             |             |      |
|---------------|-------------|-------------|-------------|-------------|-------------|------|
| acaatctatc    | gagctaaaac  | actgaagcag  | acattagcgt  | tgagaaaaaW  | aaaaaaaaagt | 60   |
| aagaacgaga    | gagagaaaagc | catgtctgcg  | aaaacaatcc  | tatcatcagt  | agtttttggtg | 120  |
| gttctcgtcg    | ccgcatacgc  | agcggctaata | atcggattcg  | atgagtcaaa  | cccgatccga  | 180  |
| atggctctccg   | atggctctccg | ggaggtagaa  | gaatctgttt  | cccagatctt  | aggtcaatct  | 240  |
| cgtcacgttc    | tctcttttcgc | tgcgttcact  | caccgatatg  | gtaaaaagta  | tcagaacgtg  | 300  |
| gaggagatga    | agcttcgatt  | ctcgaattttc | aaggagaatc  | ttgatttgat  | gagatccacc  | 360  |
| aacaagaaag    | gcttattctta | caaatccggt  | gttaattcaat | ttgtgtgattt | gcgatggcaa  | 420  |
| gagtttcaaa    | ggaccaagct  | tggtgctgct  | cagaactgct  | ctgccacttt  | aaagggcagc  | 480  |
| cacaaggtca    | cagaagcagc  | tcttctctgaa | acaaaagact  | ggagagaaga  | tggtatcggt  | 540  |
| agtccggtca    | aagatcaggg  | aggttgtgga  | tcttgctgga  | cattcagcac  | aactggagct  | 600  |
| cttgaggcag    | cttaccatca  | ggcattttgga | aaaggaatat  | ctctctctga  | gcaacagctt  | 660  |
| gtggattgtg    | ctggaagcttt | caataactat  | ggttgcaatg  | gtggccttcc  | ttctcaagcc  | 720  |
| tttgaataca    | taaaaatccaa | cgggtggcctc | gacacagaga  | aagcttatcc  | ttataccggt  | 780  |
| aaagatgaaa    | cctgcaaatt  | ttcagctgaa  | aacgttggtg  | tacaagtcct  | caactcagtc  | 840  |
| aacattactc    | tgggtgctga  | agatgaactg  | aagcatcgcg  | ttgBgattgg  | tacggccagt  | 900  |
| aagcatagca    | tttgaggtta  | tacactcggt  | cgggctttac  | aagagtggag  | tttacactga  | 960  |
| tagtcactgt    | ggaagtactc  | caatggatgt  | gaaccacgcg  | gttttgccg   | ttggttatgg  | 1020 |
| agttgaagac    | ggtgtaccat  | attggcttat  | taagaactca  | tggggagcgg  | attggggcga  | 1080 |
| caaaggttac    | ttcaagatgg  | agatggggaa  | gaacatgtgt  | ggtattgcta  | catgtgcata  | 1140 |
| ataccccggt    | gtggcttgag  | atgatcagcg  | aatctgggtg  | gtcaattatc  | aaattacgaa  | 1200 |
| atggttcacgt   | atttatttga  | ttaaagacatt | acgttaaaagt | tgggacttgg  | gaatgcatat  | 1260 |
| ggttttatgct   | tgtttgaaca  | tataaaaggtc | tgtaaatatg  | tacaaaaataa | agccaaaact  | 1320 |
| atagacgaca    | atatttataat | attttcatgt  | taaatattatg | aac         |             |      |

(2) INFORMATION FOR SEQ ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..304  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573562  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

Thr Ile Tyr Arg Ala Lys Thr Leu Lys Gln Thr Leu Ala Leu Arg Lys  
1                   5                   10                   15  
Xaa Lys Lys Ser Lys Asn Glu Arg Glu Lys Ala Met Ser Ala Lys Thr  
          20                   25                   30  
Ile Leu Ser Ser Val Val Leu Val Val Leu Val Ala Ala Ser Ala Ala  
          35                   40                   45  
Ala Asn Ile Gly Phe Asp Glu Ser Asn Pro Ile Arg Met Val Ser Asp  
          50                   55                   60  
Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln Ile Leu Gly Gln Ser  
65                   70                   75                   80  
Arg His Val Leu Ser Phe Ala Arg Phe Thr His Arg Tyr Gly Lys Lys  
          85                   90                   95  
Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe Ser Ile Phe Lys Glu  
          100                   105                   110  
Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys Gly Leu Ser Tyr Lys  
          115                   120                   125  
Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp Gln Glu Phe Gln Arg  
          130                   135                   140  
Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala Thr Leu Lys Gly Ser  
145                   150                   155                   160  
His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr Lys Asp Trp Arg Glu  
          165                   170                   175  
Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly Gly Cys Gly Ser Cys  
          180                   185                   190  
Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala Ala Tyr His Gln Ala  
          195                   200                   205  
Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Ala  
          210                   215                   220  
Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly Leu Pro Ser Gln Ala  
225                   230                   235                   240  
Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp Thr Glu Lys Ala Tyr  
          245                   250                   255  
Pro Tyr Thr Gly Lys Asp Glu Thr Cys Lys Phe Ser Ala Glu Asn Val  
          260                   265                   270  
Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr Leu Gly Ala Glu Asp  
          275                   280                   285  
Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala Ser Lys His Ser Ile  
          290                   295                   300

(2) INFORMATION FOR SEQ ID NO:2509:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 277 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..277  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573563  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

Met Ser Ala Lys Thr Ile Leu Ser Ser Val Val Leu Val Val Leu Val

1 5 10 15  
Ala Ala Ser Ala Ala Asn Ile Gly Phe Asp Glu Ser Asn Pro Ile  
20 25 30  
Arg Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln  
35 40 45  
Ile Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His  
50 55 60  
Arg Tyr Gly Lys Lys Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe  
65 70 75 80  
Ser Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys  
85 90 95  
Gly Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp  
100 105 110  
Gln Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala  
115 120 125  
Thr Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr  
130 135 140  
Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly  
145 150 155 160  
Gly Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala  
165 170 175  
Ala Tyr His Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln  
180 185 190  
Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly  
195 200 205  
Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp  
210 215 220  
Thr Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys Lys Phe  
225 230 235 240  
Ser Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr  
245 250 255  
Leu Gly Ala Glu Asp Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala  
260 265 270  
Ser Lys His Ser Ile  
275

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1573564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln Ile  
1 5 10 15  
Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His Arg  
20 25 30  
Tyr Gly Lys Lys Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe Ser  
35 40 45  
Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys Gly  
50 55 60  
Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp Gln  
65 70 75 80  
Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala Thr  
85 90 95  
Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr Lys  
100 105 110

Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly Gly  
115 120 125  
Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala Ala  
130 135 140  
Tyr His Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln Leu  
145 150 155 160  
Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly Leu  
165 170 175  
Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp Thr  
180 185 190  
Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys Lys Phe Ser  
195 200 205  
Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr Leu  
210 215 220  
Gly Ala Glu Asp Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala Ser  
225 230 235 240  
Lys His Ser Ile

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..545
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ttttctttga gtcgcttcac ttctcttgca tccttcaaac tcatccacag gaatggcgac | 60  |
| agCagcagca ccagcagtga ttcatggac aagatcaggc attgtgtcca aatccggaca  | 120 |
| aaccagaag aaatctgaga tgaaagtctt ttacataact ggacttaact catatggtgg  | 180 |
| tctcaaggca cagaacaaca aggttgtctc aatgggatca ccactctgca cagaacagtg | 240 |
| ttttgctaac gttgtgatgt ctctcaaagg aagaagaggt aatggaggag ccttatccac | 300 |
| cacgtgtaac ctgtcggaga gattttcaag attgcagcaa tcatgaacgc tcttactctt | 360 |
| gttggtgttg cagttggatt cgttcttctt cgaatcgaaa cttctgttga agaagctgaa | 420 |
| gcagagtaaa tagagtaaat tgcgtctctt ataattatat atttttggtt attgtgttg  | 480 |
| tcaagctttg gtaaaacttg atggatacat gttacatttg tttatgaaga agctcttttc | 540 |
| ttggc                                                             |     |

(2) INFORMATION FOR SEQ ID NO:2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

Met Ala Thr Ala Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly  
1 5 10 15  
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val  
20 25 30  
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn  
35 40 45  
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe  
50 55 60  
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn Gly Gly Ala

(2) INFORMATION FOR SEQ ID NO:2513:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1573567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

65

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1357

(D) OTHER INFORMATION: / Ceres Seq. ID 1573568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

| (X1) SEQUENCE DESCRIPTION: SEQ ID: NO: 1 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 |
|------------------------------------------|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|------------------------------------------|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

tcatgttttc tcttttcttc atctatatatt ttactgc

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1573569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Pro | Ser | Gly | Ala | Ser | Ala | Leu | Phe | Arg | Glu | Glu | Asp | Pro | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Lys | Arg | Lys | Lys | Trp | Thr | Ile | Cys | Met | Xaa | Pro | Gly | Arg | His | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Val | Pro | Gly | Pro | Val | Asn | Ile | Pro | Glu | Pro | Val | Ile | Arg | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Arg | Asn | Asn | Glu | Asp | Tyr | Arg | Ser | Pro | Ala | Ile | Pro | Ala | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Thr | Lys | Thr | Leu | Leu | Glu | Asp | Val | Lys | Lys | Ile | Phe | Lys | Thr | Thr | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Thr | Pro | Phe | Leu | Phe | Pro | Thr | Thr | Gly | Thr | Gly | Ala | Trp | Glu | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Thr | Asn | Thr | Leu | Ser | Pro | Gly | Asp | Arg | Ile | Val | Ser | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Gln | Phe | Ser | Leu | Leu | Trp | Ile | Asp | Gln | Gln | Lys | Arg | Leu | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Asn | Val | Asp | Val | Val | Glu | Ser | Asp | Trp | Gly | Gln | Gly | Ala | Asn | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Val | Leu | Ala | Ser | Lys | Leu | Ser | Gln | Asp | Glu | Asn | His | Thr | Ile | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ile | Cys | Ile | Val | His | Asn | Glu | Thr | Ala | Thr | Gly | Val | Thr | Asn | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ser | Ala | Val | Arg | Thr | Leu | Leu | Asp | His | Tyr | Lys | His | Pro | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Val | Asp | Gly | Val | Ser | Ser | Ile | Cys | Ala | Leu | Asp | Phe | Arg | Met |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Glu | Trp | Gly | Val | Asp | Val | Ala | Leu | Thr | Gly | Ser | Gln | Lys | Ala | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Leu | Pro | Thr | Gly | Leu | Gly | Ile | Val | Cys | Ala | Ser | Pro | Lys | Ala | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ala | Thr | Lys | Thr | Ser | Lys | Ser | Leu | Lys | Val | Phe | Phe | Asp | Trp | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Tyr | Leu | Lys | Phe | Tyr | Lys | Leu | Gly | Thr | Tyr | Trp | Pro | Tyr | Thr | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ile | Gln | Leu | Leu | Tyr | Gly | Leu | Arg | Ala | Ala | Leu | Asp | Leu | Ile | Phe |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Gly | Leu | Glu | Asn | Ile | Ile | Ala | Arg | His | Ala | Arg | Leu | Gly | Lys |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Thr | Arg | Leu | Ala | Val | Glu | Ala | Trp | Gly | Leu | Lys | Asn | Cys | Thr | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Glu | Glu | Trp | Ile | Ser | Asn | Thr | Val | Thr | Ala | Val | Met | Val | Pro | Pro |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| His | Ile | Asp | Gly | Ser | Glu | Ile | Val | Arg | Arg | Ala | Trp | Gln | Arg | Tyr | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Ser | Leu | Gly | Leu | Gly | Leu | Asn | Lys | Val | Ala | Gly | Lys | Val | Phe | Arg |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Ile | Gly | His | Leu | Gly | Asn | Val | Asn | Glu | Leu | Gln | Leu | Leu | Gly | Cys | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2516:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1573570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Pro | Gly | Arg | His | His | Leu | Phe | Val | Pro | Gly | Pro | Val | Asn | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Glu | Pro | Val | Ile | Arg | Ala | Met | Asn | Arg | Asn | Asn | Glu | Asp | Tyr | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Ala | Ile | Pro | Ala | Leu | Thr | Lys | Thr | Leu | Leu | Glu | Asp | Val | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Phe | Lys | Thr | Thr | Ser | Gly | Thr | Pro | Phe | Leu | Phe | Pro | Thr | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Thr | Gly | Ala | Trp | Glu | Ser | Ala | Leu | Thr | Asn | Thr | Leu | Ser | Pro | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Arg | Ile | Val | Ser | Phe | Leu | Ile | Gly | Gln | Phe | Ser | Leu | Leu | Trp | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Gln | Gln | Lys | Arg | Leu | Asn | Phe | Asn | Val | Asp | Val | Val | Glu | Ser | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Gly | Gln | Gly | Ala | Asn | Leu | Gln | Val | Leu | Ala | Ser | Lys | Leu | Ser | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Glu | Asn | His | Thr | Ile | Lys | Ala | Ile | Cys | Ile | Val | His | Asn | Glu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Gly | Val | Thr | Asn | Asp | Ile | Ser | Ala | Val | Arg | Thr | Leu | Leu | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Tyr | Lys | His | Pro | Ala | Leu | Leu | Leu | Val | Asp | Gly | Val | Ser | Ser | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Cys | Ala | Leu | Asp | Phe | Arg | Met | Asp | Glu | Trp | Gly | Val | Asp | Val | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Gly | Ser | Gln | Lys | Ala | Leu | Ser | Leu | Pro | Thr | Gly | Leu | Gly | Ile | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Ala | Ser | Pro | Lys | Ala | Leu | Glu | Ala | Thr | Lys | Thr | Ser | Lys | Ser | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Val | Phe | Phe | Asp | Trp | Asn | Asp | Tyr | Leu | Lys | Phe | Tyr | Lys | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Tyr | Trp | Pro | Tyr | Thr | Pro | Ser | Ile | Gln | Leu | Leu | Tyr | Gly | Leu | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala | Leu | Asp | Leu | Ile | Phe | Glu | Glu | Gly | Leu | Glu | Asn | Ile | Ile | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Arg | His | Ala | Arg | Leu | Gly | Lys | Ala | Thr | Arg | Leu | Ala | Val | Glu | Ala | Trp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Leu | Lys | Asn | Cys | Thr | Gln | Lys | Glu | Glu | Trp | Ile | Ser | Asn | Thr | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ala | Val | Met | Val | Pro | Pro | His | Ile | Asp | Gly | Ser | Glu | Ile | Val | Arg |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Ala | Trp | Gln | Arg | Tyr | Asn | Leu | Ser | Leu | Gly | Leu | Gly | Leu | Asn | Lys |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Ala | Gly | Lys | Val | Phe | Arg | Ile | Gly | His | Leu | Gly | Asn | Val | Asn | Glu |

340 345 350  
Leu Gln Leu Leu Gly Cys Leu Ala Gly Val Glu Met Ile Leu Lys Asp  
355 360 365  
Val Gly Tyr Pro Val Val Met Gly Ser Gly Val Ala Ala Ala Ser Thr  
370 375 380  
Tyr Leu Gln His His Ile Pro Leu Ile Pro Ser Arg Ile  
385 390 395

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1573571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

Met Asn Arg Asn Asn Glu Asp Tyr Arg Ser Pro Ala Ile Pro Ala Leu  
1 5 10 15  
Thr Lys Thr Leu Leu Glu Asp Val Lys Lys Ile Phe Lys Thr Thr Ser  
20 25 30  
Gly Thr Pro Phe Leu Phe Pro Thr Thr Gly Thr Gly Ala Trp Glu Ser  
35 40 45  
Ala Leu Thr Asn Thr Leu Ser Pro Gly Asp Arg Ile Val Ser Phe Leu  
50 55 60  
Ile Gly Gln Phe Ser Leu Leu Trp Ile Asp Gln Lys Arg Leu Asn  
65 70 75 80  
Phe Asn Val Asp Val Val Glu Ser Asp Trp Gly Gln Gly Ala Asn Leu  
85 90 95  
Gln Val Leu Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys  
100 105 110  
Ala Ile Cys Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp  
115 120 125  
Ile Ser Ala Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu  
130 135 140  
Leu Leu Val Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met  
145 150 155 160  
Asp Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu  
165 170 175  
Ser Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu  
180 185 190  
Glu Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn  
195 200 205  
Asp Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro  
210 215 220  
Ser Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile Phe  
225 230 235 240  
Glu Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys  
245 250 255  
Ala Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln  
260 265 270  
Lys Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro  
275 280 285  
His Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn  
290 295 300  
Leu Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg  
305 310 315 320  
Ile Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu  
325 330 335

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Ala Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met  
340 345 350  
Gly Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro  
355 360 365  
Leu Ile Pro Ser Arg Ile  
370

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1449

(D) OTHER INFORMATION: / Ceres Seq. ID 1573572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

caaaacctcc ctcaggagct tccgccttat tcagagtgtg gaggaggatc caaaagaaaa 60  
gaggaaaaaa tggactatat gtatggacca gggagacacc atctgtttgt accaggacca 120  
gtgaacatac cggaaccggg aatccggggc atgaaccgga acaacgagga ttaccgggtca 180  
ccagccattc cggcgcttac gaaaacattg ttggaggatg ttaagaagat attcaagacc 240  
acatcaggga caccttttct gtttcccacg accgggactg gtgcttgga gagtgccttg 300  
accaacacgt tatctcctgg agacaggatt gtttcgtttc tgattggaca atttagcttg 360  
ctctggattg accagcagaa gaggccta atcaatgttg atgtggttga gagtgattGg 420  
gggacaagggt gctaattctc aagtcttggc ctcaaagctc tcacaagacg agaatcatac 480  
catcaaagcc atttgcattg tccacaacga gaccgcgacc ggagttacca atgacatctc 540  
tgctgtccgc aactcctcgc atcactacaa gcacccggct ttgctgctag tggacgggtg 600  
ttcgtccatc tgcgcgcttg atttccgaat ggatgagtg ggagtggacg tggccttgac 660  
tgggtctcag aaagccttat ctcttccaac aggacttggg attgtctgcg ccagtcctaa 720  
agcttttgaa gctaccaaaa cttctaaatc tctcaaagta ttctttgact ggaatgacta 780  
ccttaagttt tacaagctag gaacctattg gccatacaca ccttccattc aacttctcta 840  
cggctcttaga gctgctcttg atcttatctt tgaggaagga cttgagaaca tcatcgcccc 900  
ccatgctcgt ttgggaaagg ccaccaggct tgcggtggaa gcatgggggc tgaaaaactg 960  
cacacagaag gaggaatgga taagtaacac agtgacagca gttatggtgc ctccgcatat 1020  
agacggttcg gagattgtga gaagggcatg gcagaggtag aacttaagtc ttggtcttgg 1080  
tctcaacaaa gtggctggaa aggttttcag aattggacat ctaggaaatg tgaatgagtt 1140  
gcaacttctc ggggtgcttg cgggagtgga gatgatactg aaggatgttg gatacccagt 1200  
tgtaatggga agtggagttg cagctgcctc tacttatctt cagcaccaca ttctctcat 1260  
tccctctaga atctaataca tgtggtcctt ctctttcttt ctcttctct caatgtaaac 1320  
aaactctcat gttttctctt ttcttcatct atatttttac tacattatct atgtttttat 1380  
ttgctatctc caacaaactt attgaacaaa agatcaaata tgtttattac tcactataaa 1440  
ctttgtctc

(2) INFORMATION FOR SEQ ID NO:2519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1573573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

Met Leu Met Trp Leu Arg Val Ile Gly Gly Gln Gly Ala Asn Leu Gln  
1 5 10 15  
Val Leu Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys Ala  
20 25 30  
Ile Cys Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp Ile  
35 40 45

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Ser Ala Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu Leu  
50 55 60  
Leu Val Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met Asp  
65 70 75 80  
Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu Ser  
85 90 95  
Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu Glu  
100 105 110  
Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn Asp  
115 120 125  
Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro Ser  
130 135 140  
Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile Phe Glu  
145 150 155 160  
Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys Ala  
165 170 175  
Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln Lys  
180 185 190  
Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro His  
195 200 205  
Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn Leu  
210 215 220  
Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg Ile  
225 230 235 240  
Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu Ala  
245 250 255  
Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met Gly  
260 265 270  
Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro Leu  
275 280 285  
Ile Pro Ser Arg Ile  
290

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1573574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Met Trp Leu Arg Val Ile Gly Gly Gln Gly Ala Asn Leu Gln Val Leu  
1 5 10 15  
Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys Ala Ile Cys  
20 25 30  
Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp Ile Ser Ala  
35 40 45  
Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu Leu Leu Val  
50 55 60  
Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met Asp Glu Trp  
65 70 75 80  
Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu Ser Leu Pro  
85 90 95  
Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu Glu Ala Thr  
100 105 110  
Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn Asp Tyr Leu  
115 120 125  
Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro Ser Ile Gln

SEQUENCE: 2520

|                                                                 |                                         |     |
|-----------------------------------------------------------------|-----------------------------------------|-----|
| 130                                                             | 135                                     | 140 |
| Leu Leu Tyr Gly Leu Arg                                         | Ala Ala Leu Asp Leu Ile Phe Glu Glu Gly |     |
| 145                                                             | 150                                     | 155 |
| Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys Ala Thr Arg |                                         | 160 |
|                                                                 | 165                                     | 170 |
| Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln Lys Glu Glu |                                         | 175 |
|                                                                 | 180                                     | 185 |
| Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro His Ile Asp |                                         | 190 |
|                                                                 | 195                                     | 200 |
| Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn Leu Ser Leu |                                         | 205 |
|                                                                 | 210                                     | 215 |
| Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg Ile Gly His |                                         | 220 |
| 225                                                             | 230                                     | 235 |
| Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu Ala Gly Val |                                         | 240 |
|                                                                 | 245                                     | 250 |
| Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met Gly Ser Gly |                                         | 255 |
|                                                                 | 260                                     | 265 |
| Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro Leu Ile Pro |                                         | 270 |
|                                                                 | 275                                     | 280 |
| Ser Arg Ile                                                     |                                         | 285 |
| 290                                                             |                                         |     |

(2) INFORMATION FOR SEQ ID NO:2521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1573575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Asp Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala |     |     |
| 1                                                               | 5   | 10  |
| Leu Ser Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala |     | 15  |
|                                                                 | 20  | 25  |
| Leu Glu Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp |     | 30  |
|                                                                 | 35  | 40  |
| Asn Asp Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr |     | 45  |
|                                                                 | 50  | 55  |
| Pro Ser Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile |     | 60  |
|                                                                 | 65  | 70  |
| Phe Glu Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly |     | 75  |
|                                                                 | 80  | 85  |
| Lys Ala Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr |     | 90  |
|                                                                 | 95  | 100 |
| Gln Lys Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro |     | 105 |
|                                                                 | 110 | 115 |
| Pro His Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr |     | 120 |
|                                                                 | 125 | 130 |
| Asn Leu Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe |     | 135 |
|                                                                 | 140 | 145 |
| Arg Ile Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys |     | 150 |
|                                                                 | 155 | 160 |
| Leu Ala Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val |     | 165 |
|                                                                 | 170 | 175 |
| Met Gly Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile |     | 180 |
|                                                                 | 185 | 190 |
|                                                                 | 195 | 200 |
| Pro Leu Ile Pro Ser Arg Ile                                     |     | 205 |
| 210                                                             | 215 |     |

(2) INFORMATION FOR SEQ ID NO:2522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..581
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| aagaattatt | gttttttgat | cggaaaagag  | atctagaatc  | accaaaaggt | tttattttat | 60  |
| acaatgggtc | gtggaaacag | ctgtggtgga  | ggtcaaagct  | cattggatta | tctctttggt | 120 |
| ggtgacgctc | ctgctcctaa | gccagttcca  | gctcctcgtc  | ccgctcctac | tgagtctaac | 180 |
| aacggacctg | caccaccagt | aacagctgtg  | actgcaaccg  | cactcacgac | tgctactact | 240 |
| tctgttgagc | ctgcagagct | taacaagcag  | attcctgctg  | gtatcaaaac | tcctgttaac | 300 |
| aactatgcca | gagctgaagg | acagaacacc  | ggcaacttcc  | tactgaccg  | tccttcgacc | 360 |
| aaagttcacg | cagctccggg | aggaggatca  | tccttggtatt | atctottcac | tggtggcaag | 420 |
| taaaataatt | gcaaagacct | tatatctatcc | attgtctttg  | ctgcgttatc | tcactatgaa | 480 |
| actgtttgat | gtgagccttt | aaatgataag  | aagtcggttt  | ctgtctcaaa | ctcttatctg | 540 |
| taatatattg | ctgaaaaaAt | gtttgaatca  | aaaccttccc  | t          |            |     |

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Ile | Val | Phe | Gly | Ser | Glu | Lys | Arg | Ser | Arg | Ile | Thr | Lys | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Tyr | Phe | Ile | Gln | Trp | Val | Val | Glu | Thr | Ala | Val | Val | Glu | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | His | Trp | Ile | Ile | Ser | Leu | Val | Val | Thr | Leu | Leu | Leu | Leu | Ser | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Phe | Gln | Leu | Leu | Val | Pro | Leu | Leu | Leu | Ser | Leu | Thr | Thr | Asp | Leu | His |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |
| His | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Gly | Asn | Ser | Cys | Gly | Gly | Gly | Gln | Ser | Ser | Leu | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Phe | Gly | Gly | Asp | Ala | Pro | Ala | Pro | Lys | Pro | Val | Pro | Ala | Pro | Arg |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Pro | Ala | Pro | Thr | Glu | Ser | Asn | Asn | Gly | Pro | Ala | Pro | Pro | Val | Thr | Ala |

35 40 45  
Val Thr Ala Thr Ala Leu Thr Thr Ala Thr Thr Ser Val Glu Pro Ala  
50 55 60  
Glu Leu Asn Lys Gln Ile Pro Ala Gly Ile Lys Thr Pro Val Asn Asn  
65 70 75 80  
Tyr Ala Arg Ala Glu Gly Gln Asn Thr Gly Asn Phe Leu Thr Asp Arg  
85 90 95  
Pro Ser Thr Lys Val His Ala Ala Pro Gly Gly Gly Ser Ser Leu Asp  
100 105 110  
Tyr Leu Phe Thr Gly Gly Lys  
115

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Met Pro Glu Leu Lys Asp Arg Thr Pro Ala Thr Ser Ser Leu Thr Val  
1 5 10 15  
Leu Arg Pro Lys Phe Thr Gln Leu Arg Glu Glu Asp His Pro Trp Ile  
20 25 30  
Ile Ser Ser Leu Val Ala Ser Lys Ile Ile Ala Lys Thr Phe Ile Tyr  
35 40 45  
Pro Leu Ser Leu Leu Arg Tyr Leu Thr Met Lys Leu Phe Asp Val Ser  
50 55 60  
Leu  
65

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

aattttttttt ttgacgac ttgcttcttc ttcttcttct tcttcttctt cttcttcttc 60  
aactcggttac catcaacgct caaatcctgt atacaatctc ttctcagctg taatttctat 120  
aatctcgctca attatcatct attcaggggt aagctatggg atgtgcttct tctcttccag 180  
ataggaactc tggaaactta agtggcttta gcaattcaga gaatgctggt ccagctgatg 240  
ccaaaaatct acgtgtgaag ttagttctat taggagactc tgggtgttggg aaaagttgta 300  
ttgtccttcg atttgtacgt ggtcagtttg acgctacatc taaggtaact gttggagcct 360  
cgttcttgtc ccaaactata gcaTtgcaag actctaccac agtgaagttt gaaatatggg 420  
atacagcagg acaggagagg tattctgctc ttgcaccact atactaccgt ggagctggag 480  
ttgctgttat tgtgtatgat ataacaagcc ctgaatcggt caagaaagca cagtattggg 540  
ttaaggaact gcaaaagcat ggaagcccag atattgttat ggctctgggt ggtaacaaag 600  
ctgatctaca tgaaaaaaga gaagtaccta ctgaggatgg aatggagctt gcagagaaga 660  
acggcatggt cttcattgag acgtcagcca agacagccga taacataaat caactgtttg 720  
aggaaattgg caagaggcta cctcgtcctg ctccttcgtc atgattggag tgttgaatca 780  
tctcatcttc agccatgtct tcagactact aatctttcca tactttttta tgtaattttt 840  
caaaacaata tttctctatc tgttaagtca agtgtgttgt ataattgtgaa gatttgagtt 900  
tgaaactggg gatattacga acctcaaaag tggaaccaca agttatatca agcaatggat 960

catcagtaca tatttttagtg gg

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

Met Gly Cys Ala Ser Ser Leu Pro Asp Arg Asn Ser Gly Thr Leu Ser  
1 5 10 15  
Gly Leu Ser Asn Ser Glu Asn Ala Val Pro Ala Asp Ala Lys Asn Leu  
20 25 30  
Arg Val Lys Leu Val Leu Leu Gly Asp Ser Gly Val Gly Lys Ser Cys  
35 40 45  
Ile Val Leu Arg Phe Val Arg Gly Gln Phe Asp Ala Thr Ser Lys Val  
50 55 60  
Thr Val Gly Ala Ser Phe Leu Ser Gln Thr Ile Ala Leu Gln Asp Ser  
65 70 75 80  
Thr Thr Val Lys Phe Glu Ile Trp Asp Thr Ala Gly Gln Glu Arg Tyr  
85 90 95  
Ser Ala Leu Ala Pro Leu Tyr Tyr Arg Gly Ala Gly Val Ala Val Ile  
100 105 110  
Val Tyr Asp Ile Thr Ser Pro Glu Ser Phe Lys Lys Ala Gln Tyr Trp  
115 120 125  
Val Lys Glu Leu Gln Lys His Gly Ser Pro Asp Ile Val Met Ala Leu  
130 135 140  
Val Gly Asn Lys Ala Asp Leu His Glu Lys Arg Glu Val Pro Thr Glu  
145 150 155 160  
Asp Gly Met Glu Leu Ala Glu Lys Asn Gly Met Phe Phe Ile Glu Thr  
165 170 175  
Ser Ala Lys Thr Ala Asp Asn Ile Asn Gln Leu Phe Glu Glu Ile Gly  
180 185 190  
Lys Arg Leu Pro Arg Pro Ala Pro Ser Ser  
195 200

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..619
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

cctctgctgt cgctcgtcta caTttacact cggagcttag accttccaat ctaccggcgg 60  
cgaaaatggg tttcaagagg tacgttgaga tccggagagt agcacttggtg aactacggag 120  
aagatcatgg aaagctcgtc gttatcgtcg acgttggtga ccagaacaga gctttggtgg 180  
atgccccctga tatggagagg atccagatga acttcaagag gttgtctctt accgatattg 240  
tcattgacat caaccgtgtg ccaaagaaga aggctttgat cgaggcaatg gaaaaggctg 300  
atgtgaagaa caagtgggag aaaagctcat ggggtaggaa gcttatcgtg cagaaacgta 360  
gggctaacct taacgacttt gataggttca agatcatggt ggccaagatc aagaaagctg 420  
gtgttggtcag gcaagagctt gcaaaactca agaaggagat cactgcctga tcaaatatta 480  
tctacaattc tggtgtcttt cttttttgat tttggattcg gaaattagtg tttttggaac 540  
tatcaatatc agtatgtgct caattatcag acattattca agtttgaaac cttgtttgca 600

aaactcaaag ttttttgtc

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ala | Val | Ala | Arg | Leu | His | Leu | His | Ser | Glu | Leu | Arg | Pro | Ser | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Pro | Ala | Ala | Lys | Met | Gly | Phe | Lys | Arg | Tyr | Val | Glu | Ile | Arg | Arg |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ala | Leu | Val | Asn | Tyr | Gly | Glu | Asp | His | Gly | Lys | Leu | Val | Val | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Asp | Val | Val | Asp | Gln | Asn | Arg | Ala | Leu | Val | Asp | Ala | Pro | Asp | Met |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Arg | Ile | Gln | Met | Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Asp | Ile | Asn | Arg | Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala | Met |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Lys | Ala | Asp | Val | Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly | Arg |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Leu | Ile | Val | Gln | Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Phe | Lys | Ile | Met | Leu | Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg | Gln |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Leu | Ala | Lys | Leu | Lys | Lys | Glu | Ile | Thr | Ala |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Phe | Lys | Arg | Tyr | Val | Glu | Ile | Arg | Arg | Val | Ala | Leu | Val | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Tyr | Gly | Glu | Asp | His | Gly | Lys | Leu | Val | Val | Ile | Val | Asp | Val | Val | Asp |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asn | Arg | Ala | Leu | Val | Asp | Ala | Pro | Asp | Met | Glu | Arg | Ile | Gln | Met |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile | Val | Ile | Asp | Ile | Asn | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala | Met | Glu | Lys | Ala | Asp | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly | Arg | Lys | Leu | Ile | Val | Gln |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp | Arg | Phe | Lys | Ile | Met | Leu |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg | Gln | Glu | Leu | Ala | Lys | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |

Lys Lys Glu Ile Thr Ala  
130

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ile | Gln | Met | Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Asp | Ile | Asn | Arg | Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Glu | Lys | Ala | Asp | Val | Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Arg | Lys | Leu | Ile | Val | Gln | Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Phe | Lys | Ile | Met | Leu | Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Gln | Glu | Leu | Ala | Lys | Leu | Lys | Lys | Glu | Ile | Thr | Ala |     |     |     |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| ccttctcact | tcaaattcat | aatctctcta | cttctctctc | tctctaaatt | caaaaatggc  | 60  |
| gaaactggtg | atgttggttg | ttctttgtat | cttaccggcg | ataGccatgg | cggcaaggag  | 120 |
| gagtaatat  | gaaagaata  | caatgggtgg | tcaaggtagc | acttactgtg | acatttgcaa  | 180 |
| attcggcttc | gagactcctg | aatcctccta | cttcatcccc | ggtgcaacgg | tgaagctatc  | 240 |
| atgcaaagac | aggaagacaa | tggaagaggt | ttacacagac | aaagctgtat | cggacaaaaga | 300 |
| aggaaagtat | aagttcattg | tccacgacga | tcacagagac | cagatgtgcg | atgttttgct  | 360 |
| tgtgaaaagc | tcggataaaa | cctgctctaa | aatctccgtt | ggacgtgaga | agtctcgtgt  | 420 |
| gatcttgaac | cattacagtg | gcattgcctc | gcagatcaga | catgctaaca | acatgggatt  | 480 |
| cgagaaagaa | gtgagtgatg | tgttctgctc | tgctttgttt | cagaagtata | tggttgatga  | 540 |
| agatgaggat | gatattaaaa | accatctcta | atctctctgt | ttaatcttat | gatctgctgt  | 600 |
| tttcttcatt | aatgagtttc | gagttatgga | agagatatat | ttgtatttgt | ttgattactt  | 660 |
| atttgttgtc | tttagagatg | ttgactctgg | tgatcggata | actatctggt | tgtgtaagct  | 720 |
| tcttatatat | tgatgtgtca | tttccttg   |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171



(D) OTHER INFORMATION: / Ceres Seq. ID 1573607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile  
1 5 10 15  
Ala Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val  
20 25 30  
Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro  
35 40 45  
Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys  
50 55 60  
Asp Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp  
65 70 75 80  
Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln  
85 90 95  
Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys  
100 105 110  
Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser  
115 120 125  
Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys  
130 135 140  
Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val  
145 150 155 160  
Asp Glu Asp Glu Asp Ile Lys Asn His Leu  
165 170

(2) INFORMATION FOR SEQ ID NO:2534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:

Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg  
1 5 10 15  
Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr  
20 25 30  
Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe  
35 40 45  
Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met  
50 55 60  
Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr  
65 70 75 80  
Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met Cys Asp Val Leu  
85 90 95  
Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile Ser Val Gly Arg  
100 105 110  
Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly Ile Ala Ser Gln  
115 120 125  
Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu Val Ser Asp Val  
130 135 140  
Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp Glu Asp Glu Asp  
145 150 155 160  
Asp Ile Lys Asn His Leu  
165

(2) INFORMATION FOR SEQ ID NO:2535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..154  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573609  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:

Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln  
1 5 10 15  
Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu  
20 25 30  
Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp  
35 40 45  
Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys  
50 55 60  
Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met  
65 70 75 80  
Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile  
85 90 95  
Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly  
100 105 110  
Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu  
115 120 125  
Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp  
130 135 140  
Glu Asp Glu Asp Asp Ile Lys Asn His Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:2536:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1707  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

atacacacaa ttcaatat ttt gacttcacat agagagagat agagagatgg cgacggaaac 60  
ggaagtgtga gctccggtaa cggtaagcaa cggcgggaagc aaaggatggt gcaagtacgg 120  
tggtcctggt tacgcgactc ctctcgccgc tatgtctggt ccacgggaga aacttatcta 180  
cgtaaccgcc gtctacaccg gaactggaat agataaaccg gattatttgg cgacgggtgga 240  
tgtagatcca agctcgccct cgtattcaag tggtattcat agattaccaa tgccttttgt 300  
tggtgatgag cttcatcatt ctggttgga ctcttgtagt tcttgccatg gtgatgcttc 360  
tggtgataga cgttatctcg tgttaccgtc tcttatatct ggtcgattt atgcgattga 420  
tactaaggaa aacccgaggg ctccgtcttt gtataagtat gttgatccta aagagattgc 480  
tgataagMac tggattggcg tttcctcaca cggctcattg cctcgccacg ggcgagatct 540  
tggtgtcctg tcttgagat gaagagggga atgctaaggg gaatgggttt cttcttsttg 600  
actctgattt taacatcaag aataggtggg agaaaccagg acatagtcct ttgtatgggt 660  
atgatgttct agatgttttt ggtaccaacc tcggcacaag accatgatca gcacatcttg 720  
gggagcacct aaagccttct cttaaaggtt caatcttcag cacgttgctg atggcttgta 780  
tggaagtcat ctacatgttt atagttggcc aggaggtgaa atgaaacaat taattgacct 840  
tggaccgact ggtctcttac ctttgagat tagattcttg catgatccat cttaaagatac 900  
agggtttgtt gggagtgcct tgtcgagtaa tatgataaga tttttcaaga acagtgatga 960  
aacatggagc catgagggtt ttatatcggt taaaccgttg aaagtcgaaa actggatact 1020  
tcacgaaatg ccggggctaa tcaccgactt cttgatctcc ctcgatgacc gatttattta 1080  
ctttgtgaac tggctccatg gagacattcg tcagtacaac atagaggacc ctaaaaaccc 1140  
tgtattaaca gggcaaattt ggggttgagg attactacaa aagggcagtc ctgttaaggc 1200

ggttggagaa gacggaaaca ctttccagtt cgaggttcct cagatcaagg ggaaatcttt 1260  
acgaggtgga cctcaaataa ttcagctgag cctcgatggg aaacgattgt atgcaacaaa 1320  
ctcgcgtgttt agcgcagtggt atcgtcagtt ttatcctgaa atcatggaga aaggctcaca 1380  
cataattcag attgatgttg atacagaaaa aggtgggtctc accataaacc ctgattttctt 1440  
tgtggacttt ggtgatgaac cagacggtcc ttactagacc cacgagatga gatattccagg 1500  
tgagagactgc acttccgata tctggatttg aatttggctt tgttttagagt gtgttttgtg 1560  
ttaagtttaa attgagtttt attatttgtt gtgtgttttag taCgagttga ataaaaaagg 1620  
gagtaagatg actcagacaa ttaacacttg tttgtacatt ttgactccta tgtgtcttaa 1680  
gtaataaaac tttctacaat tcgactg

(2) INFORMATION FOR SEQ ID NO:2537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..275

(D) OTHER INFORMATION: / Ceres Seq. ID 1573625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

Met Ile Ser Thr Ser Trp Gly Ala Pro Lys Ala Phe Ser Lys Gly Phe  
1 5 10 15  
Asn Leu Gln His Val Ala Asp Gly Leu Tyr Gly Ser His Leu His Val  
20 25 30  
Tyr Ser Trp Pro Gly Gly Glu Met Lys Gln Leu Ile Asp Leu Gly Pro  
35 40 45  
Thr Gly Leu Leu Pro Leu Glu Ile Arg Phe Leu His Asp Pro Ser Lys  
50 55 60  
Asp Thr Gly Phe Val Gly Ser Ala Leu Ser Ser Asn Met Ile Arg Phe  
65 70 75 80  
Phe Lys Asn Ser Asp Glu Thr Trp Ser His Glu Val Val Ile Ser Val  
85 90 95  
Lys Pro Leu Lys Val Glu Asn Trp Ile Leu Pro Glu Met Pro Gly Leu  
100 105 110  
Ile Thr Asp Phe Leu Ile Ser Leu Asp Asp Arg Phe Ile Tyr Phe Val  
115 120 125  
Asn Trp Leu His Gly Asp Ile Arg Gln Tyr Asn Ile Glu Asp Pro Lys  
130 135 140  
Asn Pro Val Leu Thr Gly Gln Ile Trp Val Gly Gly Leu Leu Gln Lys  
145 150 155 160  
Gly Ser Pro Val Lys Ala Val Gly Glu Asp Gly Asn Thr Phe Gln Phe  
165 170 175  
Glu Val Pro Gln Ile Lys Gly Lys Ser Leu Arg Gly Gly Pro Gln Met  
180 185 190  
Ile Gln Leu Ser Leu Asp Gly Lys Arg Leu Tyr Ala Thr Asn Ser Leu  
195 200 205  
Phe Ser Ala Trp Asp Arg Gln Phe Tyr Pro Glu Ile Met Glu Lys Gly  
210 215 220  
Ser His Ile Ile Gln Ile Asp Val Asp Thr Glu Lys Gly Gly Leu Thr  
225 230 235 240  
Ile Asn Pro Asp Phe Phe Val Asp Phe Gly Asp Glu Pro Asp Gly Pro  
245 250 255  
Ser Leu Ala His Glu Met Arg Tyr Pro Gly Gly Asp Cys Thr Ser Asp  
260 265 270  
Ile Trp Ile  
275

(2) INFORMATION FOR SEQ ID NO:2538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

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- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..236  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573626  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

Met Lys Gln Leu Ile Asp Leu Gly Pro Thr Gly Leu Leu Pro Leu Glu  
1 5 10 15  
Ile Arg Phe Leu His Asp Pro Ser Lys Asp Thr Gly Phe Val Gly Ser  
20 25 30  
Ala Leu Ser Ser Asn Met Ile Arg Phe Phe Lys Asn Ser Asp Glu Thr  
35 40 45  
Trp Ser His Glu Val Val Ile Ser Val Lys Pro Leu Lys Val Glu Asn  
50 55 60  
Trp Ile Leu Pro Glu Met Pro Gly Leu Ile Thr Asp Phe Leu Ile Ser  
65 70 75 80  
Leu Asp Asp Arg Phe Ile Tyr Phe Val Asn Trp Leu His Gly Asp Ile  
85 90 95  
Arg Gln Tyr Asn Ile Glu Asp Pro Lys Asn Pro Val Leu Thr Gly Gln  
100 105 110  
Ile Trp Val Gly Gly Leu Leu Gln Lys Gly Ser Pro Val Lys Ala Val  
115 120 125  
Gly Glu Asp Gly Asn Thr Phe Gln Phe Glu Val Pro Gln Ile Lys Gly  
130 135 140  
Lys Ser Leu Arg Gly Gly Pro Gln Met Ile Gln Leu Ser Leu Asp Gly  
145 150 155 160  
Lys Arg Leu Tyr Ala Thr Asn Ser Leu Phe Ser Ala Trp Asp Arg Gln  
165 170 175  
Phe Tyr Pro Glu Ile Met Glu Lys Gly Ser His Ile Ile Gln Ile Asp  
180 185 190  
Val Asp Thr Glu Lys Gly Gly Leu Thr Ile Asn Pro Asp Phe Phe Val  
195 200 205  
Asp Phe Gly Asp Glu Pro Asp Gly Pro Ser Leu Ala His Glu Met Arg  
210 215 220  
Tyr Pro Gly Gly Asp Cys Thr Ser Asp Ile Trp Ile  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2539:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..199  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573627  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

Met Ile Arg Phe Phe Lys Asn Ser Asp Glu Thr Trp Ser His Glu Val  
1 5 10 15  
Val Ile Ser Val Lys Pro Leu Lys Val Glu Asn Trp Ile Leu Pro Glu  
20 25 30  
Met Pro Gly Leu Ile Thr Asp Phe Leu Ile Ser Leu Asp Asp Arg Phe  
35 40 45  
Ile Tyr Phe Val Asn Trp Leu His Gly Asp Ile Arg Gln Tyr Asn Ile  
50 55 60  
Glu Asp Pro Lys Asn Pro Val Leu Thr Gly Gln Ile Trp Val Gly Gly  
65 70 75 80  
Leu Leu Gln Lys Gly Ser Pro Val Lys Ala Val Gly Glu Asp Gly Asn

85 90 95  
Thr Phe Gln Phe Glu Val Pro Gln Ile Lys Gly Lys Ser Leu Arg Gly  
100 105 110  
Gly Pro Gln Met Ile Gln Leu Ser Leu Asp Gly Lys Arg Leu Tyr Ala  
115 120 125  
Thr Asn Ser Leu Phe Ser Ala Trp Asp Arg Gln Phe Tyr Pro Glu Ile  
130 135 140  
Met Glu Lys Gly Ser His Ile Ile Gln Ile Asp Val Asp Thr Glu Lys  
145 150 155 160  
Gly Gly Leu Thr Ile Asn Pro Asp Phe Phe Val Asp Phe Gly Asp Glu  
165 170 175  
Pro Asp Gly Pro Ser Leu Ala His Glu Met Arg Tyr Pro Gly Gly Asp  
180 185 190  
Cys Thr Ser Asp Ile Trp Ile  
195

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..777
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcttcacaa ttttttttcg tctctcaaac caacgcaaaa gaacaatgtc taacgttgta   | 60  |
| gtaatcgccg ttgtttctcat cgtagcatcg ctaacaggac atgtgtcagc acaaattggat | 120 |
| atgtctccgt cgtcaggacc atcgggtgca ccagactgca tggcgaaacct aatgaacatg  | 180 |
| acaggctgtc tctcgtacgt tacggtcgga gaagggtgtg gtgcggccaa gccggacaag   | 240 |
| acgtgttggtc cggcgctaGc ggggctagtg gagagctcgc cgcaatgctt atgttacctc  | 300 |
| ctctccggtg acatggcggc acaacttgga atcaagattg ataaggcaaa ggctctcaaa   | 360 |
| cttcccggag tttgcggcgt gatcactccc gatccttcac tttgttctct ttttggaatt   | 420 |
| cctgtttggag cacctgtagc tatgggagac gagggagcct ccccagccta tgctccaggt  | 480 |
| togatgtcag aatcaccagg aggatttggg tcgggtCctt cggctagtag agggagcgat   | 540 |
| gcaccaagca gtgcacctta ttctcgtttt ctcaatctta taattttccc attagctttt   | 600 |
| gcattttaca tcttttgctg atttcattct cttccaacca ttaacaacac cattatttgt   | 660 |
| tatgtatttt cttaaaagag tattattgct tttgtaggct atgttcttga atttattact   | 720 |
| ttgtgtatoc acggattatt tcttcattca tcttattgaa taaagattgt tttttttt     |     |

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

Ile Phe Thr Ile Phe Phe Arg Leu Ser Asn Gln Arg Lys Arg Thr Met  
1 5 10 15  
Ser Asn Val Val Val Ile Ala Val Val Leu Ile Val Ala Ser Leu Thr  
20 25 30  
Gly His Val Ser Ala Gln Met Asp Met Ser Pro Ser Ser Gly Pro Ser  
35 40 45  
Gly Ala Pro Asp Cys Met Ala Asn Leu Met Asn Met Thr Gly Cys Leu  
50 55 60  
Ser Tyr Val Thr Val Gly Glu Gly Gly Gly Ala Ala Lys Pro Asp Lys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Pro | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Met | Ser | Glu | Ser | Pro | Gly | Gly | Phe | Gly | Ser | Gly | Pro | Ser | Ala | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Gly | Ser | Asp | Ala | Pro | Ser | Ser | Ala | Pro | Tyr | Ser | Arg | Phe | Leu | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ile | Ile | Phe | Pro | Leu | Ala | Phe | Ala | Phe | Tyr | Ile | Phe | Cys |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1573630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Thr | Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Gly | Ala | Ala | Lys | Pro | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Cys | Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Thr | Pro | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gly | Ser | Met | Ser | Glu | Ser | Pro | Gly | Gly | Phe | Gly | Ser | Gly | Pro | Ser | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Arg | Gly | Ser | Asp | Ala | Pro | Ser | Ser | Ala | Pro | Tyr | Ser | Arg | Phe | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asn | Leu | Ile | Ile | Phe | Pro | Leu | Ala | Phe | Ala | Phe | Tyr | Ile | Phe | Cys |     |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

(2) INFORMATION FOR SEQ ID NO:2544:

(A) LENGTH: 788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..788

(D) OTHER INFORMATION: / Ceres Seq. ID 1573632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

| (X1) SEQUENCE DESCRIPTION | SIZE       | SCORE      |            |             |             |     |
|---------------------------|------------|------------|------------|-------------|-------------|-----|
| atttatcttc                | aCaatttttG | tttcgtctct | caaaccaacg | caaaagaaca  | atgtctaacg  | 60  |
| ttgtagtaat                | cgccgttggt | ctcatcgtag | catcgctaac | aggacatgtg  | tcagcacaaa  | 120 |
| tggatatgtc                | tccgtcgtca | ggaccatcgg | gtgcaccaga | ctgcatggcg  | aacctaatga  | 180 |
| acatgacagg                | ctgtctctcg | tacgttacgg | tcggagaagg | tggtgggtgc  | Ggccaagccgg | 240 |
| acaagacgtg                | ttgtccggcg | ctaGcggggc | tagtgagag  | ctcgccgcaa  | tgcttatggt  | 300 |
| acctcctctc                | cggtgacatg | gcggcacaa  | ttggaatcaa | gattgataag  | gcaaaaggctc | 360 |
| tcaaactttc                | cggagtttgc | ggcgtgatca | cttcgatcc  | tctcactttgt | tctctttttg  | 420 |
| gaattcctgt                | tggagcacct | gtagctatgg | gagacgaggg | agcctcccca  | gcctatgctc  | 480 |
| caggttcgat                | gtcaggtgca | gaatcaccag | gaggatttgg | gtcgggtCct  | tcggctagta  | 540 |
| gagggagcga                | tgcaccaagc | agtgcacctt | attctcgttt | tctcaatctt  | ataattttcc  | 600 |
| cattagcttt                | tgcattttac | atcttttget | gatttcattc | tctccaacc   | attaacaaca  | 660 |
| ccattatttg                | ttatgtattt | tcttaaaaga | gtattattgc | ttttgtaggc  | tatgttcttg  | 720 |
| aatttattac                | tttgtgtatc | cacggattat | ttcttcattc | atcttattga  | ataaagattg  | 780 |
| tttttttc                  |            |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1573633

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1573634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Gly | Ala | Ala | Lys | Pro | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Thr | Cys | Cys | Pro | Ala | Leu | Ala | Gly | Leu | Val | Glu | Ser | Ser | Pro | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Leu | Cys | Tyr | Leu | Leu | Ser | Gly | Asp | Met | Ala | Ala | Gln | Leu | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ile | Asp | Lys | Ala | Lys | Ala | Leu | Lys | Leu | Pro | Gly | Val | Cys | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Ser | Asp | Pro | Ser | Leu | Cys | Ser | Leu | Phe | Gly | Ile | Pro | Val | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Val | Ala | Met | Gly | Asp | Glu | Gly | Ala | Ser | Pro | Ala | Tyr | Ala | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

[illegible]



Gly Ser Met Ser Gly Ala Glu Ser Pro Gly Gly Phe Gly Ser Gly Pro  
145 150 155 160  
Ser Ala Ser Arg Gly Ser Asp Ala Pro Ser Ser Ala Pro Tyr Ser Arg  
165 170 175  
Phe Leu Asn Leu Ile Ile Phe Pro Leu Ala Phe Ala Phe Tyr Ile Phe  
180 185 190  
Cys

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1573635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:

Met Asp Met Ser Pro Ser Ser Gly Pro Ser Gly Ala Pro Asp Cys Met  
1 5 10 15  
Ala Asn Leu Met Asn Met Thr Gly Cys Leu Ser Tyr Val Thr Val Gly  
20 25 30  
Glu Gly Gly Gly Ala Ala Lys Pro Asp Lys Thr Cys Cys Pro Ala Leu  
35 40 45  
Ala Gly Leu Val Glu Ser Ser Pro Gln Cys Leu Cys Tyr Leu Leu Ser  
50 55 60  
Gly Asp Met Ala Ala Gln Leu Gly Ile Lys Ile Asp Lys Ala Lys Ala  
65 70 75 80  
Leu Lys Leu Pro Gly Val Cys Gly Val Ile Thr Ser Asp Pro Ser Leu  
85 90 95  
Cys Ser Leu Phe Gly Ile Pro Val Gly Ala Pro Val Ala Met Gly Asp  
100 105 110  
Glu Gly Ala Ser Pro Ala Tyr Ala Pro Gly Ser Met Ser Gly Ala Glu  
115 120 125  
Ser Pro Gly Gly Phe Gly Ser Gly Pro Ser Ala Ser Arg Gly Ser Asp  
130 135 140  
Ala Pro Ser Ser Ala Pro Tyr Ser Arg Phe Leu Asn Leu Ile Ile Phe  
145 150 155 160  
Pro Leu Ala Phe Ala Phe Tyr Ile Phe Cys  
165 170

(2) INFORMATION FOR SEQ ID NO:2548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1403 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1403

(D) OTHER INFORMATION: / Ceres Seq. ID 1573636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

aaaatttttt aaaaggcaag acctcctctg ttcccatatt ctcaccacag aagaactctt 60  
gaggctttct cttttctcta ccatggcgaa accggtgtcc attgaagtgt ataattcctaa 120  
tggaataac agagttgtta gcacaaaacc gatgcctgga actcgctgga tcaatctctt 180  
ggtagaccaa ggtgtcgcg ttgagatatg tcatttgaag aagacaatct tgtctgtaga 240  
agatatcatt gatctgatcg gagacaagtg tgatggagtc atcggtcagt tgacggaaga 300  
ttggggagag actctgttct cagctttgag caaagctgga gggaaagctt tcagtaacat 360  
ggcgttggt tataacaacg ttgatgttga agctgccaat aagtatggaa ttgctgtcgg 420

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| taacactccg  | ggagtgttga | ctgagacgac | ggctgaacta | gctgcttctc | tttccttggc | 480  |
| tgctgcaaga  | agaattgttg | aagccgacga | attcatgaga | ggtggcttgt | acgagggatg | 540  |
| gcttcctcat  | ctgtttgttg | ggaacttact | taaaggacag | actgttggag | ttattggagc | 600  |
| tggacgtatt  | ggatctgctt | atgctagaat | gatggtggaa | gggttcaaga | tgaatttgat | 660  |
| ctactttgat  | ctttaccaat | ccactcgtct | tgagaaattt | gtgacagctt | atggacagtt | 720  |
| cttgaaagca  | aatggagaac | aacctgtgac | atggaaacga | gcttcgtcca | tggaggaggt | 780  |
| gctgcgtgag  | gctgatctga | taagtcttca | cccgtgtctg | gacaaaacca | cttaccatct | 840  |
| tgtcaacaag  | gagaggcttg | ccatgatgaa | aaaggaagca | atccttgtga | actgcagcag | 900  |
| aggtcctgtg  | atcgatgagg | cagctttggt | cgaacatctc | aaagagaacc | cgatgttccg | 960  |
| agttgggtctc | gatgtgttcg | aggaagagcc | attcatgaaa | ccagggcttg | ctgatatgaa | 1020 |
| aaacgctatt  | gttgttcctc | acattgcttc | tgcttccaag | tggactcgtg | aaggaatggc | 1080 |
| tNacgcttgc  | agctctcaac | gtcctcggaa | gagtcaaagg | gtacccgatt | tggcatgacc | 1140 |
| cgaaccgagt  | cgatccattc | ttgaacgaaa | acgcttcacc | gccaatgcc  | agtccaagca | 1200 |
| tcgtcaactc  | aaaggcctta | ggattgcctg | tttcgaagct | atgagttaag | tatgaagaag | 1260 |
| gggagatttg  | gaagaatcct | tttagtgaat | atatgatggt | gtcaagttgt | gtttatgtat | 1320 |
| tgtatatgaa  | acaaccatgt | tggatcatat | aatcactcc  | tttaaagtgt | tacattgttg | 1380 |

atgagtctat tagacgatta ccc

(2) INFORMATION FOR SEQ ID NO:2549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1573637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Phe | Phe | Lys | Arg | Gln | Asp | Leu | Leu | Cys | Phe | His | Ile | Leu | Thr | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Glu | Leu | Leu | Arg | Leu | Ser | Leu | Phe | Ser | Thr | Met | Ala | Lys | Pro | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Ile | Glu | Val | Tyr | Asn | Pro | Asn | Gly | Lys | Tyr | Arg | Val | Val | Ser | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Pro | Met | Pro | Gly | Thr | Arg | Trp | Ile | Asn | Leu | Leu | Val | Asp | Gln | Gly |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Arg | Val | Glu | Ile | Cys | His | Leu | Lys | Lys | Thr | Ile | Leu | Ser | Val | Glu |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Ile | Ile | Asp | Leu | Ile | Gly | Asp | Lys | Cys | Asp | Gly | Val | Ile | Gly | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Glu | Asp | Trp | Gly | Glu | Thr | Leu | Phe | Ser | Ala | Leu | Ser | Lys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Lys | Ala | Phe | Ser | Asn | Met | Ala | Val | Gly | Tyr | Asn | Asn | Val | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Glu | Ala | Ala | Asn | Lys | Tyr | Gly | Ile | Ala | Val | Gly | Asn | Thr | Pro | Gly |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Leu | Thr | Glu | Thr | Thr | Ala | Glu | Leu | Ala | Ala | Ser | Leu | Ser | Leu | Ala |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ala | Arg | Arg | Ile | Val | Glu | Ala | Asp | Glu | Phe | Met | Arg | Gly | Gly | Leu |
|     |     |     |     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |
| Tyr | Glu | Gly | Trp | Leu | Pro | His | Leu | Phe | Val | Gly | Asn | Leu | Leu | Lys | Gly |
|     |     |     |     |     |     | 180 |     |     |     | 185 |     |     |     | 190 |     |
| Gln | Thr | Val | Gly | Val | Ile | Gly | Ala | Gly | Arg | Ile | Gly | Ser | Ala | Tyr | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Met | Met | Val | Glu | Gly | Phe | Lys | Met | Asn | Leu | Ile | Tyr | Phe | Asp | Leu |
|     |     |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Tyr | Gln | Ser | Thr | Arg | Leu | Glu | Lys | Phe | Val | Thr | Ala | Tyr | Gly | Gln | Phe |
| 225 |     |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Lys | Ala | Asn | Gly | Glu | Gln | Pro | Val | Thr | Trp | Lys | Arg | Ala | Ser | Ser |
|     |     |     |     |     |     | 245 |     |     |     | 250 |     |     |     | 255 |     |

(2) INFORMATION FOR SEQ ID NO:2550:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1573638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

|            |            |     |            |            |            |     |            |            |            |            |            |            |            |            |            |
|------------|------------|-----|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Ala        | Lys | Pro        | Val<br>5   | Ser        | Ile | Glu        | Val        | Tyr<br>10  | Asn        | Pro        | Asn        | Gly        | Lys<br>15  | Tyr        |
| Arg        | Val        | Val | Ser        | Thr<br>20  | Lys        | Pro | Met        | Pro        | Gly        | Thr        | Arg        | Trp        | Ile<br>30  | Asn        | Leu        |
| Leu        | Val        | Asp | Gln        | Gly        | Cys        | Arg | Val<br>40  | Glu        | Ile        | Cys        | His        | Leu<br>45  | Lys        | Lys        | Thr        |
| Ile        | Leu        | Ser | Val        | Glu        | Asp        | Ile | Ile<br>55  | Asp        | Leu        | Ile        | Gly<br>60  | Asp        | Lys        | Cys        | Asp        |
| Gly<br>65  | Val        | Ile | Gly        | Gln        | Leu<br>70  | Thr | Glu        | Asp        | Trp        | Gly<br>75  | Glu        | Thr        | Leu        | Phe        | Ser<br>80  |
| Ala        | Leu        | Ser | Lys        | Ala<br>85  | Gly        | Gly | Lys        | Ala        | Phe<br>90  | Ser        | Asn        | Met        | Ala<br>95  | Val        | Gly        |
| Tyr        | Asn        | Asn | Val        | Asp<br>100 | Val        | Glu | Ala        | Ala<br>105 | Asn        | Lys        | Tyr        | Gly        | Ile<br>110 | Ala        | Val        |
| Gly        | Asn        | Thr | Pro        | Gly<br>115 | Val        | Leu | Thr<br>120 | Glu        | Thr        | Thr        | Ala        | Glu<br>125 | Leu        | Ala        | Ala        |
| Ser<br>130 | Leu        | Ser | Leu        | Ala        | Ala        | Ala | Arg<br>135 | Arg        | Ile        | Val        | Glu<br>140 | Ala        | Asp        | Glu        | Phe        |
| Met<br>145 | Arg        | Gly | Gly        | Leu<br>150 | Tyr        | Glu | Gly        | Trp        | Leu        | Pro<br>155 | His        | Leu        | Phe        | Val        | Gly<br>160 |
| Asn        | Leu        | Leu | Lys        | Gly<br>165 | Gln        | Thr | Val        | Gly<br>170 | Val        | Ile        | Gly        | Ala        | Gly<br>175 | Arg        | Ile        |
| Gly        | Ser        | Ala | Tyr<br>180 | Ala        | Arg        | Met | Met<br>185 | Val        | Glu        | Gly        | Phe        | Lys        | Met<br>190 | Asn        | Leu        |
| Ile        | Tyr        | Phe | Asp<br>195 | Leu        | Tyr        | Gln | Ser<br>200 | Thr        | Arg        | Leu        | Glu        | Lys<br>205 | Phe        | Val        | Thr        |
| Ala        | Tyr<br>210 | Gly | Gln        | Phe        | Leu        | Lys | Ala<br>215 | Asn        | Gly        | Glu        | Gln        | Pro        | Val        | Thr        | Trp        |
| Lys<br>225 | Arg        | Ala | Ser        | Ser        | Met<br>230 | Glu | Glu        | Val        | Leu        | Arg<br>235 | Glu        | Ala        | Asp        | Leu        | Ile<br>240 |
| Ser        | Leu        | His | Pro        | Val<br>245 | Leu        | Asp | Lys        | Thr        | Thr<br>250 | Tyr        | His        | Leu        | Val        | Asn<br>255 | Lys        |
| Glu        | Arg        | Leu | Ala        | Met        | Met        | Lys | Lys        | Glu        | Ala        | Ile        | Leu        | Val        | Asn        | Cys        | Ser        |

|                                 |                                 |     |
|---------------------------------|---------------------------------|-----|
| 260                             | 265                             | 270 |
| Arg Gly Pro Val Ile Asp Glu Ala | Ala Leu Val Glu His Leu Lys Glu |     |
| 275                             | 280                             | 285 |
| Asn Pro Met Phe Arg Val Gly Leu | Asp Val Phe Glu Glu Glu Pro Phe |     |
| 290                             | 295                             | 300 |
| Met Lys Pro Gly Leu Ala Asp Met | Lys Asn Ala Ile Val Val Pro His |     |
| 305                             | 310                             | 315 |
| Ile Ala Ser Ala Ser Lys Trp Thr | Arg Glu Gly Met Ala Xaa Ala Cys |     |
| 325                             | 330                             | 335 |
| Ser Ser Gln Arg Pro Arg Lys Ser | Gln Arg Val Pro Asp Leu Ala     |     |
| 340                             | 345                             | 350 |

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1573639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Thr | Arg | Trp | Ile | Asn | Leu | Leu | Val | Asp | Gln | Gly | Cys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Glu | Ile | Cys | His | Leu | Lys | Lys | Thr | Ile | Leu | Ser | Val | Glu | Asp | Ile |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asp | Leu | Ile | Gly | Asp | Lys | Cys | Asp | Gly | Val | Ile | Gly | Gln | Leu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Trp | Gly | Glu | Thr | Leu | Phe | Ser | Ala | Leu | Ser | Lys | Ala | Gly | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ala | Phe | Ser | Asn | Met | Ala | Val | Gly | Tyr | Asn | Asn | Val | Asp | Val | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ala | Asn | Lys | Tyr | Gly | Ile | Ala | Val | Gly | Asn | Thr | Pro | Gly | Val | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Glu | Thr | Thr | Ala | Glu | Leu | Ala | Ala | Ser | Leu | Ser | Leu | Ala | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Ile | Val | Glu | Ala | Asp | Glu | Phe | Met | Arg | Gly | Gly | Leu | Tyr | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Trp | Leu | Pro | His | Leu | Phe | Val | Gly | Asn | Leu | Leu | Lys | Gly | Gln | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Gly | Val | Ile | Gly | Ala | Gly | Arg | Ile | Gly | Ser | Ala | Tyr | Ala | Arg | Met |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Met | Val | Glu | Gly | Phe | Lys | Met | Asn | Leu | Ile | Tyr | Phe | Asp | Leu | Tyr | Gln |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ser | Thr | Arg | Leu | Glu | Lys | Phe | Val | Thr | Ala | Tyr | Gly | Gln | Phe | Leu | Lys |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asn | Gly | Glu | Gln | Pro | Val | Thr | Trp | Lys | Arg | Ala | Ser | Ser | Met | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Val | Leu | Arg | Glu | Ala | Asp | Leu | Ile | Ser | Leu | His | Pro | Val | Leu | Asp |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Thr | Thr | Tyr | His | Leu | Val | Asn | Lys | Glu | Arg | Leu | Ala | Met | Met | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Glu | Ala | Ile | Leu | Val | Asn | Cys | Ser | Arg | Gly | Pro | Val | Ile | Asp | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ala | Leu | Val | Glu | His | Leu | Lys | Glu | Asn | Pro | Met | Phe | Arg | Val | Gly |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Asp | Val | Phe | Glu | Glu | Glu | Pro | Phe | Met | Lys | Pro | Gly | Leu | Ala | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Met | Lys | Asn | Ala | Ile | Val | Val | Pro | His | Ile | Ala | Ser | Ala | Ser | Lys | Trp |
|     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |

Thr Arg Glu Gly Met Ala Xaa Ala Cys Ser Ser Gln Arg Pro Arg Lys  
305 310 315 320  
Ser Gln Arg Val Pro Asp Leu Ala  
325

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| aaaacccaaa ccctcactca ctattttcac attcttcttc tctctcgata tcatctaaat   | 60   |
| ctctctcttg atctcaattt cgcaaaatgg ctgacaagaa gatcagaatc ggaatcaacg   | 120  |
| gtttcggaag aatcggctcg ttggttgcta gagttgttct tcagagggat gatgttgagc   | 180  |
| tcgtcgtctg taacgatcct ttcatcacca ccgagtacat gacatacatg ttttaagtatg  | 240  |
| acagtgttca cggtcagttg aagcaccatg agcttaaggt gaaggatgac aaaactcttc   | 300  |
| tcttcggtga gaagccagtc actgttttctg gcatcaggaa ccctgaggac atccccatggg | 360  |
| gtgaggtctg agctgacttt gttgttgagt ctactggtgt cttcactgac aaagacaagg   | 420  |
| ctgctgctca cttgaagggt ggtgctaaaa aggttgatcat ctctgcccc aagcaaagatg  | 480  |
| cgccccatgtt cgttggttgg gtcAacgagc acgagtacaa gtctgacctt gacattgttt  | 540  |
| ccaacgctag ttgcaccact aactgccttg ctccctcttg caaggttatt aatgacaggt   | 600  |
| ttggcattgt tgagggaactc atgaccactg tccactctat cactgctact cagaagacag  | 660  |
| ttgatggtcc atcaatgaag gactggagag gtggaagagc tgcttccttc aacattattc   | 720  |
| ctagcagcac tgggtgcgccc aaggctgttg ggaaagtgtt gccatccctc aatggaaaat  | 780  |
| tgaccggaat gtctttccgt gttccaaccg ttgatgtctc agttgttgat ctccaccgtta  | 840  |
| gacttgagaa agctgcaaca taagacgaaa tcaagaaggc catcaaggag gaatctgaag   | 900  |
| gcaaaatgaa gggaattttg ggatacactg aggatgatgt tgtgtctacc gactttgttg   | 960  |
| gtgacaacag gtcaagcatt ttcatgcca aggctgggat tgcattgagc gacaagtgtg    | 1020 |
| tgaagttggt gtcattggtac gacaacgaat ggggttacag ttctcgtgtc gttgacctta  | 1080 |
| tcgttcacat gtcaaaggcc taagcttaca ccggcgagag tttgtgtgtg gttgagttcg   | 1140 |
| tactgttctg aataaaaaaa aggagaaaag aaaactcgag ttgttatgtt ttttcaactga  | 1200 |
| ttccatgcgc agtcatgaga gtttgtagct tttgtctttt tgctttctct taatgtttcc   | 1260 |
| ctgctttatt tactgaaacc attggtttgg ttttttatgt taattaagtt ttttagtcc    |      |

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Asp Lys Lys Ile Arg Ile Gly Ile Asn Gly Phe Gly Arg Ile |  |
| 1 5 10 15                                                       |  |
| Gly Arg Leu Val Ala Arg Val Val Leu Gln Arg Asp Asp Val Glu Leu |  |
| 20 25 30                                                        |  |
| Val Ala Val Asn Asp Pro Phe Ile Thr Thr Glu Tyr Met Thr Tyr Met |  |
| 35 40 45                                                        |  |
| Phe Lys Tyr Asp Ser Val His Gly Gln Trp Lys His His Glu Leu Lys |  |
| 50 55 60                                                        |  |
| Val Lys Asp Asp Lys Thr Leu Leu Phe Gly Glu Lys Pro Val Thr Val |  |
| 65 70 75 80                                                     |  |
| Phe Gly Ile Arg Asn Pro Glu Asp Ile Pro Trp Gly Glu Ala Gly Ala |  |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

(B) LOCATION: 1..294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Tyr | Met | Phe | Lys | Tyr | Asp | Ser | Val | His | Gly | Gln | Trp | Lys | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Glu | Leu | Lys | Val | Lys | Asp | Asp | Lys | Thr | Leu | Leu | Phe | Gly | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Val | Thr | Val | Phe | Gly | Ile | Arg | Asn | Pro | Glu | Asp | Ile | Pro | Trp | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Gly | Ala | Asp | Phe | Val | Val | Glu | Ser | Thr | Gly | Val | Phe | Thr | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asp | Lys | Ala | Ala | Ala | His | Leu | Lys | Gly | Gly | Ala | Lys | Lys | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Ser | Ala | Pro | Ser | Lys | Asp | Ala | Pro | Met | Phe | Val | Val | Gly | Val | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | His | Glu | Tyr | Lys | Ser | Asp | Leu | Asp | Ile | Val | Ser | Asn | Ala | Ser | Cys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Thr | Thr | Asn | Cys | Leu | Ala | Pro | Leu | Ala | Lys | Val | Ile | Asn | Asp | Arg | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ser Ile Thr Ala Thr  
130 135 140  
Gln Lys Thr Val Asp Gly Pro Ser Met Lys Asp Trp Arg Gly Gly Arg  
145 150 155 160  
Ala Ala Ser Phe Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala  
165 170 175  
Val Gly Lys Val Leu Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ser  
180 185 190  
Phe Arg Val Pro Thr Val Asp Val Ser Val Val Asp Leu Thr Val Arg  
195 200 205  
Leu Glu Lys Ala Ala Thr Tyr Asp Glu Ile Lys Lys Ala Ile Lys Glu  
210 215 220  
Glu Ser Glu Gly Lys Met Lys Gly Ile Leu Gly Tyr Thr Glu Asp Asp  
225 230 235 240  
Val Val Ser Thr Asp Phe Val Gly Asp Asn Arg Ser Ser Ile Phe Asp  
245 250 255  
Ala Lys Ala Gly Ile Ala Leu Ser Asp Lys Phe Val Lys Leu Val Ser  
260 265 270  
Trp Tyr Asp Asn Glu Trp Gly Tyr Ser Ser Arg Val Val Asp Leu Ile  
275 280 285  
Val His Met Ser Lys Ala  
290

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Met Phe Lys Tyr Asp Ser Val His Gly Gln Trp Lys His His Glu Leu  
1 5 10 15  
Lys Val Lys Asp Asp Lys Thr Leu Leu Phe Gly Glu Lys Pro Val Thr  
20 25 30  
Val Phe Gly Ile Arg Asn Pro Glu Asp Ile Pro Trp Gly Glu Ala Gly  
35 40 45  
Ala Asp Phe Val Val Glu Ser Thr Gly Val Phe Thr Asp Lys Asp Lys  
50 55 60  
Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Val Ile Ser Ala  
65 70 75 80  
Pro Ser Lys Asp Ala Pro Met Phe Val Val Gly Val Asn Glu His Glu  
85 90 95  
Tyr Lys Ser Asp Leu Asp Ile Val Ser Asn Ala Ser Cys Thr Thr Asn  
100 105 110  
Cys Leu Ala Pro Leu Ala Lys Val Ile Asn Asp Arg Phe Gly Ile Val  
115 120 125  
Glu Gly Leu Met Thr Thr Val His Ser Ile Thr Ala Thr Gln Lys Thr  
130 135 140  
Val Asp Gly Pro Ser Met Lys Asp Trp Arg Gly Gly Arg Ala Ala Ser  
145 150 155 160  
Phe Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala Val Gly Lys  
165 170 175  
Val Leu Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ser Phe Arg Val  
180 185 190  
Pro Thr Val Asp Val Ser Val Val Asp Leu Thr Val Arg Leu Glu Lys  
195 200 205  
Ala Ala Thr Tyr Asp Glu Ile Lys Lys Ala Ile Lys Glu Glu Ser Glu

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210 215 220  
Gly Lys Met Lys Gly Ile Leu Gly Tyr Thr Glu Asp Asp Val Val Ser  
225 230 235 240  
Thr Asp Phe Val Gly Asp Asn Arg Ser Ser Ile Phe Asp Ala Lys Ala  
245 250 255  
Gly Ile Ala Leu Ser Asp Lys Phe Val Lys Leu Val Ser Trp Tyr Asp  
260 265 270  
Asn Glu Trp Gly Tyr Ser Ser Arg Val Val Asp Leu Ile Val His Met  
275 280 285  
Ser Lys Ala  
290

(2) INFORMATION FOR SEQ ID NO:2556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..532
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| ataacacaaa | tacacacaaa | aaaaaaaaaac | agaaagtaac | atgagatctc  | tcttattagc  | 60  |
| cgtgtgcctg | gttcttgctt | tacactgcgg  | tgaagcagcc | gtgtcttgca  | acacgggtgat | 120 |
| tgcggatctt | tacccttgct | tatcctacgt  | gactcagggc | ggaccgggtcc | caaccctctg  | 180 |
| ctgcaacggt | ctcacaaac  | tcaagagtca  | ggctcaaact | tctgtggacc  | gtcaSgggGg  | 240 |
| tctgtcgttg | catcaaact  | gctattggag  | gactcactct | ctctcctaga  | accatccaaa  | 300 |
| atgctttgga | attgccttct | aaatgtggtg  | tcgatctccc | ttacaagttc  | agcccttcca  | 360 |
| ctgactgcga | cagtatccag | tgagacaagc  | agaaaatctt | aaaggaagct  | actacaagaa  | 420 |
| ctataataac | ctaataatta | ataaatgagg  | gcattgggtt | gctagttgct  | aaAttgatca  | 480 |
| gtgatgtatt | Cgycattttg | aatgthctaa  | tTctcagcag | gcacttatct  | cc          |     |

(2) INFORMATION FOR SEQ ID NO:2557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Arg Ser Leu Leu Ala Val Cys Leu Val Leu Ala Leu His Cys     |  |
| 1 5 10 15                                                       |  |
| Gly Glu Ala Ala Val Ser Cys Asn Thr Val Ile Ala Asp Leu Tyr Pro |  |
| 20 25 30                                                        |  |
| Cys Leu Ser Tyr Val Thr Gln Gly Gly Pro Val Pro Thr Leu Cys Cys |  |
| 35 40 45                                                        |  |
| Asn Gly Leu Thr Thr Leu Lys Ser Gln Ala Gln Thr Ser Val Asp Arg |  |
| 50 55 60                                                        |  |
| Xaa Gly Gly Leu Ser Leu His Gln Ile Cys Tyr Trp Arg Thr His Ser |  |
| 65 70 75 80                                                     |  |
| Leu Ser                                                         |  |

(2) INFORMATION FOR SEQ ID NO:2558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..533  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ataacacaaa | tacacacaaa | aaaaandRaa | Wacagaaagt  | aacatgagat | ctctcttatt | 60  |
| agccgtgtgc | ctgggtcttg | ctttacactg | cgggtgaagca | gccgtgtctt | gcaacacggt | 120 |
| gattgcggat | ctttaccctt | gcttatccta | cgtgactcag  | ggcggaccgg | tcccaaccct | 180 |
| ctgctgcaac | ggtctcaca  | cactcaagag | tcagggtcaa  | acttctgtgg | accgtcaggg | 240 |
| gNgtctgtcg | ttgcatcaaa | tctgctattg | gaggactcac  | tctctctcct | agaaccatcc | 300 |
| aaaatgcttt | ggaattgcct | tctaaatgtg | gtgtcgatct  | cccttacaag | ttcagccctt | 360 |
| ccactgactg | cgacagtatc | cagtgagaca | agcagaaaat  | cttaaaggaa | gctactacaa | 420 |
| gaactataat | aacctataa  | ttaataaatg | agggcattgg  | tttgctagtt | gctaattgat | 480 |
| cagtgatgta | ttgtcatttt | gaatgttcta | atatcagcag  | gcacttatct | ctg        |     |

(2) INFORMATION FOR SEQ ID NO:2559:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 82 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..82  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Leu | Leu | Ala | Val | Cys | Leu | Val | Leu | Ala | Leu | His | Cys |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Glu | Ala | Ala | Val | Ser | Cys | Asn | Thr | Val | Ile | Ala | Asp | Leu | Tyr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  | Pro |
| Cys | Leu | Ser | Tyr | Val | Thr | Gln | Gly | Gly | Pro | Val | Pro | Thr | Leu | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  | Cys |
| Asn | Gly | Leu | Thr | Thr | Leu | Lys | Ser | Gln | Ala | Gln | Thr | Ser | Val | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  | Arg |
| Gln | Gly | Xaa | Leu | Ser | Leu | His | Gln | Ile | Cys | Tyr | Trp | Arg | Thr | His |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     |     |     | 80  |
| Leu | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2560:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 896 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..896  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| accattaggg  | ctctctctaa | attcctcagt | ctcgtgagaa | tcgtcatcgt | cttcacggag | 60  |
| ctcactcgaa  | gatgttaaag | gcagatatat | caccgaatca | ttcaatctac | atccaGaaac | 120 |
| ctcaatgaaa  | ggatcaagaa | agaggaattg | aagagatctc | tttactgttt | gttctctcag | 180 |
| tttgggagaa  | tacttgatgt | ggttgctttg | aagactccga | agctccgagg | acaagcttgg | 240 |
| gttaactttta | gtgaagtcac | tgctgctggg | catgctgttc | gtcagatgca | aaattttccc | 300 |
| ttvtatgata  | aaccaatgag | cttacaatat | gcaaaagcaa | agtcagattg | tctagctaaa | 360 |
| gctgagggaa  | ctttcgtttc | aaaagataag | aagaggaagc | aagaagaaaa | agttgaaaga | 420 |
| aagcgtgaag  | aatcccaacg | accaaacaca | gctaattggc | caagtgctaa | tggtccaagt | 480 |
| gccaataaag  | gagtccttgc | gccttcgttc | cagccgagcg | ggcaagaaac | aatgccacca | 540 |

aacaacatac tcttcattca gaatctccca caccagacaa caagcatgat gctccagctt 600  
ctcttcgaac agtaccctgg attcaaagag ataagaatga tcgacgcaaa accaggaatc 660  
gcgtttgtag agtacgaaga cgatgttcaa gcttccatag ctatgcaacc tcttcaagggt 720  
ttcaaaatca ctccccagaa tccaatggtc atctctttcg ccaagaaatg ataagagtct 780  
tggttttggt tggttggtgt cctttaagac gatagtactg gaccaaccaa acctgggtgtg 840  
tataaccaac caacggttct attggttaac ggattaatcc gggttttggt taatcg

(2) INFORMATION FOR SEQ ID NO:2561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1573649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

Met Gln Asn Phe Pro Xaa Tyr Asp Lys Pro Met Arg Leu Gln Tyr Ala  
1 5 10 15  
Lys Ala Lys Ser Asp Cys Leu Ala Lys Ala Glu Gly Thr Phe Val Pro  
20 25 30  
Lys Asp Lys Lys Arg Lys Gln Glu Glu Lys Val Glu Arg Lys Arg Glu  
35 40 45  
Glu Ser Gln Arg Pro Asn Thr Ala Asn Gly Pro Ser Ala Asn Gly Pro  
50 55 60  
Ser Ala Asn Asn Gly Val Pro Ala Pro Ser Phe Gln Pro Ser Gly Gln  
65 70 75 80  
Glu Thr Met Pro Pro Asn Asn Ile Leu Phe Ile Gln Asn Leu Pro His  
85 90 95  
Glu Thr Thr Ser Met Met Leu Gln Leu Leu Phe Glu Gln Tyr Pro Gly  
100 105 110  
Phe Lys Glu Ile Arg Met Ile Asp Ala Lys Pro Gly Ile Ala Phe Val  
115 120 125  
Glu Tyr Glu Asp Asp Val Gln Ala Ser Ile Ala Met Gln Pro Leu Gln  
130 135 140  
Gly Phe Lys Ile Thr Pro Gln Asn Pro Met Val Ile Ser Phe Ala Lys  
145 150 155 160  
Lys

(2) INFORMATION FOR SEQ ID NO:2562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1573650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

Met Arg Leu Gln Tyr Ala Lys Ala Lys Ser Asp Cys Leu Ala Lys Ala  
1 5 10 15  
Glu Gly Thr Phe Val Pro Lys Asp Lys Lys Arg Lys Gln Glu Glu Lys  
20 25 30  
Val Glu Arg Lys Arg Glu Glu Ser Gln Arg Pro Asn Thr Ala Asn Gly  
35 40 45  
Pro Ser Ala Asn Gly Pro Ser Ala Asn Asn Gly Val Pro Ala Pro Ser  
50 55 60  
Phe Gln Pro Ser Gly Gln Glu Thr Met Pro Pro Asn Asn Ile Leu Phe

65 70 75 80  
Ile Gln Asn Leu Pro His Glu Thr Thr Ser Met Met Leu Gln Leu Leu  
85 90 95  
Phe Glu Gln Tyr Pro Gly Phe Lys Glu Ile Arg Met Ile Asp Ala Lys  
100 105 110  
Pro Gly Ile Ala Phe Val Glu Tyr Glu Asp Asp Val Gln Ala Ser Ile  
115 120 125  
Ala Met Gln Pro Leu Gln Gly Phe Lys Ile Thr Pro Gln Asn Pro Met  
130 135 140  
Val Ile Ser Phe Ala Lys Lys  
145 150

(2) INFORMATION FOR SEQ ID NO:2563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1070
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| acattttttca | cgtctccgac  | aacttcttct  | tctccaaccc | aaattcctct | cttctcaacc | 60   |
| togtctcttc  | cgttctcttc  | ctccaacatt  | tctccgatca | ttgatgggtt | cgtcttcttc | 120  |
| tttctctctct | tcttctctga  | agcttctctt  | tctgcaactc | tttgagaacg | aatcttccac | 180  |
| ctttacttat  | cttctcgccg  | acgtttctca  | tcttgataaa | cctgctttgt | tgattgatcc | 240  |
| ggtggacaag  | actgtggata  | gagacttgaa  | actgattgat | gagttaggat | taaagcttat | 300  |
| ctatgctatg  | aacactcatg  | ttcatgctga  | tcatgtcact | ggtactggac | ttcttaagac | 360  |
| gaagctcccc  | ggtgtgaaat  | ccgttatttc  | gaaagcaagt | ggttccaaag | ctgatttggt | 420  |
| tcttgaaacct | ggtgacaaaag | tatctattgg  | tgatatatac | cttgagggtc | gtgctacacc | 480  |
| tggacacact  | acaggatgtg  | ttacatatgt  | gactggtgaa | ggagctgac  | agccccaacc | 540  |
| aagaatggct  | tttacogggg  | atgctgtact  | catCcggtgt | tgtgggagga | ctgactttca | 600  |
| gggaggaagc  | tcagatcaac  | tctacgagtc  | tgtacattca | cagatatttt | cattgccaaa | 660  |
| ggacacattg  | atctatccag  | ctcacgacta  | caaagggttc | gaggtaagta | cagttggaga | 720  |
| agagatgcaa  | cacaacccgc  | gtctaactaa  | agataaagaa | acattcaaaa | ccattatgtc | 780  |
| aaatctgaat  | ctgtcgtatc  | cgaagatgat  | tgatgttgca | gtaccagcaa | atatggtctg | 840  |
| tgggttacaa  | gatgtgcctt  | ctcaagccaa  | ctaaaaaaaa | ctcttacata | taatgtttgt | 900  |
| ctttttatcg  | atgtcattct  | atattttacca | aagccaataa | aaactcttga | gagtaatttc | 960  |
| tacaataaga  | tttgcttccg  | ttgtagataa  | gttcattaga | aaattgtgta | aattagattg | 1020 |
| aacatgtgga  | atttgttatg  | aagatgaaga  | cagtatttgc | gtgttcgact |            |      |

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

His Phe Ser Arg Leu Arg Gln Leu Leu Leu Gln Pro Lys Phe Leu  
1 5 10 15  
Ser Ser Gln Pro Arg Pro Leu Arg Ser Pro Pro Pro Thr Phe Leu Arg  
20 25 30  
Ser Leu Met Gly Ser Ser Ser Ser Phe Ser Ser Ser Ser Ser Lys Leu  
35 40 45  
Leu Phe Arg Gln Leu Phe Glu Asn Glu Ser Ser Thr Phe Thr Tyr Leu  
50 55 60

Leu Ala Asp Val Ser His Pro Asp Lys Pro Ala Leu Leu Ile Asp Pro  
65 70 75 80  
Val Asp Lys Thr Val Asp Arg Asp Leu Lys Leu Ile Asp Glu Leu Gly  
85 90 95  
Leu Lys Leu Ile Tyr Ala Met Asn Thr His Val His Ala Asp His Val  
100 105 110  
Thr Gly Thr Gly Leu Leu Lys Thr Lys Leu Pro Gly Val Lys Ser Val  
115 120 125  
Ile Ser Lys Ala Ser Gly Ser Lys Ala Asp Leu Phe Leu Glu Pro Gly  
130 135 140  
Asp Lys Val Ser Ile Gly Asp Ile Tyr Leu Glu Val Arg Ala Thr Pro  
145 150 155 160  
Gly His Thr Thr Gly Cys Val Thr Tyr Val Thr Gly Glu Gly Ala Asp  
165 170 175  
Gln Pro Gln Pro Arg Met Ala Phe Thr Gly Asp Ala Val Leu Ile Arg  
180 185 190  
Gly Cys Gly Arg Thr Asp Phe Gln Gly Gly Ser Ser Asp Gln Leu Tyr  
195 200 205  
Glu Ser Val His Ser Gln Ile Phe Ser Leu Pro Lys Asp Thr Leu Ile  
210 215 220  
Tyr Pro Ala His Asp Tyr Lys Gly Phe Glu Val Ser Thr Val Gly Glu  
225 230 235 240  
Glu Met Gln His Asn Pro Arg Leu Thr Lys Asp Lys Glu Thr Phe Lys  
245 250 255  
Thr Ile Met Ser Asn Leu Asn Leu Ser Tyr Pro Lys Met Ile Asp Val  
260 265 270  
Ala Val Pro Ala Asn Met Val Cys Gly Leu Gln Asp Val Pro Ser Gln  
275 280 285  
Ala Asn  
290

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Gly Ser Ser Ser Ser Phe Ser Ser Ser Ser Ser Lys Leu Leu Phe  
1 5 10 15  
Arg Gln Leu Phe Glu Asn Glu Ser Ser Thr Phe Thr Tyr Leu Leu Ala  
20 25 30  
Asp Val Ser His Pro Asp Lys Pro Ala Leu Leu Ile Asp Pro Val Asp  
35 40 45  
Lys Thr Val Asp Arg Asp Leu Lys Leu Ile Asp Glu Leu Gly Leu Lys  
50 55 60  
Leu Ile Tyr Ala Met Asn Thr His Val His Ala Asp His Val Thr Gly  
65 70 75 80  
Thr Gly Leu Leu Lys Thr Lys Leu Pro Gly Val Lys Ser Val Ile Ser  
85 90 95  
Lys Ala Ser Gly Ser Lys Ala Asp Leu Phe Leu Glu Pro Gly Asp Lys  
100 105 110  
Val Ser Ile Gly Asp Ile Tyr Leu Glu Val Arg Ala Thr Pro Gly His  
115 120 125  
Thr Thr Gly Cys Val Thr Tyr Val Thr Gly Glu Gly Ala Asp Gln Pro  
130 135 140  
Gln Pro Arg Met Ala Phe Thr Gly Asp Ala Val Leu Ile Arg Gly Cys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Arg | Thr | Asp | Phe | Gln | Gly | Gly | Ser | Ser | Asp | Gln | Leu | Tyr | Glu | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | His | Ser | Gln | Ile | Phe | Ser | Leu | Pro | Lys | Asp | Thr | Leu | Ile | Tyr | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | His | Asp | Tyr | Lys | Gly | Phe | Glu | Val | Ser | Thr | Val | Gly | Glu | Glu | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | His | Asn | Pro | Arg | Leu | Thr | Lys | Asp | Lys | Glu | Thr | Phe | Lys | Thr | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Ser | Asn | Leu | Asn | Leu | Ser | Tyr | Pro | Lys | Met | Ile | Asp | Val | Ala | Val |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Ala | Asn | Met | Val | Cys | Gly | Leu | Gln | Asp | Val | Pro | Ser | Gln | Ala | Asn |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |

(2) INFORMATION FOR SEQ ID NO:2566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1573654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Thr | His | Val | His | Ala | Asp | His | Val | Thr | Gly | Thr | Gly | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Thr | Lys | Leu | Pro | Gly | Val | Lys | Ser | Val | Ile | Ser | Lys | Ala | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Lys | Ala | Asp | Leu | Phe | Leu | Glu | Pro | Gly | Asp | Lys | Val | Ser | Ile | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ile | Tyr | Leu | Glu | Val | Arg | Ala | Thr | Pro | Gly | His | Thr | Thr | Gly | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Thr | Tyr | Val | Thr | Gly | Glu | Gly | Ala | Asp | Gln | Pro | Gln | Pro | Arg | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Phe | Thr | Gly | Asp | Ala | Val | Leu | Ile | Arg | Gly | Cys | Gly | Arg | Thr | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gln | Gly | Gly | Ser | Ser | Asp | Gln | Leu | Tyr | Glu | Ser | Val | His | Ser | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Phe | Ser | Leu | Pro | Lys | Asp | Thr | Leu | Ile | Tyr | Pro | Ala | His | Asp | Tyr |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Gly | Phe | Glu | Val | Ser | Thr | Val | Gly | Glu | Glu | Met | Gln | His | Asn | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Leu | Thr | Lys | Asp | Lys | Glu | Thr | Phe | Lys | Thr | Ile | Met | Ser | Asn | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Leu | Ser | Tyr | Pro | Lys | Met | Ile | Asp | Val | Ala | Val | Pro | Ala | Asn | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Cys | Gly | Leu | Gln | Asp | Val | Pro | Ser | Gln | Ala | Asn |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1151 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1151

(D) OTHER INFORMATION: / Ceres Seq. ID 1573655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

|            |             |            |            |            |            |      |
|------------|-------------|------------|------------|------------|------------|------|
| acacatctta | aaaagtaaaa  | acacattcat | ctatccaaca | aaaaaaaaaa | aaaaaaggag | 60   |
| aaatggaagg | aatcgatcat  | agaatggtga | gtgtcaatgg | cataactatg | cacattgccg | 120  |
| agaaaggtcc | caaagaagga  | cctgtggtgc | ttctcctcca | tggattccct | gatctctggt | 180  |
| acacgtggcg | tcaccagatt  | agtgggttat | catctctagg | ttaccgcgct | gtagctccag | 240  |
| acctccgagg | ctacggagac  | tctgattcgc | cagagtcctt | ctccgagtac | acgtgtctta | 300  |
| acgtcgttgg | ggacctcgta  | gctcttctgg | acagtgttgc | tggaaatcaa | gagaagggtg | 360  |
| ttctggtcgg | tcattgattg  | ggagccatta | tcggatggtt | tctctgtttg | tttcgacctg | 420  |
| aaaagattaa | cggcttttgt  | tgtttgagt  | tgccgtatag | atcaagaaac | cctaaagtca | 480  |
| agcccgttca | agggttcaag  | gctgtattg  | gagatgatta | ctacatttgt | agatttcagg | 540  |
| aaccggggaa | gattgaagga  | gagattgcaa | gtgcagatcc | aagaatattt | ctgaggaacc | 600  |
| tcttcacagg | gaggacactc  | ggtcgcgcga | ttttacctaa | ggataatccc | tttggggaaa | 660  |
| aacctaaccc | taatagcgaa  | aacattgaat | tgccatgaat | gttttctaag | aaagatctcg | 720  |
| atttctatgt | ctccaaattc  | gagaaggcag | gatttaccgg | tggattgaac | tactacagag | 780  |
| ccatggatct | gaattgggag  | ctcactgcac | catggaccgg | agctaagatt | caagttccag | 840  |
| tgaagtccat | gacagggtgac | ttcgacatgg | tttacaccac | accagggatg | aaagagtaca | 900  |
| ttcacgggtg | tggattttgt  | gcagatgttc | caactcttca | agagatagtg | gtgattgaag | 960  |
| atgctggKYM | Ytcgttaacc  | aagagaaacc | tcaagaggtc | actgctcaca | tcaatgacct | 1020 |
| cttcaccaag | cttcggggaca | acaacaaaag | cttttagagt | tctcgtttgg | ttctattatg | 1080 |
| ttggctctca | aaacaagttg  | gttcttgcac | gtgttggttc | gacaagattt | tgaataagac | 1140 |
| ttggcattat | g           |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..356

(D) OTHER INFORMATION: / Ceres Seq. ID 1573656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Ile | Asp | His | Arg | Met | Val | Ser | Val | Asn | Gly | Ile | Thr | Met |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ile | Ala | Glu | Lys | Gly | Pro | Lys | Glu | Gly | Pro | Val | Val | Leu | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gly | Phe | Pro | Asp | Leu | Trp | Tyr | Thr | Trp | Arg | His | Gln | Ile | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Ser | Leu | Gly | Tyr | Arg | Ala | Val | Ala | Pro | Asp | Leu | Arg | Gly | Tyr |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Asp | Ser | Asp | Ser | Pro | Glu | Ser | Phe | Ser | Glu | Tyr | Thr | Cys | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Val | Gly | Asp | Leu | Val | Ala | Leu | Leu | Asp | Ser | Val | Ala | Gly | Asn | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Val | Phe | Leu | Val | Gly | His | Asp | Trp | Gly | Ala | Ile | Ile | Gly | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Cys | Leu | Phe | Arg | Pro | Glu | Lys | Ile | Asn | Gly | Phe | Val | Cys | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Pro | Tyr | Arg | Ser | Arg | Asn | Pro | Lys | Val | Lys | Pro | Val | Gln | Gly |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Lys | Ala | Val | Phe | Gly | Asp | Asp | Tyr | Tyr | Ile | Cys | Arg | Phe | Gln | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Gly | Lys | Ile | Glu | Gly | Glu | Ile | Ala | Ser | Ala | Asp | Pro | Arg | Ile | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Arg | Asn | Leu | Phe | Thr | Gly | Arg | Thr | Leu | Gly | Pro | Pro | Ile | Leu | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Lys | Asp | Asn | Pro | Phe | Gly | Glu | Lys | Pro | Asn | Pro | Asn | Ser | Glu | Asn | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Leu | Pro | Glu | Trp | Phe | Ser | Lys | Lys | Asp | Leu | Asp | Phe | Tyr | Val | Ser |

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(2) INFORMATION FOR SEQ ID NO:2569:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..349
 (D) OTHER INFORMATION: / Ceres Seq. ID 1573657
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:
```

|            |            |            |            |            |           |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Val        | Ser        | Val        | Asn<br>5   | Gly       | Ile        | Thr        | Met<br>10  | His        | Ile        | Ala        | Glu        | Lys        | Gly<br>15 | Pro        |
| Lys        | Glu        | Gly        | Pro<br>20  | Val        | Val       | Leu        | Leu        | Leu<br>25  | His        | Gly        | Phe        | Pro        | Asp<br>30  | Leu       | Trp        |
| Tyr        | Thr        | Trp<br>35  | Arg        | His        | Gln       | Ile        | Ser<br>40  | Gly        | Leu        | Ser        | Ser        | Leu<br>45  | Gly        | Tyr       | Arg        |
| Ala        | Val<br>50  | Ala        | Pro        | Asp        | Leu       | Arg<br>55  | Gly        | Tyr        | Gly        | Asp        | Ser<br>60  | Asp        | Ser        | Pro       | Glu        |
| Ser<br>65  | Phe        | Ser        | Glu        | Tyr        | Thr<br>70 | Cys        | Leu        | Asn        | Val        | Val<br>75  | Gly        | Asp        | Leu        | Val       | Ala<br>80  |
| Leu        | Leu        | Asp        | Ser        | Val<br>85  | Ala       | Gly        | Asn        | Gln        | Glu<br>90  | Lys        | Val        | Phe        | Leu        | Val<br>95 | Gly        |
| His        | Asp        | Trp        | Gly<br>100 | Ala        | Ile       | Ile        | Gly        | Trp<br>105 | Phe        | Leu        | Cys        | Leu        | Phe<br>110 | Arg       | Pro        |
| Glu        | Lys        | Ile<br>115 | Asn        | Gly        | Phe       | Val        | Cys<br>120 | Leu        | Ser        | Val        | Pro        | Tyr<br>125 | Arg        | Ser       | Arg        |
| Asn        | Pro<br>130 | Lys        | Val        | Lys        | Pro       | Val<br>135 | Gln        | Gly        | Phe        | Lys        | Ala<br>140 | Val        | Phe        | Gly       | Asp        |
| Asp<br>145 | Tyr        | Tyr        | Ile        | Cys<br>150 | Arg       | Phe        | Gln        | Glu        | Pro        | Gly<br>155 | Lys        | Ile        | Glu        | Gly       | Glu<br>160 |
| Ile        | Ala        | Ser        | Ala<br>165 | Asp        | Pro       | Arg        | Ile        | Phe        | Leu<br>170 | Arg        | Asn        | Leu        | Phe<br>175 | Thr       | Gly        |
| Arg        | Thr<br>180 | Leu        | Gly        | Pro        | Pro       | Ile        | Leu        | Pro<br>185 | Lys        | Asp        | Asn        | Pro        | Phe<br>190 | Gly       | Glu        |
| Lys        | Pro<br>195 | Asn        | Pro        | Asn        | Ser       | Glu        | Asn<br>200 | Ile        | Glu        | Leu        | Pro        | Glu<br>205 | Trp        | Phe       | Ser        |
| Lys        | Lys<br>210 | Asp        | Leu        | Asp        | Phe       | Tyr<br>215 | Val        | Ser        | Lys        | Phe        | Glu<br>220 | Lys        | Ala        | Gly       | Phe        |
| Thr<br>225 | Gly        | Gly        | Leu        | Asn<br>230 | Tyr       | Arg        | Ala        | Met        | Asp<br>235 | Leu        | Asn        | Trp        | Glu        | Leu       | Leu<br>240 |

Thr Ala Pro Trp Thr Gly Ala Lys Ile Gln Val Pro Val Lys Phe Met  
245 250 255  
Thr Gly Asp Phe Asp Met Val Tyr Thr Thr Pro Gly Met Lys Glu Tyr  
260 265 270  
Ile His Gly Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu Ile  
275 280 285  
Val Val Ile Glu Asp Ala Xaa Xaa Ser Leu Thr Lys Arg Asn Leu Lys  
290 295 300  
Arg Ser Leu Leu Thr Ser Met Thr Ser Ser Pro Ser Phe Gly Thr Thr  
305 310 315 320  
Thr Lys Ala Phe Arg Val Leu Val Trp Phe Tyr Tyr Val Gly Ser Gln  
325 330 335  
Asn Lys Leu Val Leu Ala Cys Val Val Ser Thr Arg Phe  
340 345

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1573658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

Met His Ile Ala Glu Lys Gly Pro Lys Glu Gly Pro Val Val Leu Leu  
1 5 10 15  
Leu His Gly Phe Pro Asp Leu Trp Tyr Thr Trp Arg His Gln Ile Ser  
20 25 30  
Gly Leu Ser Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly  
35 40 45  
Tyr Gly Asp Ser Asp Ser Pro Glu Ser Phe Ser Glu Tyr Thr Cys Leu  
50 55 60  
Asn Val Val Gly Asp Leu Val Ala Leu Leu Asp Ser Val Ala Gly Asn  
65 70 75 80  
Gln Glu Lys Val Phe Leu Val Gly His Asp Trp Gly Ala Ile Ile Gly  
85 90 95  
Trp Phe Leu Cys Leu Phe Arg Pro Glu Lys Ile Asn Gly Phe Val Cys  
100 105 110  
Leu Ser Val Pro Tyr Arg Ser Arg Asn Pro Lys Val Lys Pro Val Gln  
115 120 125  
Gly Phe Lys Ala Val Phe Gly Asp Asp Tyr Tyr Ile Cys Arg Phe Gln  
130 135 140  
Glu Pro Gly Lys Ile Glu Gly Glu Ile Ala Ser Ala Asp Pro Arg Ile  
145 150 155 160  
Phe Leu Arg Asn Leu Phe Thr Gly Arg Thr Leu Gly Pro Pro Ile Leu  
165 170 175  
Pro Lys Asp Asn Pro Phe Gly Glu Lys Pro Asn Pro Asn Ser Glu Asn  
180 185 190  
Ile Glu Leu Pro Glu Trp Phe Ser Lys Lys Asp Leu Asp Phe Tyr Val  
195 200 205  
Ser Lys Phe Glu Lys Ala Gly Phe Thr Gly Gly Leu Asn Tyr Tyr Arg  
210 215 220  
Ala Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys  
225 230 235 240  
Ile Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asp Met Val Tyr  
245 250 255  
Thr Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Gly Phe Ala Ala  
260 265 270  
Asp Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Xaa Xaa



275 280 285  
Ser Leu Thr Lys Arg Asn Leu Lys Arg Ser Leu Leu Thr Ser Met Thr  
290 295 300  
Ser Ser Pro Ser Phe Gly Thr Thr Thr Lys Ala Phe Arg Val Leu Val  
305 310 315 320  
Trp Phe Tyr Tyr Val Gly Ser Gln Asn Lys Leu Val Leu Ala Cys Val  
325 330 335  
Val Ser Thr Arg Phe  
340

(2) INFORMATION FOR SEQ ID NO:2571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

atcttaaaaa gtaaaaacac attcatctat ccaacaaaaa aaggagaaat 60  
ggaaggaatc gatcatagaa tggtagtgt caatggcata actatgcaca ttgccgagaa 120  
aggtoccaaa gaaggacctg tggtagttct cctccatgga ttccctgac tcgtacacgt 180  
ggcgtaacca gattagtggg ttatcatctc taggttaccg cgctgtagct ccagacctcc 240  
gaggctacgg agactctgat tcgccagagt ctttctccga gtacacgtgt cttaacgtcg 300  
ttggggacct cgtagctctt ctggacagtg ttgctggaaa tcagagaagg tgtttctggt 360  
cggtoatgat tggggagcca ttatcggatg gtttctctgt ttgtttcgac ctgaaaagat 420  
taacggcttt gtGgtgtttg agtgtgccgt atagatcaaG gaaaccctaa agtcaagccc 480  
gttcaagggt tcaaggctgt atttgagat gattactaca tttgtagatt tcaggaaccg 540  
gggaagattg aaggagagat tgcaagtga gatccaagaa tatttctgag gaacctcttc 600  
acagggagga cactcgggtc gccgatttta cctaaggata atccctttgg ggaaaaacct 660  
aaccctaata gcgaaaacat tgaattgcct gaatggtttt ctaagaaaga tctcgatttc 720  
tatgtctcca aattcgagaa ggcaggattt accggtggat tgaactacta cagagccatg 780  
gatctgaatt gggagctcac tgcacatgg accggagcta agattcaagt tccagtgaag 840  
ttcatgacag gtgacttcaa catggtttac accacaccag ggatgaaaga gtacattcac 900  
ggtggtggat ttgctgcaga tgttccaact cttcaagaga tagtggtgat tgaagatgct 960  
ggtcacttcg ttaaccaaga gaaacctcaa gaggtcactg ctcacatcaa tgacttcttc 1020  
accaatcttc gggacaacaa caaagcttt tagagttctc gtttggttct attatgttg 1080  
ctctcaaac aagttggttc ttgcatgtgt tgtttcgaca agattttgaa taagacttgg 1140  
cattatgaag ccc

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Met Asp Ser Leu Ile Ser Tyr Thr Trp Arg His Gln Ile Ser Gly Leu  
1 5 10 15  
Ser Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly Tyr Gly  
20 25 30  
Asp Ser Asp Ser Pro Glu Ser Phe Ser Glu Tyr Thr Cys Leu Asn Val  
35 40 45  
Val Gly Asp Leu Val Ala Leu Leu Asp Ser Val Ala Gly Asn Gln Arg  
50 55 60

Arg Cys Phe Trp Ser Val Met Ile Gly Glu Pro Leu Ser Asp Gly Phe  
65 70 75 80  
Ser Val Cys Phe Asp Leu Lys Arg Leu Thr Ala Leu Trp Cys Leu Ser  
85 90 95  
Val Pro Tyr Arg Ser Arg Lys Pro  
100

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1573661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys Ile  
1 5 10 15  
Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asn Met Val Tyr Thr  
20 25 30  
Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Gly Phe Ala Ala Asp  
35 40 45  
Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Gly His Phe  
50 55 60  
Val Asn Gln Glu Lys Pro Gln Glu Val Thr Ala His Ile Asn Asp Phe  
65 70 75 80  
Phe Thr Asn Leu Arg Asp Asn Asn Lys Ser Phe  
85 90

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1573662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

Met Thr Gly Asp Phe Asn Met Val Tyr Thr Thr Pro Gly Met Lys Glu  
1 5 10 15  
Tyr Ile His Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu  
20 25 30  
Ile Val Val Ile Glu Asp Ala Gly His Phe Val Asn Gln Glu Lys Pro  
35 40 45  
Gln Glu Val Thr Ala His Ile Asn Asp Phe Phe Thr Asn Leu Arg Asp  
50 55 60  
Asn Asn Lys Ser Phe  
65

(2) INFORMATION FOR SEQ ID NO:2575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1155

(D) OTHER INFORMATION: / Ceres Seq. ID 1573663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

|             |             |             |            |            |             |      |
|-------------|-------------|-------------|------------|------------|-------------|------|
| acatcttaaa  | aagtaaaaaac | acattcatct  | atccaacaaa | aaaaaaaaaa | aaaaaggaga  | 60   |
| aatggaagga  | atcgatcata  | gaatgggtgag | tgtcaatggc | ataactatgc | acattgccga  | 120  |
| gaaaggtccc  | aaagaaggac  | ctgtgggtgct | tctcctccat | ggattcccta | atctctggta  | 180  |
| cacgtggcgt  | caccagatta  | gtgggttatc  | atctctaggt | taccgcgctg | tagctccaga  | 240  |
| cctccgaggg  | tacggagact  | ctgattcgcc  | agagtctttc | tccgagtaca | cgtgtcttaa  | 300  |
| cgctcgttggg | gacctcgtag  | ctcttctgga  | cagtgttgct | ggaaatcaag | agaagggtgtt | 360  |
| tctggtcggg  | catgattggg  | gagccattat  | cggatggttt | ctctgtttgt | ttcgacctga  | 420  |
| aaagattaac  | ggctttgtgt  | gtttgagtg   | gccgtataga | tcaagaaacc | ctaaagtcaa  | 480  |
| gcccgttcaa  | gggttcaagg  | ctgtatttgg  | agatgattac | tacatttgta | gatttcagga  | 540  |
| accggggaag  | attgaaggag  | agattgcaag  | tgcagatcca | agaatatttc | tgaggaaacct | 600  |
| cttcacaggg  | aggacactcg  | gtccgccgat  | tttacctaag | gataatccct | ttggggaaaa  | 660  |
| acctaaccct  | aatagcgaaa  | acattgaatt  | gcctgaatgg | ttttctaaga | aagatctoga  | 720  |
| tttctatgtc  | tccaaattcg  | agaaggcagg  | atttaccggg | ggattgaact | actacagagc  | 780  |
| catggatctg  | aattgggagc  | tactgcacc   | atggaccgga | gctaagattc | aagttccagt  | 840  |
| gaagttcatg  | acaggtgact  | tgcacatggt  | ttacaccaca | ccagggatga | aagagtacat  | 900  |
| tcacggtggt  | ggatttgctg  | cagatgttcc  | aactcttcaa | gagatagtgg | tgattgaaga  | 960  |
| tgctggTchc  | ttogttaacc  | aagagaaacc  | tcaagaggtc | actgctcaca | tcaatgactt  | 1020 |
| cttcaccaag  | cttcgggaca  | acaacaaaag  | cttttagagt | tctcgtttgg | ttctattatg  | 1080 |
| ttggctctca  | aaacaagttg  | gttcttgcac  | gtgttgtttc | gacaagattt | tgaataagac  | 1140 |
| ttggcattat  | gaagc       |             |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1573664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Ile | Asp | His | Arg | Met | Val | Ser | Val | Asn | Gly | Ile | Thr | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Ile | Ala | Glu | Lys | Gly | Pro | Lys | Glu | Gly | Pro | Val | Val | Leu | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gly | Phe | Pro | Asn | Leu | Trp | Tyr | Thr | Trp | Arg | His | Gln | Ile | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Ser | Ser | Leu | Gly | Tyr | Arg | Ala | Val | Ala | Pro | Asp | Leu | Arg | Gly | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Asp | Ser | Asp | Ser | Pro | Glu | Ser | Phe | Ser | Glu | Tyr | Thr | Cys | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Val | Gly | Asp | Leu | Val | Ala | Leu | Leu | Asp | Ser | Val | Ala | Gly | Asn | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Lys | Val | Phe | Leu | Val | Gly | His | Asp | Trp | Gly | Ala | Ile | Ile | Gly | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Cys | Leu | Phe | Arg | Pro | Glu | Lys | Ile | Asn | Gly | Phe | Val | Cys | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Pro | Tyr | Arg | Ser | Arg | Asn | Pro | Lys | Val | Lys | Pro | Val | Gln | Gly |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Phe | Lys | Ala | Val | Phe | Gly | Asp | Asp | Tyr | Tyr | Ile | Cys | Arg | Phe | Gln | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Gly | Lys | Ile | Glu | Gly | Glu | Ile | Ala | Ser | Ala | Asp | Pro | Arg | Ile | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Arg | Asn | Leu | Phe | Thr | Gly | Arg | Thr | Leu | Gly | Pro | Pro | Ile | Leu | Pro |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asp | Asn | Pro | Phe | Gly | Glu | Lys | Pro | Asn | Pro | Asn | Ser | Glu | Asn | Ile |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Pro | Glu | Trp | Phe | Ser | Lys | Lys | Asp | Leu | Asp | Phe | Tyr | Val | Ser |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Phe | Glu | Lys | Ala | Gly | Phe | Thr | Gly | Gly | Leu | Asn | Tyr | Tyr | Arg | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Asp | Leu | Asn | Trp | Glu | Leu | Thr | Ala | Pro | Trp | Thr | Gly | Ala | Lys | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Val | Pro | Val | Lys | Phe | Met | Thr | Gly | Asp | Phe | Asp | Met | Val | Tyr | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Pro | Gly | Met | Lys | Glu | Tyr | Ile | His | Gly | Gly | Gly | Phe | Ala | Ala | Asp |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Pro | Thr | Leu | Gln | Glu | Ile | Val | Val | Ile | Glu | Asp | Ala | Gly | Xaa | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Asn | Gln | Glu | Lys | Pro | Gln | Glu | Val | Thr | Ala | His | Ile | Asn | Asp | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Thr | Lys | Leu | Arg | Asp | Asn | Asn | Lys | Ser | Phe |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1573665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Val | Asn | Gly | Ile | Thr | Met | His | Ile | Ala | Glu | Lys | Gly | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Gly | Pro | Val | Val | Leu | Leu | Leu | His | Gly | Phe | Pro | Asn | Leu | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Thr | Trp | Arg | His | Gln | Ile | Ser | Gly | Leu | Ser | Ser | Leu | Gly | Tyr | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Val | Ala | Pro | Asp | Leu | Arg | Gly | Tyr | Gly | Asp | Ser | Asp | Ser | Pro | Glu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Phe | Ser | Glu | Tyr | Thr | Cys | Leu | Asn | Val | Val | Gly | Asp | Leu | Val | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Leu | Asp | Ser | Val | Ala | Gly | Asn | Gln | Glu | Lys | Val | Phe | Leu | Val | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Asp | Trp | Gly | Ala | Ile | Ile | Gly | Trp | Phe | Leu | Cys | Leu | Phe | Arg | Pro |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Lys | Ile | Asn | Gly | Phe | Val | Cys | Leu | Ser | Val | Pro | Tyr | Arg | Ser | Arg |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asn | Pro | Lys | Val | Lys | Pro | Val | Gln | Gly | Phe | Lys | Ala | Val | Phe | Gly | Asp |
|     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Asp | Tyr | Tyr | Ile | Cys | Arg | Phe | Gln | Glu | Pro | Gly | Lys | Ile | Glu | Gly | Glu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Ala | Ser | Ala | Asp | Pro | Arg | Ile | Phe | Leu | Arg | Asn | Leu | Phe | Thr | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Arg | Thr | Leu | Gly | Pro | Pro | Ile | Leu | Pro | Lys | Asp | Asn | Pro | Phe | Gly | Glu |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Lys | Pro | Asn | Pro | Asn | Ser | Glu | Asn | Ile | Glu | Leu | Pro | Glu | Trp | Phe | Ser |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Lys | Lys | Asp | Leu | Asp | Phe | Tyr | Val | Ser | Lys | Phe | Glu | Lys | Ala | Gly | Phe |
|     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Thr | Gly | Gly | Leu | Asn | Tyr | Tyr | Arg | Ala | Met | Asp | Leu | Asn | Trp | Glu | Leu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Thr | Ala | Pro | Trp | Thr | Gly | Ala | Lys | Ile | Gln | Val | Pro | Val | Lys | Phe | Met |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Thr | Gly | Asp | Phe | Asp | Met | Val | Tyr | Thr | Thr | Pro | Gly | Met | Lys | Glu | Tyr |

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
|                                                                 | 260 |     | 265 |     | 270 |
| Ile His Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu Ile     |     |     |     |     |     |
| 275                                                             |     | 280 |     | 285 |     |
| Val Val Ile Glu Asp Ala Gly Xaa Phe Val Asn Gln Glu Lys Pro Gln |     |     |     |     |     |
| 290                                                             |     | 295 |     | 300 |     |
| Glu Val Thr Ala His Ile Asn Asp Phe Phe Thr Lys Leu Arg Asp Asn |     |     |     |     |     |
| 305                                                             |     | 310 |     | 315 | 320 |
| Asn Lys Ser Phe                                                 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1573666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ile | Ala | Glu | Lys | Gly | Pro | Lys | Glu | Gly | Pro | Val | Val | Leu | Leu |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | His | Gly | Phe | Pro | Asn | Leu | Trp | Tyr | Thr | Trp | Arg | His | Gln | Ile | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Leu | Ser | Ser | Leu | Gly | Tyr | Arg | Ala | Val | Ala | Pro | Asp | Leu | Arg | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Tyr | Gly | Asp | Ser | Asp | Ser | Pro | Glu | Ser | Phe | Ser | Glu | Tyr | Thr | Cys | Leu |
| 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Asn | Val | Val | Gly | Asp | Leu | Val | Ala | Leu | Leu | Asp | Ser | Val | Ala | Gly | Asn |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Glu | Lys | Val | Phe | Leu | Val | Gly | His | Asp | Trp | Gly | Ala | Ile | Ile | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Trp | Phe | Leu | Cys | Leu | Phe | Arg | Pro | Glu | Lys | Ile | Asn | Gly | Phe | Val | Cys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Ser | Val | Pro | Tyr | Arg | Ser | Arg | Asn | Pro | Lys | Val | Lys | Pro | Val | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Lys | Ala | Val | Phe | Gly | Asp | Asp | Tyr | Tyr | Ile | Cys | Arg | Phe | Gln |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Glu | Pro | Gly | Lys | Ile | Glu | Gly | Glu | Ile | Ala | Ser | Ala | Asp | Pro | Arg | Ile |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Phe | Leu | Arg | Asn | Leu | Phe | Thr | Gly | Arg | Thr | Leu | Gly | Pro | Pro | Ile | Leu |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |
| Pro | Lys | Asp | Asn | Pro | Phe | Gly | Glu | Lys | Pro | Asn | Pro | Asn | Ser | Glu | Asn |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ile | Glu | Leu | Pro | Glu | Trp | Phe | Ser | Lys | Lys | Asp | Leu | Asp | Phe | Tyr | Val |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Lys | Phe | Glu | Lys | Ala | Gly | Phe | Thr | Gly | Gly | Leu | Asn | Tyr | Tyr | Arg |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Met | Asp | Leu | Asn | Trp | Glu | Leu | Thr | Ala | Pro | Trp | Thr | Gly | Ala | Lys |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Gln | Val | Pro | Val | Lys | Phe | Met | Thr | Gly | Asp | Phe | Asp | Met | Val | Tyr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Thr | Thr | Pro | Gly | Met | Lys | Glu | Tyr | Ile | His | Gly | Gly | Gly | Phe | Ala | Ala |
|     |     | 260 |     |     |     | 265 |     |     |     |     |     |     | 270 |     |     |
| Asp | Val | Pro | Thr | Leu | Gln | Glu | Ile | Val | Val | Ile | Glu | Asp | Ala | Gly | Xaa |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Phe | Val | Asn | Gln | Glu | Lys | Pro | Gln | Glu | Val | Thr | Ala | His | Ile | Asn | Asp |
| 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |     |
| Phe | Phe | Thr | Lys | Leu | Arg | Asp | Asn | Asn | Lys | Ser | Phe |     |     |     |     |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1213

(D) OTHER INFORMATION: / Ceres Seq. ID 1573682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

|            |             |            |             |            |            |      |
|------------|-------------|------------|-------------|------------|------------|------|
| aaagagaaMa | acgtatgagt  | tgcttaaacc | ataaacctca  | agctcaaaat | tttatcaacc | 60   |
| ttataaagtt | tcgtWWtctc  | gagattttga | atcttttcag  | ctaaaaaaga | tcacagcttt | 120  |
| ttgcgttttc | tggtatgagt  | tgagataaga | gaagatgaag  | attcagtgtg | acgtttgtga | 180  |
| ggcgccggaa | gcgacgggtc  | tatgwtgcgc | cgaygaggct  | gctctttgtt | gggcttgcca | 240  |
| tgagaaaatt | cacgccgcta  | ataaactcgc | cggaaaacat  | cagagagtcc | ctctctctgc | 300  |
| ctctgcctct | tccataccca  | aatgtgacat | ttgtcarraa  | gcctctggat | tcttcttttg | 360  |
| tctgcaagat | agagctttgc  | tatgtaggaa | atgtgatgtt  | gcaatccaca | ctgtgaatcc | 420  |
| tcatgtttca | gctcaccaga  | gRdttYcttM | ctcactggaa  | tcaaagttgg | tcttgaatct | 480  |
| atagacactg | gtcctttctac | taaactctca | cctaccaatg  | atgataaaac | catggagacc | 540  |
| aaaccttttg | ttcaatctat  | acctgagcct | caaaagatgg  | ccttcgatca | tcctcatcac | 600  |
| cagcagcagc | aggaacagca  | ggaaggagtt | ataccgggaa  | ctaaagtcaa | tgatcagaca | 660  |
| tcgacaaagc | ttctctctgt  | aagtagcgga | tcaactactg  | gaagcattcc | tcagtggcaa | 720  |
| atagaggaga | ttttcgggct  | aaccgacttt | gatcagagct  | atgaatacat | ggagaataat | 780  |
| ggatcatcta | aggcggatac  | tagtagacga | ggagattcag  | acagtctctc | gatgatgaga | 840  |
| tctgcagaag | aagatggaga  | agataacaat | aactgcttgg  | gaggtgagac | atcatgggag | 900  |
| gttccacaga | ttcagtctcc  | acctacagcg | tctgggtctaa | actggcctaa | gcattttcac | 960  |
| caccactctg | tgtttggtcc  | ggacataact | tcttcaactc  | cttataccgg | ttcatccccg | 1020 |
| aatcaaaggg | ttgggaaacg  | gcggcgacgg | ttctagcatt  | tgtaattatc | ttttagccgc | 1080 |
| ttgagaaaag | agattggcag  | ctttctcagt | agatgtaaga  | tcacataaat | gatttggaag | 1140 |
| cttgtaatgt | agtgatctgt  | gagagtcggt | gttctttgtt  | agctgaaaaa | acaaaaagat | 1200 |
| gtttatttgg | tcg         |            |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1573683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Gln | Cys | Asn | Val | Cys | Glu | Ala | Glu | Ala | Thr | Val | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Cys | Ala | Xaa | Glu | Ala | Ala | Leu | Cys | Trp | Ala | Cys | Asp | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  | Ile |
| His | Ala | Ala | Asn | Lys | Leu | Ala | Gly | Lys | His | Gln | Arg | Val | Pro | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  | Ser |
| Ala | Ser | Ala | Ser | Ser | Ile | Pro | Lys | Cys | Asp | Ile | Cys | Xaa | Xaa | Ala |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  | Ser |
| Gly | Phe | Phe | Phe | Cys | Leu | Gln | Asp | Arg | Ala | Leu | Cys | Arg | Lys | Cys |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Asp | Val | Ala | Ile | His | Thr | Val | Asn | Pro | His | Val | Ser | Ala | His | Gln |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |
| Xaa | Xaa | Xaa | Ser | Leu | Glu | Ser | Lys | Leu | Val | Leu | Asn | Leu |     |     |
|     |     |     |     | 100 |     |     |     |     |     |     |     | 105 |     |     |

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..174
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

Met Glu Thr Lys Pro Phe Val Gln Ser Ile Pro Glu Pro Gln Lys Met  
1 5 10 15  
Ala Phe Asp His His His His Gln Gln Gln Gln Glu Gln Gln Glu Gly  
20 25 30  
Val Ile Pro Gly Thr Lys Val Asn Asp Gln Thr Ser Thr Lys Leu Pro  
35 40 45  
Leu Val Ser Ser Gly Ser Thr Thr Gly Ser Ile Pro Gln Trp Gln Ile  
50 55 60  
Glu Glu Ile Phe Gly Leu Thr Asp Phe Asp Gln Ser Tyr Glu Tyr Met  
65 70 75 80  
Glu Asn Asn Gly Ser Ser Lys Ala Asp Thr Ser Arg Arg Gly Asp Ser  
85 90 95  
Asp Ser Ser Ser Met Met Arg Ser Ala Glu Glu Asp Gly Glu Asp Asn  
100 105 110  
Asn Asn Cys Leu Gly Gly Glu Thr Ser Trp Ala Val Pro Gln Ile Gln  
115 120 125  
Ser Pro Pro Thr Ala Ser Gly Leu Asn Trp Pro Lys His Phe His His  
130 135 140  
His Ser Val Phe Val Pro Asp Ile Thr Ser Ser Thr Pro Tyr Thr Gly  
145 150 155 160  
Ser Ser Pro Asn Gln Arg Val Gly Lys Arg Arg Arg Arg Phe  
165 170

(2) INFORMATION FOR SEQ ID NO:2582:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 159 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..159
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573685
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

Met Ala Phe Asp His His His His Gln Gln Gln Glu Gln Gln Glu  
1 5 10 15  
Gly Val Ile Pro Gly Thr Lys Val Asn Asp Gln Thr Ser Thr Lys Leu  
20 25 30  
Pro Leu Val Ser Ser Gly Ser Thr Thr Gly Ser Ile Pro Gln Trp Gln  
35 40 45  
Ile Glu Glu Ile Phe Gly Leu Thr Asp Phe Asp Gln Ser Tyr Glu Tyr  
50 55 60  
Met Glu Asn Asn Gly Ser Ser Lys Ala Asp Thr Ser Arg Arg Gly Asp  
65 70 75 80  
Ser Asp Ser Ser Ser Met Met Arg Ser Ala Glu Glu Asp Gly Glu Asp  
85 90 95  
Asn Asn Asn Cys Leu Gly Gly Glu Thr Ser Trp Ala Val Pro Gln Ile  
100 105 110  
Gln Ser Pro Pro Thr Ala Ser Gly Leu Asn Trp Pro Lys His Phe His  
115 120 125  
His His Ser Val Phe Val Pro Asp Ile Thr Ser Ser Thr Pro Tyr Thr

00000000-00000000

130 135 140  
Gly Ser Ser Pro Asn Gln Arg Val Gly Lys Arg Arg Arg Phe  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1583
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

```
aaaaaagcta gaaaaacctt tccaaaaaat gcaaagaacc gtaacttagt cttctttotta 60
gggggtattag cgtctttttac actctccagt ttcccggtaa ctgtttccgg cgagccccct 120
atcttattca ctttcggcga ctcttcctac gatgtgggca acacgaagtt cttctcgtag 180
gagttcgatc cagccaccac gtggccttac ggcgattcca tcgatgatcc ctccggtcgt 240
tggtctgacg gccacattgt cccagatttc gtcggtcgat tgattggtea tegtgaaccg 300
attcctccgg tacttgatcc aaaagctgat ctttctcgtag gagcaagctt tgccattgct 360
ggagcagttg ttcttgatc tcaatctact actgcatcca tgaattttgg acaacagata 420
tcgaagtttt tagagttaca taagcaatgg actgataaag aacgagcaga agctatatac 480
atggtaaaca taggagctga ggactacttg aatttcgcaa aggtcatcc aaatgccaat 540
actgtggagc agctaactca agttgccac gttctccaaa ggataccaag agagctcacg 600
agtttatata gggcaggttg agcgaggaag tttgcggtac agaatttggg accgcttggt 660
tgtttaccga tagtgagaca agagtttaag accggtgaga attgtatgga gatggtcaac 720
ttcatggtga aaacgcacaa tgaaaggctt agtcgtttgc tcgttgcat aaccgtaccg 780
atactgtacc gtggcttccg gtacagcctc tttgatttca atggtgaaat tctccggagg 840
atcaatgaac catcactcca tggatatact gatacaacga cttcttgctg cggaactgga 900
tcgagaaatg catacgggtg cggttatagt aacgtgcatg ctaagctctg cagctaccag 960
aaatcatttt tgttcttcga cgggcgtcac aacaccgaga aaaccgatga agaagttgct 1020
aatctgtttt attccggaga caaacatgtc gtctctccga tgaatataaa ggatctcgta 1080
ggtaaagcag cgaccgatct tcttgacaaa gaaatctaga aatcccaatc gtgttctggt 1140
ctgtttcttt gaaataagta CCaatgggtt ttgttgtaaa ctgtaaaact ctgtattcaa 1200
cttcatatat atatgatgat aaagaaaaaa taaaccggtt acattgcaaa aaaaaaaaaa 1260
aaaaacgatg acaagaccac cgtcaaggcc gcctgggga aggtcggcgc gcacgctggc 1320
gagtatgggt cggagggcct ggagaggatg ttctgtcct tccccaccac caagacctac 1380
ttcccgcact tgacactgag ccacggctct gccacggtta agggccacgg caagaagggtg 1440
gccgacgcgc tgaccaacgc cgtggcgcac gtggacgaca tgccaacgc gctgtccgcc 1500
ctgagcgacc tgcacgcgca caagcttcgg gtggacccGG Tcaacttcaa gctcctaagc 1560
cactgcctgc tggtagccc atc
```

(2) INFORMATION FOR SEQ ID NO:2584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

```
Lys Lys Ala Arg Lys Thr Phe Pro Lys Met Ala Lys Asn Arg Asn Leu
1 5 10 15
Val Phe Phe Leu Gly Val Leu Ala Ser Phe Thr Leu Ser Ser Phe Pro
20 25 30
Val Thr Val Ser Gly Glu Pro Pro Ile Leu Phe Thr Phe Gly Asp Ser
35 40 45
Ser Tyr Asp Val Gly Asn Thr Lys Phe Phe Ser Ser Glu Phe Asp Pro
```



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Ala Thr Thr Trp Pro Tyr Gly Asp Ser Ile Asp Asp Pro Ser Gly Arg |     |     |
| 65                                                              | 70  | 75  |
| Trp Ser Asp Gly His Ile Val Pro Asp Phe Val Gly Arg Leu Ile Gly |     | 80  |
|                                                                 | 85  | 90  |
| His Arg Glu Pro Ile Pro Pro Val Leu Asp Pro Lys Ala Asp Leu Ser |     | 95  |
|                                                                 | 100 | 105 |
| Arg Gly Ala Ser Phe Ala Ile Ala Gly Ala Val Val Leu Gly Ser Gln |     | 110 |
|                                                                 | 115 | 120 |
| Ser Thr Thr Ala Ser Met Asn Phe Gly Gln Gln Ile Ser Lys Phe Leu |     | 125 |
|                                                                 | 130 | 135 |
| Glu Leu His Lys Gln Trp Thr Asp Lys Glu Arg Ala Glu Ala Ile Tyr |     | 140 |
| 145                                                             | 150 | 155 |
| Met Val Asn Ile Gly Ala Glu Asp Tyr Leu Asn Phe Ala Lys Ala His |     | 160 |
|                                                                 | 165 | 170 |
| Pro Asn Ala Asn Thr Val Glu Gln Leu Thr Gln Val Ala His Val Leu |     | 175 |
|                                                                 | 180 | 185 |
| Gln Arg Ile Pro Arg Glu Leu Thr Ser Leu Tyr Arg Ala Gly Gly Ala |     | 190 |
|                                                                 | 195 | 200 |
| Arg Lys Phe Ala Val Gln Asn Leu Gly Pro Leu Gly Cys Leu Pro Ile |     | 205 |
|                                                                 | 210 | 215 |
| Val Arg Gln Glu Phe Lys Thr Gly Glu Asn Cys Met Glu Met Val Asn |     | 220 |
| 225                                                             | 230 | 235 |
| Phe Met Val Lys Thr His Asn Glu Arg Leu Ser Arg Leu Leu Val Ala |     | 240 |
|                                                                 | 245 | 250 |
| Ile Thr Val Pro Ile Leu Tyr Arg Gly Phe Arg Tyr Ser Leu Phe Asp |     | 255 |
|                                                                 | 260 | 265 |
| Phe Asn Gly Glu Ile Leu Arg Arg Ile Asn Glu Pro Ser Leu His Gly |     | 270 |
|                                                                 | 275 | 280 |
| Tyr Thr Asp Thr Thr Thr Ser Cys Cys Gly Thr Gly Ser Arg Asn Ala |     | 285 |
|                                                                 | 290 | 295 |
| Tyr Gly Cys Gly Tyr Ser Asn Val His Ala Lys Leu Cys Ser Tyr Gln |     | 300 |
| 305                                                             | 310 | 315 |
| Lys Ser Phe Leu Phe Phe Asp Gly Arg His Asn Thr Glu Lys Thr Asp |     | 320 |
|                                                                 | 325 | 330 |
| Glu Glu Val Ala Asn Leu Phe Tyr Ser Gly Asp Lys His Val Val Ser |     | 335 |
|                                                                 | 340 | 345 |
| Pro Met Asn Ile Lys Asp Leu Val Gly Lys Ala Ala Thr Asp Leu Leu |     | 350 |
|                                                                 | 355 | 360 |
| Ala Gln Glu Ile                                                 |     | 365 |
| 370                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:2585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1573703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Ala Lys Asn Arg Asn Leu Val Phe Phe Leu Gly Val Leu Ala Ser |    |    |
| 1                                                               | 5  | 10 |
| Phe Thr Leu Ser Ser Phe Pro Val Thr Val Ser Gly Glu Pro Pro Ile |    | 15 |
|                                                                 | 20 | 25 |
| Leu Phe Thr Phe Gly Asp Ser Ser Tyr Asp Val Gly Asn Thr Lys Phe |    | 30 |
|                                                                 | 35 | 40 |
| Phe Ser Ser Glu Phe Asp Pro Ala Thr Thr Trp Pro Tyr Gly Asp Ser |    | 45 |
|                                                                 | 50 | 55 |
|                                                                 |    | 60 |

```

Ile Asp Asp Pro Ser Gly Arg Trp Ser Asp Gly His Ile Val Pro Asp
65 70 75 80
Phe Val Gly Arg Leu Ile Gly His Arg Glu Pro Ile Pro Pro Val Leu
 85 90 95
Asp Pro Lys Ala Asp Leu Ser Arg Gly Ala Ser Phe Ala Ile Ala Gly
 100 105 110
Ala Val Val Leu Gly Ser Gln Ser Thr Thr Ala Ser Met Asn Phe Gly
 115 120 125
Gln Gln Ile Ser Lys Phe Leu Glu Leu His Lys Gln Trp Thr Asp Lys
 130 135 140
Glu Arg Ala Glu Ala Ile Tyr Met Val Asn Ile Gly Ala Glu Asp Tyr
145 150 155 160
Leu Asn Phe Ala Lys Ala His Pro Asn Ala Asn Thr Val Glu Gln Leu
 165 170 175
Thr Gln Val Ala His Val Leu Gln Arg Ile Pro Arg Glu Leu Thr Ser
 180 185 190
Leu Tyr Arg Ala Gly Gly Ala Arg Lys Phe Ala Val Gln Asn Leu Gly
 195 200 205
Pro Leu Gly Cys Leu Pro Ile Val Arg Gln Glu Phe Lys Thr Gly Glu
 210 215 220
Asn Cys Met Glu Met Val Asn Phe Met Val Lys Thr His Asn Glu Arg
225 230 235 240
Leu Ser Arg Leu Leu Val Ala Ile Thr Val Pro Ile Leu Tyr Arg Gly
 245 250 255
Phe Arg Tyr Ser Leu Phe Asp Phe Asn Gly Glu Ile Leu Arg Arg Ile
 260 265 270
Asn Glu Pro Ser Leu His Gly Tyr Thr Asp Thr Thr Thr Ser Cys Cys
 275 280 285
Gly Thr Gly Ser Arg Asn Ala Tyr Gly Cys Gly Tyr Ser Asn Val His
 290 295 300
Ala Lys Leu Cys Ser Tyr Gln Lys Ser Phe Leu Phe Phe Asp Gly Arg
305 310 315 320
His Asn Thr Glu Lys Thr Asp Glu Glu Val Ala Asn Leu Phe Tyr Ser
 325 330 335
Gly Asp Lys His Val Val Ser Pro Met Asn Ile Lys Asp Leu Val Gly
 340 345 350
Lys Ala Ala Thr Asp Leu Leu Ala Gln Glu Ile
 355 360

```

(2) INFORMATION FOR SEQ ID NO:2586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

```

Met Asn Phe Gly Gln Gln Ile Ser Lys Phe Leu Glu Leu His Lys Gln
1 5 10 15
Trp Thr Asp Lys Glu Arg Ala Glu Ala Ile Tyr Met Val Asn Ile Gly
 20 25 30
Ala Glu Asp Tyr Leu Asn Phe Ala Lys Ala His Pro Asn Ala Asn Thr
 35 40 45
Val Glu Gln Leu Thr Gln Val Ala His Val Leu Gln Arg Ile Pro Arg
 50 55 60
Glu Leu Thr Ser Leu Tyr Arg Ala Gly Gly Ala Arg Lys Phe Ala Val
65 70 75 80
Gln Asn Leu Gly Pro Leu Gly Cys Leu Pro Ile Val Arg Gln Glu Phe

```

SEQUENCE - THE

| 85  |     |     |     |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Gly | Glu | Asn | Cys | Met | Glu | Met | Val | Asn | Phe | Met | Val | Lys | Thr |
| 100 |     |     |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| His | Asn | Glu | Arg | Leu | Ser | Arg | Leu | Leu | Val | Ala | Ile | Thr | Val | Pro | Ile |
| 115 |     |     |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Leu | Tyr | Arg | Gly | Phe | Arg | Tyr | Ser | Leu | Phe | Asp | Phe | Asn | Gly | Glu | Ile |
| 130 |     |     |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Leu | Arg | Arg | Ile | Asn | Glu | Pro | Ser | Leu | His | Gly | Tyr | Thr | Asp | Thr | Thr |
| 145 |     |     |     |     |     |     |     | 150 |     |     |     | 155 |     |     |     |
| Thr | Ser | Cys | Cys | Gly | Thr | Gly | Ser | Arg | Asn | Ala | Tyr | Gly | Cys | Gly | Tyr |
| 165 |     |     |     |     |     |     |     | 170 |     |     |     | 175 |     |     |     |
| Ser | Asn | Val | His | Ala | Lys | Leu | Cys | Ser | Tyr | Gln | Lys | Ser | Phe | Leu | Phe |
| 180 |     |     |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Phe | Asp | Gly | Arg | His | Asn | Thr | Glu | Lys | Thr | Asp | Glu | Glu | Val | Ala | Asn |
| 195 |     |     |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Leu | Phe | Tyr | Ser | Gly | Asp | Lys | His | Val | Val | Ser | Pro | Met | Asn | Ile | Lys |
| 210 |     |     |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |
| Asp | Leu | Val | Gly | Lys | Ala | Ala | Thr | Asp | Leu | Leu | Ala | Gln | Glu | Ile |     |
| 225 |     |     |     |     |     |     |     | 230 |     |     |     | 235 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| atcattctcg | gtttaactga | aacacataat  | aaaacaaaga  | gaaagagata  | taatattgggt | 60   |
| gggtgggcaa | tgcagtaga  | cggtgggtgcc | ggtatcgacc  | ctaattcttcc | ggcagagaga  | 120  |
| caagaagagg | cgaacagct  | tttaactcgt  | tgtctcaacc  | tcggcataat  | agctttgcgt  | 180  |
| tccaatgttt | cggccattga | cgtcggttag  | ctcgtcatta  | gagaattgga  | gacggatcct  | 240  |
| ctgtttaatt | caggccgtgg | atcttctttg  | acggagaaaag | gaacggttga  | gatggaagct  | 300  |
| agcattatgg | acggtacgaa | gagacgatgc  | ggtgccggtt  | cggggataac  | caccgtgaaa  | 360  |
| aatcctatat | ctcttgctcg | tctcgtcatg  | gacaaatctc  | cccactctta  | ccttgctttc  | 420  |
| tcaggtgcag | aggattttcg | ccgcaaacag  | ggagttgaaa  | ttgtggacaa  | cgagtacttt  | 480  |
| gtcacggacg | acaacgtagg | aatgctcaag  | ttggccaagg  | aagctaaactc | catcttgttt  | 540  |
| gattaccgga | ttccgcgat  | gggatgtgcc  | ggcgcagctg  | cgaccgacag  | tccaatccaa  | 600  |
| atgaacggtc | ttccgatcag | cattttacgca | ccGggagaca  | gtcgggtgctg | ttgtggttga  | 660  |
| cgggaaagga | cattgtgccc | ccgggacatc  | cacgggtggt  | ttaatgaaca  | agatgatggg  | 720  |
| aaggattggt | gactogccgc | tgataggagc  | cgggacgtat  | gcgtcggagt  | tttgtggtgt  | 780  |
| gtcgtgtacc | ggagaaggag | aagccattat  | aagagcaacc  | ctagctcgtg  | atgtgtcagc  | 840  |
| tgttatggag | tataaaggac | ttaacctcca  | agaagcgggt  | gattacgtca  | tcaagcatcg  | 900  |
| acttgacgaa | gggttcgctg | gactcattgc  | tgtctcgaat  | aaaggagagg  | tggtttgtgg  | 960  |
| ttttaactct | aatgggatgt | tcaggggatg  | tgcaactgag  | gatggattca  | tggacgttgc  | 1020 |
| tatttgggag | tgagaaatat | tttagattaa  | gaaaatgtct  | tactagtatt  | taatcagtca  | 1080 |
| tcgctctatt | aatttggtta | ttcattatca  | taaagctgga  | gtagtaaatt  | tagttctgtc  | 1140 |
| gttatcacca | gtcctatatt | gatttgtgtt  | taatgcggtt  | tcaaattgg   |             |      |

(2) INFORMATION FOR SEQ ID NO:2588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219

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(D) OTHER INFORMATION: / Ceres Seq. ID 1573706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

Ile Ile Leu Gly Leu Thr Glu Thr His Asn Lys Thr Lys Arg Lys Arg  
1 5 10 15  
Tyr Asn Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile  
20 25 30  
Asp Pro Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu  
35 40 45  
Thr Arg Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser  
50 55 60  
Ala Ile Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro  
65 70 75 80  
Leu Phe Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val  
85 90 95  
Glu Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala  
100 105 110  
Val Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu  
115 120 125  
Val Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu  
130 135 140  
Asp Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe  
145 150 155 160  
Val Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn  
165 170 175  
Ser Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala  
180 185 190  
Ala Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile  
195 200 205  
Tyr Ala Pro Gly Asp Ser Arg Val Arg Cys Gly  
210 215

(2) INFORMATION FOR SEQ ID NO:2589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1573707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile Asp Pro  
1 5 10 15  
Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu Thr Arg  
20 25 30  
Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser Ala Ile  
35 40 45  
Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro Leu Phe  
50 55 60  
Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val Glu Met  
65 70 75 80  
Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val Ser  
85 90 95  
Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val Met  
100 105 110  
Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp Phe  
115 120 125  
Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val Thr  
130 135 140  
Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser Ile

(2) INFORMATION FOR SEO ID NO:2590:

(A) LENGTH: 122 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAM

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1573708

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ala | Ser | Ile | Met | Asp | Gly | Thr | Lys | Arg | Arg | Cys | Gly | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gly | Ile | Thr | Thr | Val | Lys | Asn | Pro | Ile | Ser | Leu | Ala | Arg | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Asp | Lys | Ser | Pro | His | Ser | Tyr | Leu | Ala | Phe | Ser | Gly | Ala | Glu | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ala | Arg | Lys | Gln | Gly | Val | Glu | Ile | Val | Asp | Asn | Glu | Tyr | Phe | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Asp | Asp | Asn | Val | Gly | Met | Leu | Lys | Leu | Ala | Lys | Glu | Ala | Asn | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Leu | Phe | Asp | Tyr | Arg | Ile | Pro | Pro | Met | Gly | Cys | Ala | Gly | Ala | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Thr | Asp | Ser | Pro | Ile | Gln | Met | Asn | Gly | Leu | Pro | Ile | Ser | Ile | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Pro | Gly | Asp | Ser | Arg | Val | Arg | Cys | Gly |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1048

(D) OTHER INFORMATION: / Ceres Seq. ID 1573713

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aacgcattta | aattaatat  | tatggataat | atggttaata | aataaggaac  | ttctatttat | 60  |
| atcacaaaag | gtcactggtc | ttcttcgtgt | gacttcacca | ctttctcatc  | tcccacaaaa | 120 |
| atggctctct | cacttccttc | agtctttatc | tttttccatg | tctttaccaaa | tggtgttttt | 180 |
| gctgcttcaa | atgaggaatc | caaggcctta | gtttctttac | caacgccaac  | acttccatcg | 240 |
| ccatctccgg | ctaccaaacc | gcgcgtcgca | gctctcaaac | cgcgcagcc   | gtcgtacaag | 300 |
| ccaccacgc  | tgccaactac | tctattataa | ccaccacca  | cgaaacctcc  | ggctaaaCct | 360 |
| ccaactactt | cggttacacc | agtaaaacct | ccggtttcaa | ctcctccgat  | caaactaccg | 420 |
| ccggtacaac | cacctacgta | caaaacccca | acgccaacag | ttaaaccacc  | gtcgcgtcaa | 480 |
| ccacctacgt | acaaaccccc | aactccaacg | gttaaaccac | ccactacatc  | accggttaaa | 540 |
| ccaccacta  | cgccaccagt | ccaatcaccg | ccggtccaac | cacctacgta  | caaaccccca | 600 |
| acgtcacccg | ttaaaccacc | caccacaact | ccaccggtta | aacccccac   | cacgacgcca | 660 |
| ccggtccaac | cacctacgta | caatcccca  | actacccgg  | ttaaacacc   | tacagcgccg | 720 |
| cctgtcaaac | ctccgacacc | acctccogta | agaactcgga | tgattgcgt   | gcctttatgt | 780 |
| gggacgaggt | gtgggcaaca | ctcgaggaag | aacgtatgta | tgagagcggtg | cgtcacgtgc | 840 |

(2) INFORMATION FOR SEQ ID NO:2592:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..275

(D) OTHER INFORMATION: / Ceres Seq. ID 1573714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..836

(D) OTHER INFORMATION: / Ceres Seq. ID 1573727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

|             |            |             |             |             |            |     |
|-------------|------------|-------------|-------------|-------------|------------|-----|
| cttttttttt  | tgtttattat | ttttttgact  | ttgatctccc  | atcagttcat  | cttttttttc | 60  |
| ttctttctgat | caaccatggc | tgctgtctata | agtgtctgcag | tctctttacc  | ttcctccaag | 120 |
| tcatoctctc  | tcctcaccaa | aatctcctct  | gtatcccctc  | aaaggatttt  | cctcaagaag | 180 |
| agcacagtgt  | gttacagaag | agttgtgtca  | gtgaaggctc  | aggtgacaac  | agatactacc | 240 |
| gaggcaccac  | cagttaaagt | agtcaaggag  | tctaagaaac  | aggaagaagg  | gattgttgtc | 300 |
| aacaaattca  | aacctaagaa | cccttacact  | ggctcgctgcc | ttttgaacac  | caagatcacc | 360 |
| ggtgatgacg  | ctcccggtga | gacttggcac  | attgtcttca  | ccaccgaagg  | TGagWgNttc | 420 |
| cgtatagaga  | aggacaatcg | ataggagtga  | ttccagaggg  | aatagacaag  | aacgggaagc | 480 |
| cgcacaagct  | caggctttac | tctatcgcg   | gtagtgccat  | tgggtgacttt | ggagactcca | 540 |
| agaccgtttc  | tctctgtgtc | aagagactag  | tttacacaaa  | tgatggcgga  | gagattgtta | 600 |
| agggggtctg  | ctccaacttc | ttgtgtgact  | tgaagccggg  | tgatgaagct  | aagatcactg | 660 |
| gacctgttgg  | caaggaaatg | cttatgcaa   | aagaccccaa  | tgccaccatc  | atcatgcttg | 720 |
| gaacaggaac  | tggaatagct | ccattcagat  | cattttttgtg | gaaaatgttc  | tttgaggagc | 780 |
| acgaggacta  | caagttcaat | ggtttggcgt  | ggcttttctt  | gggtgtaccc  | acaagc     |     |

(2) INFORMATION FOR SEQ ID NO:2594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1573728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Phe | Phe | Ala | Tyr | Tyr | Phe | Phe | Asp | Phe | Asp | Leu | Pro | Ser | Val | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Leu | Leu | Leu | Leu | Ile | Asn | His | Gly | Cys | Cys | Tyr | Lys | Cys | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Leu | Phe | Thr | Phe | Leu | Gln | Val | Ile | Leu | Ser | Pro | His | Gln | Asn | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Leu | Cys | Ile | Pro | Ser | Lys | Asp | Phe | Pro | Gln | Glu | Glu | His | Ser | Val | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Gln | Lys | Ser | Cys | Val | Ser | Glu | Gly | Ser | Gly | Asp | Asn | Arg | Tyr | Tyr | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Thr | Thr | Ser |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1573729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Ile | Ser | Ala | Ala | Val | Ser | Leu | Pro | Ser | Ser | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Leu | Leu | Thr | Lys | Ile | Ser | Ser | Val | Ser | Pro | Gln | Arg | Ile | Phe |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Leu | Lys | Lys | Ser | Thr | Val | Cys | Tyr | Arg | Arg | Val | Val | Ser | Val | Lys | Ala |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Gln | Val | Thr | Thr | Asp | Thr | Thr | Glu | Ala | Pro | Pro | Val | Lys | Val | Val | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |

Glu Ser Lys Lys Gln Glu Glu Gly Ile Val Val Asn Lys Phe Lys Pro  
65 70 75 80  
Lys Asn Pro Tyr Thr Gly Arg Cys Leu Leu Asn Thr Lys Ile Thr Gly  
85 90 95  
Asp Asp Ala Pro Gly Glu Thr Trp His Ile Val Phe Thr Thr Glu Gly  
100 105 110  
Glu Xaa Phe Arg Ile Glu Lys Asp Asn Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:2596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:

aatctttttt tttttgctta ttattttttt gactttgac tcccatcagt tcatctttctt 60  
cttctttctt tgatcaacca tggctgctgc tataagtgc gcagtctctt taccttcttc 120  
caagtcattc tctctctca ccaaaatctc ctctgtatcc cctcaaagga ttttctctca 180  
gaagagcaca gtgtgtttaca gaagagttgt gtcagtgaag gctcaggtga caacagatac 240  
taccgaggca ccaccagtta aagtagtcaa ggagtctaag aaacaggaag aagggattgt 300  
tgtcaacaaa ttcaaaccta agaaccctta cactggctgc tgccttttga acaccaagat 360  
caccggtgat gacgctccc gtagacttg gcacattgtc ttcaccaccg aaggtgaggt 420  
tccgtataga gaaggacaat cgataggagt gattccagag ggaatagaca agaacgggaa 480  
gccgcacaag ctcaggcttt actctatcgc gagtagtgcc attggtgact ttggagactc 540  
caagaccgtt tctctctgtg tcaagagact agtttacaca aatgatggcg gagagattgt 600  
taaggggggc tgctccaact tcttgtgtga cttgaagccg ggtgatgaag ctaagatcac 660  
tggacctgtt ggcaaggaaa tgcttatgcc aaaagacccc aatgccacca tcatcatgct 720  
tggaacagga actggaatag ctccattcag atcatttttg tggaaaatgt tctttgagga 780  
gcacgaggac tacaagttca atggtttggc gtggcttttc ttgggtgtac ccagaagcag 840  
ctcactgcta tacaaggagg agtttgagaa gatgaaggag aagaaccag acaacttcag 900  
gctggacttt gcggtgagca gagagcagac gaacgagaag ggagagaaaa tgtacattca 960  
gacaagaatg gcagagtatg cagAaagagc tgtgggagtt gctgaagaaa gacaacacct 1020  
ttgtttacat gtgtggtctt aagggtatgg agaagggtat cgatgacatt atggtctcgc 1080  
ttgctgctaa agatgggac gattggttgg agtacaagaa gcaattgaag aggagtgaac 1140  
agtggaatgt tgaagtctac taaggagct tctgaggag taattatata atgtagataa 1200  
aaagcttcag atgcattgtg aaatcttcat atctgcttct tttttcttct tcaaggattt 1260  
tcaatcaaaa catcc

(2) INFORMATION FOR SEQ ID NO:2597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..320
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:

Met Ala Ala Ala Ile Ser Ala Ala Val Ser Leu Pro Ser Ser Lys Ser  
1 5 10 15  
Ser Ser Leu Leu Thr Lys Ile Ser Ser Val Ser Pro Gln Arg Ile Phe  
20 25 30  
Leu Lys Lys Ser Thr Val Cys Tyr Arg Arg Val Val Ser Val Lys Ala  
35 40 45  
Gln Val Thr Thr Asp Thr Thr Glu Ala Pro Pro Val Lys Val Val Lys



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Glu Ser Lys Lys Gln Glu Glu Gly Ile Val Val Asn Lys Phe Lys Pro |     |     |
| 65                                                              | 70  | 75  |
| Lys Asn Pro Tyr Thr Gly Arg Cys Leu Leu Asn Thr Lys Ile Thr Gly |     | 80  |
|                                                                 | 85  | 90  |
| Asp Asp Ala Pro Gly Glu Thr Trp His Ile Val Phe Thr Thr Glu Gly |     | 95  |
|                                                                 | 100 | 105 |
| Glu Val Pro Tyr Arg Glu Gly Gln Ser Ile Gly Val Ile Pro Glu Gly |     | 110 |
|                                                                 | 115 | 120 |
| Ile Asp Lys Asn Gly Lys Pro His Lys Leu Arg Leu Tyr Ser Ile Ala |     | 125 |
|                                                                 | 130 | 135 |
| Ser Ser Ala Ile Gly Asp Phe Gly Asp Ser Lys Thr Val Ser Leu Cys |     | 140 |
| 145                                                             | 150 | 155 |
| Val Lys Arg Leu Val Tyr Thr Asn Asp Gly Gly Glu Ile Val Lys Gly |     | 160 |
|                                                                 | 165 | 170 |
| Val Cys Ser Asn Phe Leu Cys Asp Leu Lys Pro Gly Asp Glu Ala Lys |     | 175 |
|                                                                 | 180 | 185 |
| Ile Thr Gly Pro Val Gly Lys Glu Met Leu Met Pro Lys Asp Pro Asn |     | 190 |
|                                                                 | 195 | 200 |
| Ala Thr Ile Ile Met Leu Gly Thr Gly Thr Gly Ile Ala Pro Phe Arg |     | 205 |
|                                                                 | 210 | 215 |
| Ser Phe Leu Trp Lys Met Phe Phe Glu Glu His Glu Asp Tyr Lys Phe |     | 220 |
| 225                                                             | 230 | 235 |
| Asn Gly Leu Ala Trp Leu Phe Leu Gly Val Pro Arg Ser Ser Ser Leu |     | 240 |
|                                                                 | 245 | 250 |
| Leu Tyr Lys Glu Phe Glu Lys Met Lys Glu Lys Asn Pro Asp Asn     |     | 255 |
|                                                                 | 260 | 265 |
| Phe Arg Leu Asp Phe Ala Val Ser Arg Glu Gln Thr Asn Glu Lys Gly |     | 270 |
|                                                                 | 275 | 280 |
| Glu Lys Met Tyr Ile Gln Thr Arg Met Ala Glu Tyr Ala Glu Arg Ala |     | 285 |
|                                                                 | 290 | 295 |
| Val Gly Val Ala Glu Glu Arg Gln His Leu Cys Leu His Val Trp Ser |     | 300 |
| 305                                                             | 310 | 315 |
|                                                                 |     | 320 |

(2) INFORMATION FOR SEQ ID NO:2598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| aattattact ttaatcttct ttcccgtctct ctattcttct tcttcttttag gatcaatcac | 60  |
| cgttttagctt tcttcccata cgtctctccg tttacgacca gtatacagag gctggagctg  | 120 |
| gggaagaaaa ggattgtcta tggagggaga cgtcgggaata ggtttggtat gccagaatac  | 180 |
| tatggatggg aaggcgagta atggaaatgg tttagagaag actgtacctt cttgtttgct   | 240 |
| taaggctatg gcatgtgtac ctgaggatga tgctaagtgt cactccactg ttgtttcttg   | 300 |
| gtggttttcg gaacctcacc ctgcgtctgg gaaaaaaggc ggcaaagcag tctatttcaa   | 360 |
| caaccctatg tggccaggag aagcacactc actgaaagt ggagaaagttc tgttcaaaga   | 420 |
| caagtccgat tttcaggaag tcctagtgtt cgagtcagcc acgtacggaa aggtgcttgt   | 480 |
| tctagatggt atcgtacagc tgaccgaaaa agatgaatgt gcatatcagg agatgatagc   | 540 |
| ccatctgctt ttatgtctta tatcttcccc taataatgtt cttgtttgtg gtggaggtga   | 600 |
| tgggtggtgt cttcgagaga tttctcgcca tagttctgtt gaggttattg atatctgtga   | 660 |
| gatagacaag atggttatag atgtgtctaa gaagTtcTtc cccgagtttag cggttgggtt  | 720 |
| tgacgatcct cgtgttcaac ttcacattag tgatgctgct gagttcctcc gtaaatcccc   | 780 |
| tgaagggaag tatgatgcca tcattgttga ttcttcagat cccgtaggtc ctgctcttgc   | 840 |

gcttggtgag aagcctttct tcgagacact ggctagagcg ttgaagcctg ggggagttct 900  
ttgtaacatg gcagaaagta tgtggctcca tactcatctt attgaagata tgatctccat 960  
ttgccgtcaa acattcaaaa gtgttcaacta tgcgtggagc agcgtcccca catatccaag 1020  
cggcgtgatt ggtttcgtct tgtgctctac tgaaggacca gctggttgact tcaagaaccc 1080  
aatcaaccct attgagaaac tagacggtgc gatgacccat aaaagagaat tgaagttcta 1140  
taactctgat atgcacagag ccgcatttgc tttgcccaca ttCctgcgga gagaagtagc 1200  
ttcacttctg gcttcttgac ttctgtttgg ctctaccata tccctcatat caaactttgt 1260  
agaactcttg aagaggaata ataatcatt gaaggctttg tatctctaag tttactcctt 1320  
tataaaaaaga cttatatatt

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Asp | Val | Gly | Ile | Gly | Leu | Val | Cys | Gln | Asn | Thr | Met | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Lys | Ala | Ser | Asn | Gly | Asn | Gly | Leu | Glu | Lys | Thr | Val | Pro | Ser | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Leu | Lys | Ala | Met | Ala | Cys | Val | Pro | Glu | Asp | Asp | Ala | Lys | Cys | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Val | Val | Ser | Gly | Trp | Phe | Ser | Glu | Pro | His | Pro | Arg | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Lys | Gly | Gly | Lys | Ala | Val | Tyr | Phe | Asn | Asn | Pro | Met | Trp | Pro | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ala | His | Ser | Leu | Lys | Val | Glu | Lys | Val | Leu | Phe | Lys | Asp | Lys | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Phe | Gln | Glu | Val | Leu | Val | Phe | Glu | Ser | Ala | Thr | Tyr | Gly | Lys | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Val | Leu | Asp | Gly | Ile | Val | Gln | Leu | Thr | Glu | Lys | Asp | Glu | Cys | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Tyr | Gln | Glu | Met | Ile | Ala | His | Leu | Pro | Leu | Cys | Ser | Ile | Ser | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Asn | Val | Leu | Val | Val | Gly | Gly | Gly | Asp | Gly | Gly | Val | Leu | Arg | Glu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Ser | Arg | His | Ser | Ser | Val | Glu | Val | Ile | Asp | Ile | Cys | Glu | Ile | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Met | Val | Ile | Asp | Val | Ser | Lys | Lys | Phe | Phe | Pro | Glu | Leu | Ala | Val |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Gly | Phe | Asp | Asp | Pro | Arg | Val | Gln | Leu | His | Ile | Ser | Asp | Ala | Ala | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Leu | Arg | Lys | Ser | Pro | Glu | Gly | Lys | Tyr | Asp | Ala | Ile | Ile | Val | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Ser | Ser | Asp | Pro | Val | Gly | Pro | Ala | Leu | Ala | Leu | Val | Glu | Lys | Pro | Phe |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Phe | Glu | Thr | Leu | Ala | Arg | Ala | Leu | Lys | Pro | Gly | Gly | Val | Leu | Cys | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Ala | Glu | Ser | Met | Trp | Leu | His | Thr | His | Leu | Ile | Glu | Asp | Met | Ile |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ile | Cys | Arg | Gln | Thr | Phe | Lys | Ser | Val | His | Tyr | Ala | Trp | Ser | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Pro | Thr | Tyr | Pro | Ser | Gly | Val | Ile | Gly | Phe | Val | Leu | Cys | Ser | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Gly | Pro | Ala | Val | Asp | Phe | Lys | Asn | Pro | Ile | Asn | Pro | Ile | Glu | Lys |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |

Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser  
325 330 335  
Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu  
340 345 350  
Val Ala Ser Leu Leu Ala Ser  
355

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1573734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro  
1 5 10 15  
Ser Cys Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys  
20 25 30  
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg  
35 40 45  
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp  
50 55 60  
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp  
65 70 75 80  
Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly  
85 90 95  
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu  
100 105 110  
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser  
115 120 125  
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu  
130 135 140  
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu  
145 150 155 160  
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu  
165 170 175  
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Ser Asp Ala  
180 185 190  
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile  
195 200 205  
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys  
210 215 220  
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu  
225 230 235 240  
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp  
245 250 255  
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp  
260 265 270  
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys  
275 280 285  
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile  
290 295 300  
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr  
305 310 315 320  
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg  
325 330 335  
Arg Glu Val Ala Ser Leu Leu Ala Ser

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340 345  
(2) INFORMATION FOR SEQ ID NO:2601:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 323 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..323  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573735  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:  
Met Ala Cys Val Pro Glu Asp Asp Ala Lys Cys His Ser Thr Val Val  
1 5 10 15  
Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly Lys Lys Gly Gly  
20 25 30  
Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly Glu Ala His Ser  
35 40 45  
Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser Asp Phe Gln Glu  
50 55 60  
Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val Leu Val Leu Asp  
65 70 75 80  
Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala Tyr Gln Glu Met  
85 90 95  
Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro Lys Asn Val Leu  
100 105 110  
Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Ile Ser Arg His  
115 120 125  
Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp Lys Met Val Ile  
130 135 140  
Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val Gly Phe Asp Asp  
145 150 155 160  
Pro Arg Val Gln Leu His Ile Ser Asp Ala Ala Glu Phe Leu Arg Lys  
165 170 175  
Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp Ser Ser Asp Pro  
180 185 190  
Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe Phe Glu Thr Leu  
195 200 205  
Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn Met Ala Glu Ser  
210 215 220  
Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile Ser Ile Cys Arg  
225 230 235 240  
Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser Val Pro Thr Tyr  
245 250 255  
Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr Glu Gly Pro Ala  
260 265 270  
Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys Leu Asp Gly Ala  
275 280 285  
Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser Asp Met His Arg  
290 295 300  
Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu Val Ala Ser Leu  
305 310 315 320  
Leu Ala Ser

(2) INFORMATION FOR SEQ ID NO:2602:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 1444 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1444

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2602:

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| aaaatatcaa | aacacgagac | agatttgatt | ccatttttat | tactgttact  | atcatccaaa | 60   |
| accttggtat | ttgtagccat | gagtcctgtt | tcagatctca | tcaaccttaa  | cctctcagac | 120  |
| tccactgaca | aaatcattgc | tgaatacata | tgggttggtg | gttctggaat  | ggacatgaga | 180  |
| agcaaagcca | ggactctacc | tggaccagtg | actgaccctt | cgcagctacc  | aaagtggaac | 240  |
| tatgatgggt | caagcacagg | acaagctcct | ggtgaagaca | gtgaagtcat  | cttatagtta | 300  |
| ataatctttt | tttcttgatc | tttaataaag | tttcttctca | ttggtttttt  | tttcgattct | 360  |
| tgtttactaa | tcttttgtgt | gtttgtatat | ctttgtttag | ccttcaagcc  | atatccaag  | 420  |
| atcctttcog | tagaggaaac | aacattcttg | tcatgtgcga | tgcgtacct   | cccgcggtg  | 480  |
| aaccaatccc | gactaacaaa | agacacgtcg | cggctaagg  | cttagcaac   | cctgatgttg | 540  |
| cagctgaagt | gccatggtat | ggtattgagc | aagaatacac | tttactccag  | aaagatgtga | 600  |
| ggtggcctgt | tggttggcct | attggcgggt | atcccgccc  | tcagggaccg  | tactattgcg | 660  |
| gtattggagc | agacaaatct | tttggcagag | atgttgttga | ttctcactac  | aaggcctgtt | 720  |
| tatacgctgg | aatcaacatt | agtggcatca | atggagaagt | catgccgggt  | cagtgggagt | 780  |
| tccaggtcgg | tccagctggt | ggtatctcgg | ctgctgatga | aatttggggtc | gctcggtaca | 840  |
| ttttggagag | gatcacagag | attgctgggt | tagtggatc  | ttttgacccg  | aaaccgatto | 900  |
| ccggtgactg | gaacggtgct | ggtgctcact | gcaactacag | taccaagtca  | atgaggaag  | 960  |
| aaggcgggta | cgagatcatc | aagaagcaa  | tcgataaat  | gggactgaga  | cacaagarc  | 1020 |
| rcattgctgc | ttacsgtgaa | ggcaatgagc | gtcgtctcac | aggacaccac  | gagactgctg | 1080 |
| acatcaacac | tttcctttgg | ggtgttgcg  | accgtggagc | atcgatccga  | gtaggacgtg | 1140 |
| atacgagaa  | agaagggaaa | ggatactttg | aggacaggag | gccagcttcg  | aacatggatc | 1200 |
| cttacattgt | tacttccatg | attgcagaga | ccaccatcct | ctggaatcct  | tgatgatcat | 1260 |
| cagatcaaga | aaaaatcttg | aatgtcactc | aaatttgtgt | ttcttgcaag  | attcaaagtt | 1320 |
| tgtgttctct | atcaagcaat | gtcttaggat | aagtcaaaga | tttgctctgc  | ttattctgct | 1380 |
| ttttatttac | ttcacatcct | attgaaaaca | tttctgtgta | ttatttatga  | ataaacatta | 1440 |
| tott       |            |            |            |             |            |      |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1573737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Asp | Ala | Tyr | Thr | Pro | Ala | Gly | Glu | Pro | Ile | Pro | Thr | Asn | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | His | Ala | Ala | Ala | Lys | Val | Phe | Ser | Asn | Pro | Asp | Val | Ala | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Pro | Trp | Tyr | Gly | Ile | Glu | Gln | Glu | Tyr | Thr | Leu | Leu | Gln | Lys | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Trp | Pro | Val | Gly | Trp | Pro | Ile | Gly | Gly | Tyr | Pro | Gly | Pro | Gln |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Pro | Tyr | Tyr | Cys | Gly | Ile | Gly | Ala | Asp | Lys | Ser | Phe | Gly | Arg | Asp |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Val | Asp | Ser | His | Tyr | Lys | Ala | Cys | Leu | Tyr | Ala | Gly | Ile | Asn | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Ile | Asn | Gly | Glu | Val | Met | Pro | Gly | Gln | Trp | Glu | Phe | Gln | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Pro | Ala | Val | Gly | Ile | Ser | Ala | Ala | Asp | Glu | Ile | Trp | Val | Ala | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Ile | Leu | Glu | Arg | Ile | Thr | Glu | Ile | Ala | Gly | Val | Val | Val | Ser | Phe |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly Ala Gly Ala His Cys  
145 150 155 160  
Asn Tyr Ser Thr Lys Ser Met Arg Glu Glu Gly Gly Tyr Glu Ile Ile  
165 170 175  
Lys Lys Ala Ile Asp Lys Leu Gly Leu Arg His Lys Xaa Xaa Ile Ala  
180 185 190  
Ala Tyr Xaa Glu Gly Asn Glu Arg Arg Leu Thr Gly His His Glu Thr  
195 200 205  
Ala Asp Ile Asn Thr Phe Leu Trp Gly Val Ala Asn Arg Gly Ala Ser  
210 215 220  
Ile Arg Val Gly Arg Asp Thr Glu Lys Glu Gly Lys Gly Tyr Phe Glu  
225 230 235 240  
Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr Ser Met  
245 250 255  
Ile Ala Glu Thr Thr Ile Leu Trp Asn Pro  
260 265

(2) INFORMATION FOR SEQ ID NO:2604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1573738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ala Val Gly Ile Ser  
1 5 10 15  
Ala Ala Asp Glu Ile Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile Thr  
20 25 30  
Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro Gly  
35 40 45  
Asp Trp Asn Gly Ala Gly Ala His Cys Asn Tyr Ser Thr Lys Ser Met  
50 55 60  
Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys Leu  
65 70 75 80  
Gly Leu Arg His Lys Xaa Xaa Ile Ala Ala Tyr Xaa Glu Gly Asn Glu  
85 90 95  
Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe Leu  
100 105 110  
Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp Thr  
115 120 125  
Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser Asn  
130 135 140  
Met Asp Pro Tyr Ile Val Thr Ser Met Ile Ala Glu Thr Thr Ile Leu  
145 150 155 160  
Trp Asn Pro

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1464 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1464

(D) OTHER INFORMATION: / Ceres Seq. ID 1573751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aagttcctac  | gcgaagtttt  | caacagattc  | gccggagaat  | cttcgaatca  | acggcggaga | 60   |
| aatggctcta  | tcacgcctct  | catcacgac   | caacatcatc  | actcgccct   | tctcgcgcgc | 120  |
| cttcagccga  | ttaatctcaa  | cggacacaac  | tccgatcaca  | atcgagactt  | cgcttccttt | 180  |
| cacagctcac  | ttatgtgatc  | caccgtcacg  | ctccgtcgaa  | tcacgagtc   | ragagcttct | 240  |
| cgatttcttc  | agaanccatg  | gcgttgatgc  | gacgtatgga  | aatcgcmsec  | gattcgcttt | 300  |
| acaaagcgaa  | gctaattccsa | gggttttgtc  | atctctacga  | cggccaagaa  | gctgtagcta | 360  |
| tagGcvtgga  | agctgcsatt  | acaaagaaaag | acgcgattat  | tactgcttat  | cgtgatcact | 420  |
| gtattttctt  | aggctcgtgt  | ggttcgtctc  | atgagggtttt | ctcagagctt  | atgggaagac | 480  |
| aagctgggtg  | ttctaaaggg  | aaaggtggat  | ctatgcactt  | ctataagaag  | gaatcgctcg | 540  |
| tttacgggtg  | tcattgggatt | gttggtgctc  | aggttccatt  | aggttgtggt  | attgcttttg | 600  |
| ctcagaagta  | taataaggaa  | gaggctgtca  | catttgcttt  | gtatggatgat | ggtgctgcga | 660  |
| atcagggaca  | gttggttgaa  | gctttgaata  | tttctgctct  | ttgggatttg  | cctgcaattt | 720  |
| tgggtctgcga | gaacaatcac  | tatggaatgg  | gaactgctga  | atggagagcc  | gctaagagtc | 780  |
| catcttacta  | caagcgtggt  | gattatgttc  | ctggactcaa  | ggtagatggt  | atggatgcat | 840  |
| ttgctgtcaa  | acaagcttgc  | aaatttgcta  | agcagcatgc  | gttgagagaag | gggccaataa | 900  |
| ttcttgagat  | ggacacatac  | aggtagaacg  | gtcactccat  | gtctgatcct  | gggagcacat | 960  |
| accgtaccgc  | agatgagata  | tctggtgtga  | ggcaggaacg  | ggatccaatt  | gagagaataa | 1020 |
| agaagctggt  | actatctcat  | gacctagcaa  | cagagaaaga  | gcttaaggat  | atggagaagg | 1080 |
| aaattagaaa  | agaagtagat  | gacgccattg  | ccaaagctaa  | ggattgcccc  | atgccagagc | 1140 |
| cttctgagct  | ctttaccaat  | gtgtatgtga  | agggatttgg  | cacogagtca  | tttgagactg | 1200 |
| acagaaaaga  | agtcaaagct  | tcccttccat  | gatcatggag  | ctcttggtcg  | ttaaactgcc | 1260 |
| acgtgtcatg  | agaaagttgg  | ctgatagaga  | aatctatgaa  | tatgaataaa  | gatctgattg | 1320 |
| tatactctct  | ctctcccccc  | ccccccccct  | tctgagtttt  | aatctctctg  | tatctttgtt | 1380 |
| tacaaacata  | aggagaaaca  | tgttattctt  | gtgaagcttt  | agtagtctcg  | tgtttaatat | 1440 |
| tcaagcaatc  | gagttgagat  | ctct        |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1573752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Met | Arg | Arg | Met | Glu | Ile | Xaa | Xaa | Asp | Ser | Leu | Tyr | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Lys | Leu | Ile | Xaa | Gly | Phe | Cys | His | Leu | Tyr | Asp | Gly | Gln | Glu | Ala |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Val | Ala | Ile | Gly | Xaa | Glu | Ala | Xaa | Ile | Thr | Lys | Lys | Asp | Ala | Ile | Ile |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |
| Thr | Ala | Tyr | Arg | Asp | His | Cys | Ile | Phe | Leu | Gly | Arg | Gly | Gly | Ser | Leu |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |
| His | Glu | Val | Phe | Ser | Glu | Leu | Met | Gly | Arg | Gln | Ala | Gly | Cys | Ser | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Lys | Gly | Gly | Ser | Met | His | Phe | Tyr | Lys | Lys | Glu | Ser | Ser | Phe | Tyr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Gly | His | Gly | Ile | Val | Gly | Ala | Gln | Val | Pro | Leu | Gly | Cys | Gly | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Phe | Ala | Gln | Lys | Tyr | Asn | Lys | Glu | Glu | Ala | Val | Thr | Phe | Ala | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Gly | Asp | Gly | Ala | Ala | Asn | Gln | Gly | Gln | Leu | Phe | Glu | Ala | Leu | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Ser | Ala | Leu | Trp | Asp | Leu | Pro | Ala | Ile | Leu | Val | Cys | Glu | Asn | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| His | Tyr | Gly | Met | Gly | Thr | Ala | Glu | Trp | Arg | Ala | Ala | Lys | Ser | Pro | Ser |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Tyr | Tyr | Lys | Arg | Gly | Asp | Tyr | Val | Pro | Gly | Leu | Lys | Val | Asp | Gly | Met |

(2) INFORMATION FOR SEO ID NO:2607:

(A) LENGTH: 321 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1573753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Met | Glu | Ile | Xaa | Xaa | Asp | Ser | Leu | Tyr | Lys | Ala | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Xaa | Gly | Phe | Cys | His | Leu | Tyr | Asp | Gly | Gln | Glu | Ala | Val | Ala | Ile |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Xaa | Glu | Ala | Xaa | Ile | Thr | Lys | Lys | Asp | Ala | Ile | Ile | Thr | Ala | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asp | His | Cys | Ile | Phe | Leu | Gly | Arg | Gly | Gly | Ser | Leu | His | Glu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ser | Glu | Leu | Met | Gly | Arg | Gln | Ala | Gly | Cys | Ser | Lys | Gly | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ser | Met | His | Phe | Tyr | Lys | Lys | Glu | Ser | Ser | Phe | Tyr | Gly | Gly | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ile | Val | Gly | Ala | Gln | Val | Pro | Leu | Gly | Cys | Gly | Ile | Ala | Phe | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Lys | Tyr | Asn | Lys | Glu | Glu | Ala | Val | Thr | Phe | Ala | Leu | Tyr | Gly | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Ala | Asn | Gln | Gly | Gln | Leu | Phe | Glu | Ala | Leu | Asn | Ile | Ser | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Trp | Asp | Leu | Pro | Ala | Ile | Leu | Val | Cys | Glu | Asn | Asn | His | Tyr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Gly | Thr | Ala | Glu | Trp | Arg | Ala | Ala | Lys | Ser | Pro | Ser | Tyr | Tyr | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Gly | Asp | Tyr | Val | Pro | Gly | Leu | Lys | Val | Asp | Gly | Met | Asp | Ala | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Val | Lys | Gln | Ala | Cys | Lys | Phe | Ala | Lys | Gln | His | Ala | Leu | Glu | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Pro | Ile | Ile | Leu | Glu | Met | Asp | Thr | Tyr | Arg | Tyr | His | Gly | His | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Ser | Asp | Pro | Gly | Ser | Thr | Tyr | Arg | Thr | Arg | Asp | Glu | Ile | Ser | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Gln | Glu | Arg | Asp | Pro | Ile | Glu | Arg | Ile | Lys | Lys | Leu | Val | Leu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ser | His | Asp | Leu | Ala | Thr | Glu | Lys | Glu | Leu | Lys | Asp | Met | Glu | Lys | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Arg | Lys | Glu | Val | Asp | Asp | Ala | Ile | Ala | Lys | Ala | Lys | Asp | Cys | Pro |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Met | Pro | Glu | Pro | Ser | Glu | Leu | Phe | Thr | Asn | Val | Tyr | Val | Lys | Gly | Phe |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Thr | Glu | Ser | Phe | Gly | Pro | Asp | Arg | Lys | Glu | Val | Lys | Ala | Ser | Leu |
|     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1573754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Xaa | Xaa | Asp | Ser | Leu | Tyr | Lys | Ala | Lys | Leu | Ile | Xaa | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Cys | His | Leu | Tyr | Asp | Gly | Gln | Glu | Ala | Val | Ala | Ile | Gly | Xaa | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Xaa | Ile | Thr | Lys | Lys | Asp | Ala | Ile | Ile | Thr | Ala | Tyr | Arg | Asp | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ile | Phe | Leu | Gly | Arg | Gly | Gly | Ser | Leu | His | Glu | Val | Phe | Ser | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Met | Gly | Arg | Gln | Ala | Gly | Cys | Ser | Lys | Gly | Lys | Gly | Gly | Ser | Met |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Phe | Tyr | Lys | Lys | Glu | Ser | Ser | Phe | Tyr | Gly | Gly | His | Gly | Ile | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ala | Gln | Val | Pro | Leu | Gly | Cys | Gly | Ile | Ala | Phe | Ala | Gln | Lys | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Lys | Glu | Glu | Ala | Val | Thr | Phe | Ala | Leu | Tyr | Gly | Asp | Gly | Ala | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gln | Gly | Gln | Leu | Phe | Glu | Ala | Leu | Asn | Ile | Ser | Ala | Leu | Trp | Asp |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Pro | Ala | Ile | Leu | Val | Cys | Glu | Asn | Asn | His | Tyr | Gly | Met | Gly | Thr |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Glu | Trp | Arg | Ala | Ala | Lys | Ser | Pro | Ser | Tyr | Tyr | Lys | Arg | Gly | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Val | Pro | Gly | Leu | Lys | Val | Asp | Gly | Met | Asp | Ala | Phe | Ala | Val | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gln | Ala | Cys | Lys | Phe | Ala | Lys | Gln | His | Ala | Leu | Glu | Lys | Gly | Pro | Ile |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Leu | Glu | Met | Asp | Thr | Tyr | Arg | Tyr | His | Gly | His | Ser | Met | Ser | Asp |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Gly | Ser | Thr | Tyr | Arg | Thr | Arg | Asp | Glu | Ile | Ser | Gly | Val | Arg | Gln |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Glu | Arg | Asp | Pro | Ile | Glu | Arg | Ile | Lys | Lys | Leu | Val | Leu | Ser | His | Asp |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Ala | Thr | Glu | Lys | Glu | Leu | Lys | Asp | Met | Glu | Lys | Glu | Ile | Arg | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Val | Asp | Asp | Ala | Ile | Ala | Lys | Ala | Lys | Asp | Cys | Pro | Met | Pro | Glu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Ser | Glu | Leu | Phe | Thr | Asn | Val | Tyr | Val | Lys | Gly | Phe | Gly | Thr | Glu |

290 295 300  
Ser Phe Gly Pro Asp Arg Lys Glu Val Lys Ala Ser Leu Pro  
305 310 315

(2) INFORMATION FOR SEQ ID NO:2609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1336
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:

tacttttggcg gtgctgagaa gaaagatgag aggggttcttg ttcttgattt ggggttcctta 60  
acaagcatct atgacagggc aaggggaattg ttctattatt tgaaaggagg ggtagttgat 120  
tttggcgaag agcatagcga Nggcttgagg acattctcgg tttggaagaa gatacgaaca 180  
agggcaatac cctgaatggg atgaggatca tcctattcat tttgtggggc attcagcggg 240  
tgcgcaagtt gtgctgtgat tgcagcaaat gcttgcagat caggcatttg aagggtttga 300  
agaaacgaat gagaattggg ttctgagtgt gacatcggtta tccggggcat tcaatggaac 360  
taccaggacc tacttagatg gcattgggac agatgatgga gtgagcatga aaccaatatg 420  
tttgttcgag ctgtgtcgta taggcgtgat aatgtacgat tggttggaca tttcatggct 480  
aaagacttat tacaatttcg ggttcgatca cttcaacatt tcttgaaga agaccggtgt 540  
gagaggtctc gttgattgcc taatgggaaa cacaggctct tttgcttctg gcgattggat 600  
cttacctgat ctcaaatcc aaggctcaac aagtattaac tccaatctcc agacgttccc 660  
aaacacttac tacttcagct acgcgactaa acgcacccgc agagtcattg gtatgacaat 720  
cccttcaggt gttcttggaa tccacccgat gctcttctc cgctctttc abatgagcNc 780  
Aatggaaatt cccacaagat gtctctctc cttataaagg ctacagggat gaggactggc 840  
aagagaacga cggggcattg aacacaatat caatgacaca tccgaggcta cctgttgagc 900  
atccgagccg gttcataagg agcgattcgg aatgtcaaac attacaaccc gggatctggt 960  
attataagat agtgggaagca gatcacataa tgttcatagt gaacagagag agagctggtg 1020  
ttcagtttga tctgatatac gacagcatct tccaacggtg caggaaacat gtttttagaa 1080  
agattcctca gactctcccc aatcaatctc cttcttctcc tcgttcatca tcatcaccca 1140  
gaataaacaa ctttgtacat tgatcacatg caaaaaaaaa atgttttagg gttgttacgt 1200  
tgagggctta agtttttgtt taggctatatt actactaata cagattattc attgttcttc 1260  
ttgttctcct ctcgatttgt tgtactgtaa aatatatata ttccattttg aaaattataa 1320  
tatttgtagg ttcgcc

(2) INFORMATION FOR SEQ ID NO:2610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

Met Leu Ala Asp Gln Ala Phe Glu Gly Phe Glu Glu Thr Asn Glu Asn  
1 5 10 15  
Trp Val Leu Ser Val Thr Ser Leu Ser Gly Ala Phe Asn Gly Thr Thr  
20 25 30  
Arg Thr Tyr Leu Asp Gly Met Arg Thr Asp Asp Gly Val Ser Met Lys  
35 40 45  
Pro Ile Cys Leu Leu Gln Leu Cys Arg Ile Gly Val Ile Met Tyr Asp  
50 55 60  
Trp Leu Asp Ile Ser Trp Leu Lys Thr Tyr Tyr Asn Phe Gly Phe Asp  
65 70 75 80  
His Phe Asn Ile Ser Trp Lys Lys Thr Gly Val Arg Gly Leu Val Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Cys | Leu | Met | Gly | Asn | Thr | Gly | Pro | Phe | Ala | Ser | Gly | Asp | Trp | Ile | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Pro | Asp | Leu | Thr | Ile | Gln | Gly | Ser | Thr | Ser | Ile | Asn | Ser | Asn | Leu | Gln |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Phe | Pro | Asn | Thr | Tyr | Tyr | Phe | Ser | Tyr | Ala | Thr | Lys | Arg | Thr | Arg |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Arg | Val | Met | Gly | Met | Thr | Ile | Pro | Ser | Gly | Val | Leu | Gly | Ile | His | Pro |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Met | Leu | Phe | Leu | Arg | Val | Phe | Xaa | Met | Ser | Xaa | Met | Glu | Ile | Pro | Thr |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Arg | Cys | Leu | Ser | Ser | Leu |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1573761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Thr | Asp | Asp | Gly | Val | Ser | Met | Lys | Pro | Ile | Cys | Leu | Leu | Gln |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Cys | Arg | Ile | Gly | Val | Ile | Met | Tyr | Asp | Trp | Leu | Asp | Ile | Ser | Trp |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Leu | Lys | Thr | Tyr | Tyr | Asn | Phe | Gly | Phe | Asp | His | Phe | Asn | Ile | Ser | Trp |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Lys | Lys | Thr | Gly | Val | Arg | Gly | Leu | Val | Asp | Cys | Leu | Met | Gly | Asn | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Pro | Phe | Ala | Ser | Gly | Asp | Trp | Ile | Leu | Pro | Asp | Leu | Thr | Ile | Gln |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Gly | Ser | Thr | Ser | Ile | Asn | Ser | Asn | Leu | Gln | Thr | Phe | Pro | Asn | Thr | Tyr |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Tyr | Phe | Ser | Tyr | Ala | Thr | Lys | Arg | Thr | Arg | Arg | Val | Met | Gly | Met | Thr |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ile | Pro | Ser | Gly | Val | Leu | Gly | Ile | His | Pro | Met | Leu | Phe | Leu | Arg | Val |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Phe | Xaa | Met | Ser | Xaa | Met | Glu | Ile | Pro | Thr | Arg | Cys | Leu | Ser | Ser | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1573762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Pro | Ile | Cys | Leu | Leu | Gln | Leu | Cys | Arg | Ile | Gly | Val | Ile | Met |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Tyr | Asp | Trp | Leu | Asp | Ile | Ser | Trp | Leu | Lys | Thr | Tyr | Tyr | Asn | Phe | Gly |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |

Phe Asp His Phe Asn Ile Ser Trp Lys Lys Thr Gly Val Arg Gly Leu  
35 40 45  
Val Asp Cys Leu Met Gly Asn Thr Gly Pro Phe Ala Ser Gly Asp Trp  
50 55 60  
Ile Leu Pro Asp Leu Thr Ile Gln Gly Ser Thr Ser Ile Asn Ser Asn  
65 70 75 80  
Leu Gln Thr Phe Pro Asn Thr Tyr Tyr Phe Ser Tyr Ala Thr Lys Arg  
85 90 95  
Thr Arg Arg Val Met Gly Met Thr Ile Pro Ser Gly Val Leu Gly Ile  
100 105 110  
His Pro Met Leu Phe Leu Arg Val Phe Xaa Met Ser Xaa Met Glu Ile  
115 120 125  
Pro Thr Arg Cys Leu Ser Ser Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atcacttact taacatacta agagagttat tagaacttgc aaaaaatggc ttccaaggct  | 60  |
| ttgattctgt taggtctctt ctcagttctt ctcgtcgtct ccgaagtgtc tgccgcaagg  | 120 |
| caatcgggca tggatgaagcc agagagttag gaaactgtgc aacctgaagg ttatggcggg | 180 |
| ggccacggag gacatggttg tcacggaggg ggaggaggcc acggacatgg aggacacaac  | 240 |
| ggaggagggg gccacggact tgacggatac ggaggacact acggaggttg tggaggagga  | 300 |
| tacggaggtg gaggaggaca ccacggagga ggaggccacg ggctaaacga acctgttcag  | 360 |
| actaagccgg gtgtttaaaa ctatataata tcttcactac catgcatgat tgcataatata | 420 |
| tatatacgct tatgtattat ctatatgcct ataaataaac catggtgagt ttgtaacgca  | 480 |
| GtgcNcttca gaaatgttcg gaataaattt ccataatatt agtataatgt ctctctgttt  | 540 |
| gaattataaaa ctgcgctgtt tgcataataa aatctcttgt agctaggtcg            |     |

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu  
1 5 10 15  
Val Val Ser Glu Val Ser Ala Ala Arg Gln Ser Gly Met Val Lys Pro  
20 25 30  
Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly Gly His Gly  
35 40 45  
Gly His Gly Gly His Gly Gly Gly Gly His Gly His Gly Gly His  
50 55 60  
Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly His Tyr Gly  
65 70 75 80  
Gly Gly Gly Gly Tyr Gly Gly Gly Gly Gly His His Gly Gly Gly  
85 90 95  
Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val

100 105 110  
(2) INFORMATION FOR SEQ ID NO:2615:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573792  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:  
Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly  
20 25 30  
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly  
35 40 45  
Gly His Tyr Gly Gly Gly Gly Gly Gly Tyr Gly Gly Gly Gly His  
50 55 60  
His Gly Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys Pro  
65 70 75 80  
Gly Val

(2) INFORMATION FOR SEQ ID NO:2616:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..57  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573793  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:  
Met Ala Val Ala Thr Glu Asp Met Val Thr Glu Gly Glu Glu Ala  
1 5 10 15  
Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp  
20 25 30  
Thr Glu Asp Thr Thr Glu Val Val Glu Glu Asp Thr Glu Val Glu Glu  
35 40 45  
Asp Thr Thr Glu Glu Glu Ala Thr Gly  
50 55

(2) INFORMATION FOR SEQ ID NO:2617:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 461 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..461  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573798  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:  
atcacttact taacatacta agagagttat tagaacttgc aaaaaatggc ttccaaggct 60  
ttgattctgt taggtctctt ctcagttctt ctcgtcgtct ccgaagtgtc tgccgcaagg 120  
aatcgggcat ggtgaagcca gagagtgagg aaactgtgca acctgaagggt tatggcggtg 180  
gccacggagg acatggtggt cacggagggg gaggaggcca cggacatgga ggacacaacg 240

gaggtggagg aggcacaccac ggaggaggag gccacgggct aaacgaacct gttcagacta 300  
agccgggtgt ttaaaactat ataatatctt cactaccatg catgattgca tatatatata 360  
tacgcttatg tattatctat atgcctataa ataaaccatg gtgagtttgt aacgcagtgc 420  
Tcttcagaaa tgttcggaat aaatttccat aatattagta t

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

His Leu Leu Asn Ile Leu Arg Glu Leu Leu Glu Leu Ala Lys Asn Gly  
1 5 10 15  
Phe Gln Gly Phe Asp Ser Val Arg Ser Leu Leu Ser Ser Ser Arg Arg  
20 25 30  
Leu Arg Ser Val Cys Arg Lys Glu Ser Gly Met Val Lys Pro Glu Ser  
35 40 45  
Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly Gly Gly His Gly Gly His  
50 55 60  
Gly Gly His Gly Gly Gly Gly Gly His Gly His Gly Gly His Asn Gly  
65 70 75 80  
Gly Gly Gly Gly His His Gly Gly Gly Gly His Gly Leu Asn Glu Pro  
85 90 95  
Val Gln Thr Lys Pro Gly Val  
100

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly  
20 25 30  
His Gly Gly His Asn Gly Gly Gly Gly Gly His His Gly Gly Gly Gly  
35 40 45  
His Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..596
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| actcatcact | tacttaacat | actaagagag | ttattagatc | ttgaaaaaca | tggtttccaa | 60  |
| ggctttgatt | ctgttgggtc | tcttcgcaat | tcttctggtg | gtctccgaag | tttctgccgc | 120 |
| aaggcaKtcg | ggcatggtga | agccagagag | gaaactgtgc | aacctgaagg | ttatcacgga | 180 |
| ggacatggtg | gtcacggagg | gggaggccac | tacggaggag | gaggccacgg | gcatggagga | 240 |
| cacaacggag | gagggggcca | cggacttgac | ggatacggag | gaggacatgg | aggacactac | 300 |
| ggaggaggag | gaggacacta | cggaggagga | ggaggccacg | gtggtggtgg | acactatgga | 360 |
| ggtggaggac | accatggagg | aggaggtcac | gggctgaacg | aacctgttca | gacgaagccg | 420 |
| ggtgtttaaa | agttataact | atcaaataaa | ttcaccatgc | ataattgcat | ctctatatac | 480 |
| acttatgtct | tatatgtatc | catcaaaata | aaccatggtg | agtttgtaat | gcagttcctt | 540 |
| cagaaatgtg | tggaataatg | tttcacaata | ataatagaat | atctctgttg | attctg     |     |

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | His | His | Leu | Leu | Asn | Ile | Leu | Arg | Glu | Leu | Leu | Asp | Leu | Glu | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Gly | Phe | Gln | Gly | Phe | Asp | Ser | Val | Gly | Ser | Leu | Arg | Asn | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Leu | Arg | Ser | Phe | Cys | Arg | Lys | Ala | Xaa | Gly | His | Gly | Glu | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Glu | Thr | Val | Gln | Pro | Glu | Gly | Tyr | His | Gly | Gly | His | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | His | Gly | His | Gly | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Asn | Gly | Gly | Gly | Gly | His | Gly | Leu | Asp | Gly | Tyr | Gly | Gly | Gly | His |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | Gly | Gly |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| His | Gly | Gly | Gly | Gly | His | Tyr | Gly | Gly | Gly | His | His | Gly | Gly | Gly | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Gly | His | Gly | Leu | Asn | Glu | Pro | Val | Gln | Thr | Lys | Pro | Gly | Val |     |     |
| 130 |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Lys | Ala | Leu | Ile | Leu | Leu | Leu | Phe | Ala | Ile | Leu | Leu |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Val | Ser | Glu | Val | Ser | Ala | Ala | Arg | Xaa | Ser | Gly | Met | Val | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Arg | Lys | Leu | Cys | Asn | Leu | Lys | Val | Ile | Thr | Glu | Asp | Met | Val | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Glu | Gly | Glu | Ala | Thr | Thr | Glu | Glu | Glu | Ala | Thr | Gly | Met | Glu | Asp |
| 50  |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |

Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Asp Met  
65 70 75 80  
Glu Asp Thr Thr Glu Glu Glu Glu Asp Thr Thr Glu Glu Glu Glu Ala  
85 90 95  
Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met Glu Glu Glu  
100 105 110  
Val Thr Gly  
115

(2) INFORMATION FOR SEQ ID NO:2623:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1573804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Met Val Lys Pro Glu Arg Lys Leu Cys Asn Leu Lys Val Ile Thr Glu  
1 5 10 15  
Asp Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr  
20 25 30  
Gly Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr  
35 40 45  
Glu Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Glu Asp Thr Thr Glu  
50 55 60  
Glu Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr  
65 70 75 80  
Met Glu Glu Glu Val Thr Gly  
85

(2) INFORMATION FOR SEQ ID NO:2624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 587 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1573809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

actcatcact tacttaacat actaagagag ttattagatc ttgaaaaaca tggcttccaa 60  
ggctttgatt ctggtgggtc tcttcgcaat tcttctggtg gtctccgaag tttctgccgc 120  
aaggCaGtNo Ngggcatggt gaagccagag agtgaggaaa ctgtgcaacc tgaaggttat 180  
cacggaggac atggtggtca cggaggggga ggccactacg gaggaggagg ccacggggcat 240  
ggaggacaca acggaggagg gggccacgga cttgacggat acggaggagg acatggaggga 300  
cactacggag gaggaggagg acactacgga ggaggatacg gtggtggtga aggaggaggt 360  
taaggaggaa gcggtggtg tggaggatgg taattccttt aattaggttt aggattacca 420  
atgaatgttc tctctctcgc ttgttatgct tctacttggt tttgtgtgtt ctctattttg 480  
ttctggttct gcttttagatt tgatgtaaca gttcgtgatt aggtattttg gtatctggaa 540  
acgtaatggt aagtcacttg tcattttcta aataacaaat ttcttcg

(2) INFORMATION FOR SEQ ID NO:2625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1573810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Thr His His Leu Leu Asn Ile Leu Arg Glu Leu Leu Asp Leu Glu Lys  
1 5 10 15  
His Gly Phe Gln Gly Phe Asp Ser Val Gly Ser Leu Arg Asn Ser Ser  
20 25 30  
Gly Gly Leu Arg Ser Phe Cys Arg Lys Ala Xaa Xaa Gly Met Val Lys  
35 40 45  
Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His Gly Gly His  
50 55 60  
Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His Gly His  
65 70 75 80  
Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly  
85 90 95  
Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly  
100 105 110  
Tyr Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly  
115 120 125  
Gly Trp  
130

(2) INFORMATION FOR SEQ ID NO:2626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1573811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
20 25 30  
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly  
35 40 45  
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr  
50 55 60  
Gly Gly Gly Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly  
65 70 75 80  
Gly Gly Gly Gly Trp  
85

(2) INFORMATION FOR SEQ ID NO:2627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1573812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

Met Val Val Thr Glu Gly Glu Ala Thr Glu Glu Glu Ala Thr Gly  
1 5 10 15

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Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu  
20 25 30  
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Glu  
35 40 45  
Asp Thr Val Val Val Lys Glu Glu Val Thr Glu Glu Ala Val Val Val  
50 55 60  
Glu Asp Gly Asn Ser Phe Asn  
65 70

(2) INFORMATION FOR SEQ ID NO:2628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..550
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcacttact taacatacta agagagttat tagaacttgc aaaaaatggc ttccaaggct   | 60  |
| ttgattctgt taggtctctt ctcagttctt ctcgtcgtct ccgaagtgtc tgccgcaagg   | 120 |
| CaaNtcgggc atggtgaagc cagagagtga ggaaactgtg caacctgaag gttatrgcgg   | 180 |
| tggccacgga ggacatggtg gtcacggarg gggaggaggc cacggacatg gaggacacaa   | 240 |
| cggaggaggg ggccacggac ttgacggata cggaggaggt ggaggacact atggaggarg   | 300 |
| tggaggacac tacggaggag gtggaggaca ctacggagga ggtggaggac actacggagg   | 360 |
| aggtggccac gggctaaacg aacctgttca gactaagccg ggtgttttaa actatataat   | 420 |
| atcttcacta ccattgcattga ttgcatatat atatatacgc ttatgtatta tctatatgcc | 480 |
| tataaataaa ccattggtgag tttgtaacgc agtgccttca gaaatgttcg gaataaattt  | 540 |
| ccataatatt                                                          |     |

(2) INFORMATION FOR SEQ ID NO:2629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Xaa  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly His Gly Xaa Gly Gly Gly His Gly  
20 25 30  
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly  
35 40 45  
Gly Gly Gly Gly His Tyr Gly Gly Xaa Gly Gly His Tyr Gly Gly Gly  
50 55 60  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His  
65 70 75 80  
Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val  
85 90

(2) INFORMATION FOR SEQ ID NO:2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1573815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

```
Met Val Val Thr Xaa Gly Glu Glu Ala Thr Asp Met Glu Asp Thr Thr
1 5 10 15
Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Val Glu Asp Thr
20 25 30
Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu
35 40 45
Glu Val Glu Asp Thr Thr Glu Glu Val Ala Thr Gly
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1573816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

```
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
1 5 10 15
Glu Val Glu Asp Thr Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val
20 25 30
Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val Ala Thr
35 40 45
Gly
```

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..597

(D) OTHER INFORMATION: / Ceres Seq. ID 1573817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

```
atcacttact taacatacta agagagttat tagatcttga aaaacatggc ttccaaggct 60
ttgattctgt tgggtctctt cgcaattctt ctggtggtct ccgaagtctc tgccgcaagg 120
CaTgTcgggc atggtgaagc cagagagtga ggaaactgtg caacctgaag gttatcacgg 180
aggacatggt ggtcacggag ggggaggcca ctacggagga ggaggccacg ggcatggagg 240
acacaacgga ggagggggcc acggacttaa cggatacggg ggaggacatg gaggacacta 300
cggaggagga ggaggacact acggaggarg aggaggccac ggtggtggtg gacactatgg 360
aggtggagga caccatggag gavgaggtca cgggctgaac gaacctgttc agacgaagcc 420
gggtgtttaa aagttataac tatcaaataa attcaccatg cataattgca tctctatata 480
cacttatgtc ttatatgtat ccatcaaaat aaaccatggt gagtttgtaa tgcagttcct 540
tcagaaatgt gtggaataat gtttcacaat aataatagaa tatctctgtt gattctg
```

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1573818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

Met Ser Gly Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu  
1 5 10 15  
Gly Tyr His Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly  
20 25 30  
Gly Gly Gly His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly  
35 40 45  
Leu Asn Gly Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly  
50 55 60  
Gly His Tyr Gly Gly Xaa Gly Gly His Gly Gly Gly Gly His Tyr Gly  
65 70 75 80  
Gly Gly Gly His His Gly Gly Xaa Gly His Gly Leu Asn Glu Pro Val  
85 90 95  
Gln Thr Lys Pro Gly Val  
100

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1573819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
20 25 30  
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asn Gly  
35 40 45  
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr  
50 55 60  
Gly Gly Xaa Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
65 70 75 80  
His His Gly Gly Xaa Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys  
85 90 95  
Pro Gly Val

(2) INFORMATION FOR SEQ ID NO:2635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1573820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

Met Val Val Thr Glu Gly Glu Ala Thr Glu Glu Glu Ala Thr Gly  
1 5 10 15  
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu

```

 20 25 30
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Xaa
 35 40 45
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met
 50 55 60
Glu Xaa Glu Val Thr Gly
 65 70
```

(2) INFORMATION FOR SEQ ID NO:2636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

```

atcacttact taacatacta agagagttat tagatcttga aaaacatggc ttccaaggct 60
ttgattctgt tgggtctctt cgcaattctt ctggtggtct ccgaagtttc tgccgcaagg 120
CaKtGcgggc atggtgaagc cagagagtga ggaaactgtg caacctgaag gttatcacgg 180
aggacatggt ggtcacggar ggggaggcca ctacggagga ggaggccacg ggcattggagg 240
acacaacgga ggagggggcc acggacttga cggatacggga ggaggacatg gaggacacta 300
cggargagga ggaggacact acggargagg aggaggccac ggtggtggtg gacactatgg 360
aggtggagga caccatggag gaggaggtca cgggctgaac gaacctgttc agacgaaggg 420
tgaggaacaa gaggcaggga agaaggattt cattcagata ctcaagactc ttgaatctga 480
gcttggagac aaaccttact ttagtggcga tgactttggc tatgtagaca ttaaggg
```

(2) INFORMATION FOR SEQ ID NO:2637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

```

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His
1 5 10 15
Gly Gly His Gly His Gly Xaa Gly Gly His Tyr Gly Gly Gly Gly
 20 25 30
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly
 35 40 45
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Xaa Gly Gly Gly His Tyr
 50 55 60
Gly Xaa Gly Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
 65 70 75 80
His His Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys
 85 90 95
Gly Glu Glu Gln Glu Ala Gly Lys Lys Asp Phe Ile Gln Ile Leu Lys
 100 105 110
Thr Leu Glu Ser Glu Leu Gly Asp Lys Pro Tyr Phe Ser Gly Asp Asp
 115 120 125
Phe Gly Tyr Val Asp Ile Lys
 130 135
```

(2) INFORMATION FOR SEQ ID NO:2638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..70
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:

```
Met Val Val Thr Xaa Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly
1 5 10 15
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
20 25 30
Glu Asp Met Glu Asp Thr Thr Xaa Glu Glu Glu Asp Thr Thr Xaa Glu
35 40 45
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met
50 55 60
Glu Glu Glu Val Thr Gly
65 70
```

(2) INFORMATION FOR SEQ ID NO:2639:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1021 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1021
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

```
aataaaaaatt tgtttctttc ttctctgttt ttttttgctt tcgtcttcaa gagagagaga 60
gagagagata caaagagaga aatttggttg tttgttgacg gaagcttctt cggctctctt 120
tctccgtctt acgattgtca acgcgtggtt ccatcttcaa ttttgtttct attttagcag 180
aagtttctcg agcttcaaat actgtttcag atcaatcaat cagtcaatca tggctagctc 240
tggaacaacg aacatcaacg ccaattggtt attactagga gatgttgagg ctggaaaatc 300
aagtcttggt ctacggtttg tgaaagatca gtttggtgaa tttcaggaat caaccattgg 360
tgcagctttt ttctctcaaa cattggctgt gaatgatgag actgtgaagt ttgagatatg 420
ggatacagct ggtcaggaac gataccacag tttggctcca atgtactaca ggggtgcagc 480
tgctgctatt attgtctttg acattactaa tcaagcctca tttgagaggg cgaaraaatg 540
ggttcaggaa ctgcaggcac aaggtaacct taatatggtg atggctcttg ctggaaacaa 600
agctgattta ttagacgcaa ggaagggtgc tgcagaggag gcagagatat atgctcaaga 660
gaacagcctt ttctttatgg aaacctcagc gaagaccgca acaaattgtc aagacatatt 720
ctacgaaata gcgaaaaggc taccacgtat acagccagct gaaaacccga caggaatggt 780
tctcccaaac gggccagggg ctacggcagt gagttcatcg tgttggtgctt agattcgtac 840
ctgaagagag atctcatttg gttagtcaca tagtagagaa catctggact ttcattgtgt 900
tgcttcttct tcgtctttgt tactttactt tgcttgcatg gacaacaaca acagtgtata 960
tcatgatgat acttattctg cttttgtgAa aatctgaaga tatttgtatt tggagagatt 1020
t
```

(2) INFORMATION FOR SEQ ID NO:2640:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

Ile Lys Ile Cys Phe Phe Leu Leu Cys Phe Phe Leu Leu Ser Ser Ser  
1 5 10 15  
Arg Glu Arg Glu Arg Glu Ile Gln Arg Glu Lys Phe Gly Cys Leu Leu  
20 25 30  
Thr Glu Ala Ser Ser Val Ser Leu Leu Arg Leu Thr Ile Val Asn Ala  
35 40 45  
Trp Phe His Leu Gln Phe Cys Phe Tyr Phe Ser Arg Ser Phe Ser Ser  
50 55 60  
Phe Lys Tyr Cys Phe Arg Ser Ile Asn Gln Ser Ile Met Ala Ser Ser  
65 70 75 80  
Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu Gly Asp Val Gly  
85 90 95  
Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys Asp Gln Phe Val  
100 105 110  
Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe Ser Gln Thr Leu  
115 120 125  
Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp Asp Thr Ala Gly  
130 135 140  
Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr Tyr Arg Gly Ala Ala  
145 150 155 160  
Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala Ser Phe Glu Arg  
165 170 175  
Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly Asn Pro Asn Met  
180 185 190  
Val Met Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu Asp Ala Arg Lys  
195 200 205  
Val Ser Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu Asn Ser Leu Phe  
210 215 220  
Phe Met Glu Thr Ser Ala Lys Thr Ala Thr Asn Val Lys Asp Ile Phe  
225 230 235 240  
Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro Ala Glu Asn Pro  
245 250 255  
Thr Gly Met Val Leu Pro Asn Gly Pro Gly Ala Thr Ala Val Ser Ser  
260 265 270  
Ser Cys Cys Ala  
275

(2) INFORMATION FOR SEQ ID NO:2641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1573834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

Met Ala Ser Ser Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu  
1 5 10 15  
Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys  
20 25 30  
Asp Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe  
35 40 45  
Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp  
50 55 60  
Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr Tyr  
65 70 75 80  
Arg Gly Ala Ala Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala  
85 90 95  
Ser Phe Glu Arg Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

Ala Gly Leu Thr Leu Trp Leu Leu Ile Thr Leu His Leu Glu Trp Arg  
1 5 10 15  
Thr Met Leu Leu Ser Val Ser Ile Leu Leu Lys Lys Leu Gly Ser Leu  
20 25 30  
Arg Ser Gln Arg Ala Ser Phe Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Met Glu Asn Asp Val Ala Phe Cys Glu Tyr Leu Ile Glu Glu Val Gly  
1 5 10 15  
Val Val Ala Ile Pro Thr Ser Val Phe Tyr Leu Asn Pro Glu Glu Gly  
20 25 30  
Lys Asn Leu Val Arg Phe Ala Phe Cys Lys Asp Glu Glu Thr Leu Arg  
35 40 45  
Gly Ala Ile Glu Arg Met Lys Gln Lys Leu Lys Arg Lys Val  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1076
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| atTTTTgatt gCGtCatttt cttcttttga aatgtctttg atttagcatt tcagttcgct   | 60   |
| caaaacatca aatcttacct tcttttagctt tcacattaga ttctggtaat tattaacaca  | 120  |
| aaaaaaagat aagccagaat acgaaacaac caaaaaaaga ggattttttt tttttttttt   | 180  |
| ttctttccga tgccctccgac caataattac cgaatctccg gcgaaccacc gtctactacg  | 240  |
| ccgtctcctc caccgccaaa accgaaaaca aggattctct ctctattcct cgttggtgta   | 300  |
| atcatgtttt caatcttctt tctcttcctc gttcttatcg gtatcgctc tgttcttctc    | 360  |
| ctccctctcc tctctctctc tctccatcgt caccaccgac gtcgtcgtcg taatcgccga   | 420  |
| caagaatcct cagatgggtt atcttcaaga ttctgtgaaa agcttctcct attcaaattc   | 480  |
| tccgaaccta gcacatacac acggtagcag agcgattgtg tggtttggtt tgatggattc   | 540  |
| agacaaggac aatgggtgctg gaatcttcct ggttggtggac acgtgtttca tcgaaagtgt | 600  |
| gtggacactt ggttgctcaa agcctcgacg tgcctattK tgcagagcta gggtagatt     | 660  |
| gtgggaggaa gatccacaag aaggagaatt aaggagatgt tttggtcata gaagaagtag   | 720  |
| tttgctagat ttgtaatttt gtgtggttat gttagcgtgg actcagtcta atggatgata   | 780  |
| agaatctcca aaactgaagc tacgaagagg tacaatacaa gccaaaggact ctttctctca  | 840  |
| tagagaagta gcgggtcgat cttatggtta tatataagca ctaagcagat gggcggttga   | 900  |
| tcataataaac cctcactacc attaccaaaa agcaatagcc aagagctttt tttttcattt  | 960  |
| tctttttgaa agccatggat cggttttcgt tcttgaatgt tataatggag gttgcgggta   | 1020 |
| ttctaaatga atcccgcaa ctcttcctca agaacaaaaa gttgatgttc tcagcc        |      |

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

(2) INFORMATION FOR SEQ ID NO:2648:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atcaatcgga ttatctgcac ttgtttcaat ggtgcatcta atatctctca agctggtgct | 60  |
| cttgcttgcc ttacacccga aggacttgag gcaatgcata aggtgattgg attctataaa | 120 |
| gaaaacacaa acataatcat tgacacattc acatctctcg ggtatgatgt atatggagga | 180 |
| aatgcgcctt acgtatgggt tcacttcccg aaccaaagct catgggatgt gtttgctgag | 240 |
| attctggaga agactcatgt gggtacaact ccaggaagtg gggttgacc agggggtgaa  | 300 |
| gggttcgttc gtgtcagtc ctttggtcac agagagaaca tcttagaggc atgtcgaaga  | 360 |
| ttcaagcagc tttaaaaatg aagaaccttg tttgtaatcg ttcctcatca tcatcacct  | 420 |
| ctttaatgac atgatttgag ttaaaataat gtcgtttcca Ttgtkktstg gaatttgtag | 480 |
| aagacacttt tgacaccagt gtttc                                       |     |

(2) INFORMATION FOR SEQ ID NO:2650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Asn Arg Ile Ile Cys Thr Cys Phe Asn Gly Ala Ser Asn Ile Ser |  |
| 1 5 10 15                                                       |  |
| Gln Ala Gly Ala Leu Ala Cys Leu Thr Pro Glu Gly Leu Glu Ala Met |  |
| 20 25 30                                                        |  |
| His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Asp     |  |
| 35 40 45                                                        |  |
| Thr Phe Thr Ser Leu Gly Tyr Asp Val Tyr Gly Gly Asn Ala Pro Tyr |  |
| 50 55 60                                                        |  |
| Val Trp Val His Phe Pro Asn Gln Ser Ser Trp Asp Val Phe Ala Glu |  |
| 65 70 75 80                                                     |  |
| Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly |  |
| 85 90 95                                                        |  |
| Pro Gly Gly Glu Gly Phe Val Arg Val Ser Ala Phe Gly His Arg Glu |  |
| 100 105 110                                                     |  |
| Asn Ile Leu Glu Ala Cys Arg Arg Phe Lys Gln Leu Tyr Lys         |  |
| 115 120 125                                                     |  |

(2) INFORMATION FOR SEQ ID NO:2651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

Met His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Ile

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(2) INFORMATION FOR SEQ ID NO:2652:

(A) LENGTH: 1687 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1687  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573899

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aattccttgc | ttcatttttc  | gtcacccctag | ccgctttact  | ctcttgcgat  | atctctgaga  | 60   |
| tttgtttgac | agtctctaac  | catgggtaaa  | gagaagtttc  | acatcaacat  | tgtggtcatt  | 120  |
| ggccacgtcg | attctggaaa  | gtcgaccacc  | actggacact  | tgatctacaa  | gttgggtggg  | 180  |
| attgacaagc | gtgtcattga  | gaggttcgag  | aaggaggctg  | ctgagatgaa  | caagagggtcc | 240  |
| ttcaagtagc | catgggtttt  | ggacaaaact  | aaggctgagc  | gtgagcgtgg  | tatcaccatt  | 300  |
| gacattgctc | tctggaagtt  | cgagaccacc  | aagtactact  | gcactgtcat  | tgtgtctcct  | 360  |
| ggccatcgtg | atttcattca  | gaacatgata  | actggtaacct | cccaggctga  | ttgtgctgkc  | 420  |
| cttatcatcg | actccaccac  | tggtgGtttt  | gaggctggta  | tctccaagga  | tggtcagacc  | 480  |
| cgtgagcaag | ctctccttgc  | tttcacccct  | ggtgtcaaac  | agatgatctg  | ctgttgtaac  | 540  |
| aagatggatg | ccactacccc  | caagtactcc  | aaggccaggt  | acgatgaaat  | tatcaaggag  | 600  |
| gtgtcttcct | acttgaagaa  | ggttggttac  | aaccccgaca  | aaatcccatt  | tgtgcccatc  | 660  |
| tctggattcg | agggtgacaa  | catgattgag  | aggtccacca  | acctagacct  | gtacaaggga  | 720  |
| ccaactcttc | ttgaggtctc  | tgaccagatc  | aacgagccca  | agaggccatc  | agacaagccc  | 780  |
| cttcgtctcc | cacttcagga  | tgctctaaag  | attggttgta  | ttggaaacgg  | gccagtgga   | 840  |
| cgtgttgaga | ctgggtatgat | caagcctggg  | atggttggtga | cctttgctcc  | cacagggttg  | 900  |
| accactgagg | tcaagtctgt  | tgagatgcac  | cacgagtctc  | ttcttgaggc  | acttccaggt  | 960  |
| gacaacgttg | ggttcaatgt  | taagaatgtt  | gctgtcaagg  | atcttaagag  | agggtaacgtc | 1020 |
| gcatccaact | ccaaggatga  | ccctgccaa   | ggtgctgcta  | acttcacctc  | ccagggtcatc | 1080 |
| atcatgaacc | accctggta   | gattggtaac  | ggttacgccc  | cagtcctgga  | ttggcacacc  | 1140 |
| tctcacattg | cagtcagatt  | ctctgagatc  | ttgaccaaga  | ttgacaggcg  | ttctggttaag | 1200 |
| gagattgaga | aggagcccaa  | gttcttgaa   | aatgggtgat  | ctgtgatggt  | gaagatgact  | 1260 |
| ccaaccaagc | ccatggttgt  | ggagaccttc  | tctgagtacc  | caccacttgg  | acgtttcgct  | 1320 |
| gtgagggaca | tgaggcagac  | tgttgacgtc  | ggtgttatca  | agagtgttga  | caagaaggac  | 1380 |
| ccaaccggag | ccaaggttac  | caaggtgcc   | gtcaagaagg  | gtgcgaagtg  | aaccatcctc  | 1440 |
| aaaactctat | ctgcgcgagg  | tgaatcaaag  | gacagtgtta  | gtttttattac | aatagtttgg  | 1500 |
| tatttggctg | cgtgtctgtg  | ttcttgtttc  | gtttttctccc | cgtcagagcg  | ttgtttctcgt | 1560 |
| aattgggttc | ttgatcggag  | gtggcggatc  | tacacacaca  | ttcttcctgt  | tttttgcctt  | 1620 |
| tatttgtttt | tctcattttg  | aactgtttaa  | aatttctgtt  | atatgaatga  | atgttttccc  | 1680 |
| tgcggtc    |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2653:

(A) LENGTH: 449 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1573900

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Glu | Lys | Phe | His | Ile | Asn | Ile | Val | Val | Ile | Gly | His | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ser | Gly | Lys | Ser | Thr | Thr | Thr | Gly | His | Leu | Ile | Tyr | Lys | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Asp | Lys | Arg | Val | Ile | Glu | Arg | Phe | Glu | Lys | Glu | Ala | Ala | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Thr | Thr | Lys | Tyr | Tyr | Cys | Thr | Val | Ile | Asp | Ala | Pro | Gly | His | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Phe | Ile | Lys | Asn | Met | Ile | Thr | Gly | Thr | Ser | Gln | Ala | Asp | Cys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Xaa | Leu | Ile | Ile | Asp | Ser | Thr | Thr | Gly | Gly | Phe | Glu | Ala | Gly | Ile | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Asp | Gly | Gln | Thr | Arg | Glu | His | Ala | Leu | Leu | Ala | Phe | Thr | Leu | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Lys | Gln | Met | Ile | Cys | Cys | Cys | Asn | Lys | Met | Asp | Ala | Thr | Thr | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Tyr | Ser | Lys | Ala | Arg | Tyr | Asp | Glu | Ile | Ile | Lys | Glu | Val | Ser | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Leu | Lys | Lys | Val | Gly | Tyr | Asn | Pro | Asp | Lys | Ile | Pro | Phe | Val | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ser | Gly | Phe | Glu | Gly | Asp | Asn | Met | Ile | Glu | Arg | Ser | Thr | Asn | Leu |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Trp | Tyr | Lys | Gly | Pro | Thr | Leu | Leu | Glu | Ala | Leu | Asp | Gln | Ile | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Pro | Lys | Arg | Pro | Ser | Asp | Lys | Pro | Leu | Arg | Leu | Pro | Leu | Gln | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Tyr | Lys | Ile | Gly | Gly | Ile | Gly | Thr | Val | Pro | Val | Gly | Arg | Val | Glu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Gly | Met | Ile | Lys | Pro | Gly | Met | Val | Val | Thr | Phe | Ala | Pro | Thr | Gly |
|     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Thr | Thr | Glu | Val | Lys | Ser | Val | Glu | Met | His | His | Glu | Ser | Leu | Leu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Ala | Leu | Pro | Gly | Asp | Asn | Val | Gly | Phe | Asn | Val | Lys | Asn | Val | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Lys | Asp | Leu | Lys | Arg | Gly | Tyr | Val | Ala | Ser | Asn | Ser | Lys | Asp | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro | Ala | Lys | Gly | Ala | Ala | Asn | Phe | Thr | Ser | Gln | Val | Ile | Ile | Met | Asn |
|     |     |     | 325 |     |     |     |     |     |     | 330 |     |     |     | 335 |     |
| His | Pro | Gly | Gln | Ile | Gly | Asn | Gly | Tyr | Ala | Pro | Val | Leu | Asp | Cys | His |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Thr | Ser | His | Ile | Ala | Val | Lys | Phe |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1573901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Arg | Ser | Phe | Lys | Tyr | Ala | Trp | Val | Leu | Asp | Lys | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Glu | Arg | Glu | Arg | Gly | Ile | Thr | Ile | Asp | Ile | Ala | Leu | Trp | Lys | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Thr | Lys | Tyr | Tyr | Cys | Thr | Val | Ile | Asp | Ala | Pro | Gly | His | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Phe | Ile | Lys | Asn | Met | Ile | Thr | Gly | Thr | Ser | Gln | Ala | Asp | Cys | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Xaa | Leu | Ile | Ile | Asp | Ser | Thr | Thr | Gly | Gly | Phe | Glu | Ala | Gly | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Asp | Gly | Gln | Thr | Arg | Glu | His | Ala | Leu | Leu | Ala | Phe | Thr | Leu | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Lys | Gln | Met | Ile | Cys | Cys | Cys | Asn | Lys | Met | Asp | Ala | Thr | Thr | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Tyr | Ser | Lys | Ala | Arg | Tyr | Asp | Glu | Ile | Ile | Lys | Glu | Val | Ser | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Leu | Lys | Lys | Val | Gly | Tyr | Asn | Pro | Asp | Lys | Ile | Pro | Phe | Val | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Ser | Gly | Phe | Glu | Gly | Asp | Asn | Met | Ile | Glu | Arg | Ser | Thr | Asn | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Trp | Tyr | Lys | Gly | Pro | Thr | Leu | Leu | Glu | Ala | Leu | Asp | Gln | Ile | Asn |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Pro | Lys | Arg | Pro | Ser | Asp | Lys | Pro | Leu | Arg | Leu | Pro | Leu | Gln | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Tyr | Lys | Ile | Gly | Gly | Ile | Gly | Thr | Val | Pro | Val | Gly | Arg | Val | Glu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Gly | Met | Ile | Lys | Pro | Gly | Met | Val | Val | Thr | Phe | Ala | Pro | Thr | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Thr | Thr | Glu | Val | Lys | Ser | Val | Glu | Met | His | His | Glu | Ser | Leu | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ala | Leu | Pro | Gly | Asp | Asn | Val | Gly | Phe | Asn | Val | Lys | Asn | Val | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Lys | Asp | Leu | Lys | Arg | Gly | Tyr | Val | Ala | Ser | Asn | Ser | Lys | Asp | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Ala | Lys | Gly | Ala | Ala | Asn | Phe | Thr | Ser | Gln | Val | Ile | Ile | Met | Asn |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| His | Pro | Gly | Gln | Ile | Gly | Asn | Gly | Tyr | Ala | Pro | Val | Leu | Asp | Cys | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ser | His | Ile | Ala | Val | Lys | Phe | Ser | Glu | Ile | Leu | Thr | Lys | Ile | Asp |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Arg | Arg | Ser | Gly | Lys | Glu | Ile | Glu | Lys | Glu | Pro | Lys | Phe | Leu | Lys | Asn |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gly | Asp | Ala | Gly | Met | Val | Lys | Met | Thr | Pro | Thr | Lys | Pro | Met | Val | Val |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Glu | Thr | Phe | Ser | Glu | Tyr | Pro | Pro | Leu | Gly | Arg | Phe | Ala | Val | Arg | Asp |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Met | Arg | Gln | Thr | Val | Ala | Val | Gly | Val | Ile | Lys | Ser | Val | Asp | Lys | Lys |
|     | 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |
| Asp | Pro | Thr | Gly | Ala | Lys | Val | Thr | Lys | Ala | Ala | Val | Lys | Lys | Gly | Ala |

U.S. PAT. & TM. OFF.

(2) INFORMATION FOR SEQ ID NO:2655:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1573902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

(2) INFORMATION FOR SEQ ID NO:2656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| agggttttctg | tttcgccgct | caggtttcgt | gaaaagaatc  | tatcttgagc | aatgtctcca  | 60  |
| gctaaagttg  | atgtcaccaa | gaaagccgac | cctaaggcta  | aggctttgaa | agctgcgaaa  | 120 |
| gcagtgaat   | ctggccaaat | cgtaaaaaag | cctgcgaaga  | agatcaggac | aaagggttact | 180 |
| ttccacaggc  | cMaaaGacat | tgaccgttcc | tagaaaagcct | aagtacccaa | agatcagtgc  | 240 |
| tactccaagg  | aacaaattgg | atcattacca | gatcctcaag  | taccctctca | ctactgaatc  | 300 |
| tgccatgaaa  | aagattgaag | acaacaacac | cttagttctc  | attgttgaca | tccgtgctga  | 360 |
| caagaaaaag  | atcaaagatg | ctgtcaagaa | gatgtatgac  | attcagacca | agaaagtcaa  | 420 |
| caccctcatt  | aggcccgatg | gaacaaagaa | ggcgtatgtg  | aggttgactc | ctgattatga  | 480 |
| tgctttggat  | gtggctaaca | aaatcgggat | catctaatac  | gatcattgtc | gctctgtgat  | 540 |
| tttacttttt  | ctggtttttc | tcttccatag | tctcagtttt  | gctagagaag | ttaagatatt  | 600 |
| actatcacca  | tctctttggt | atgcttttat | ctttggattc  | aaaaagatta | tatgtttggc  | 660 |

(2) INFORMATION FOR SEQ ID NO:2657:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Pro | Ala | Lys | Val | Asp | Val | Thr | Lys | Lys | Ala | Asp | Pro | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Leu | Lys | Ala | Ala | Lys | Ala | Val | Lys | Ser | Gly | Gln | Ile | Val | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Pro | Ala | Lys | Lys | Ile | Arg | Thr | Lys | Val | Thr | Phe | His | Arg | Xaa | Lys |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Ile | Asp | Arg | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 50  |

(2) INFORMATION FOR SEQ ID NO:2658:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Ile | Glu | Asp | Asn | Asn | Thr | Leu | Val | Phe | Ile | Val | Asp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ala | Asp | Lys | Lys | Lys | Ile | Lys | Asp | Ala | Val | Lys | Lys | Met | Tyr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Thr | Lys | Lys | Val | Asn | Thr | Leu | Ile | Arg | Pro | Asp | Gly | Thr | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Lys | Ala | Tyr | Val | Arg | Leu | Thr | Pro | Asp | Tyr | Asp | Ala | Leu | Asp | Val | Ala |



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(2) INFORMATION FOR SEQ ID NO:2660:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..559
 (D) OTHER INFORMATION: / Ceres Seq. ID 1573920
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:
aattcactga ttattgtttt aaggcaaat aagatcatct tcaaaatctt ctcagatctc 60
ttccaatttt ctagaaaaaa catgtcttgc tgtggtgtaa gctgtggttg tggatctgcc 120
tgcaagtgcg gcaatggttg cggaggttgc aaaagggtacc ctgacttgga gaacaccgcc 180
accgagactc ttgtcctcgg tgttgctccg gcgatgaact ctcagtaaga ggcttcoggT 240
cgSagacttt cgttgccgag aatgatgcct gcaaatacgg atctgactgc aagtgcacc 300
cttgtaacctg caaatgaaga acttcataaa ccctaagtct gtaataaacc taatgttatg 360
ttaggtttgc ttatatgtaa taattggctg atttttccgg tagttttgcc ggcgacgttg 420
gtctttctct tcttcttctt cttctgtgtg tgttttatg gtttggtcac taagatatct 480
ctgcaaagtt ttatctttgt gactttatta atcctaagac tattatgggt ttgtattaaa 540
gtttgcttct ttcttgctc
```

(2) INFORMATION FOR SEQ ID NO:2661:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..111
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573921
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Leu | Ile | Ile | Val | Leu | Arg | Gln | Ile | Lys | Ile | Ile | Phe | Lys | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Ser | Asp | Leu | Phe | Gln | Phe | Ser | Arg | Lys | Asn | Met | Ser | Cys | Cys | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Cys | Gly | Cys | Gly | Ser | Ala | Cys | Lys | Cys | Gly | Asn | Gly | Cys | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2662:

(D) OTHER INFORMATION: / Ceres Seq. ID 1573922

(2) INFORMATION FOR SEQ ID NO:2663:

(D) OTHER INFORMATION: / Ceres Seq. ID 1573923

(2) INFORMATION FOR SEQ ID NO:2664:

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1211

(D) OTHER INFORMATION: / Ceres Seq. ID 1573941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| aaaagcaaca  | tgaagacaa   | ttcaagctgg  | tcttgttctt  | gttcttggtc  | ttcgtggaaa | 60   |
| atatgtttgt  | tgtctgttct  | ctttctcacc  | gagacgatca  | ccgccgtgaa  | gctgccgcca | 120  |
| aaattgatta  | ttccggctgt  | aatcgctttc  | ggagactcca  | tcgtcgacac  | aggaatgaac | 180  |
| aacaatgtca  | aaaccgtggt  | taagtgtgat  | tttcttcctt  | atgggtatcaa | tttccaaagc | 240  |
| ggagttgccca | cggggagatt  | ctgcgatgga  | cgagtcacctg | ccgatttgct  | agccgaagaa | 300  |
| ctgggaataa  | aatcaattgt  | accagcatatc | ctagatccga  | atctaaaatc  | gaaagatctt | 360  |
| ttaaccggtg  | tatcgtttgc  | gtccggaggt  | tctgtttatg  | atcctataac  | accgaaactt | 420  |
| gtggcagtaa  | tatcattaga  | agatcaattg  | agttatttcg  | aggagtacat  | agagaaagtg | 480  |
| aagaatatag  | ttggggaagc  | aagaaaagac  | ttcatagtag  | ccaacagctt  | attcttattg | 540  |
| gtcgcaggca  | gcgacgacat  | agccaatata  | tactatactc  | tacgtgcaag  | acctgaatac | 600  |
| gacgtcgatt  | catacactac  | tcttatgtct  | gactctgcct  | cagaatttgt  | gactaaacta | 660  |
| tatggatatg  | gagtgagaag  | agtagctgtg  | tttgggtgcac | caccaattgg  | gtgtgtacca | 720  |
| tcacagagaa  | cgttaggagg  | aggtatcttg  | agagattgtg  | ctgataatta  | caacgaagca | 780  |
| gcaaaaacttt | ttaattcaaa  | gctctcccca  | aaattggatt  | cgttgcgtaa  | aaccctaccg | 840  |
| ggcatcaaac  | cgatctacat  | taatatctat  | gatcctcttt  | ttgacatcat  | ccagaatcct | 900  |
| gcaaatattg  | ggtttgaagt  | gtctaataaa  | ggatgctgtg  | gaacaggagc  | catagaagtt | 960  |
| gctgtgtttg  | gcaataaaaat | cacatcttct  | gtatgtcccg  | acgtgtctac  | tcatgtgttt | 1020 |
| tgggacagNt  | tatcatccta  | cagagaaaac  | ttacaaaagta | ttagtctcac  | tgttgattaa | 1080 |
| caaatttgtt  | aatcagttcg  | tctgaattaa  | aaactatttt  | cacggcataa  | tgattgatta | 1140 |
| tattttatct  | catcttgttt  | gtattatttg  | ataattgtat  | tcgattttaa  | taaaattaat | 1200 |
| attttcttgt  | t           |             |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1573942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Asn | Met | Lys | Asp | Asn | Ser | Ser | Trp | Ser | Cys | Ser | Trp |     |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ser | Ser | Trp | Lys | Ile | Cys | Leu | Leu | Ser | Val | Leu | Phe | Leu | Thr | Glu |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |
| Ile | Thr | Ala | Val | Lys | Leu | Pro | Pro | Lys | Leu | Ile | Ile | Pro | Ala | Val |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |
| Ala | Phe | Gly | Asp | Ser | Ile | Val | Asp | Thr | Gly | Met | Asn | Asn | Val | Lys |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |
| Thr | Val | Val | Lys | Cys | Asp | Phe | Leu | Pro | Tyr | Gly | Ile | Asn | Phe | Gln |
|     |     |     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     | 80  |
| Gly | Val | Ala | Thr | Gly | Arg | Phe | Cys | Asp | Gly | Arg | Val | Pro | Ala | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     |
| Leu | Ala | Glu | Glu | Leu | Gly | Ile | Lys | Ser | Ile | Val | Pro | Ala | Tyr | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |
| Pro | Asn | Leu | Lys | Ser | Lys | Asp | Leu | Leu | Thr | Gly | Val | Ser | Phe | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     |     |
| Gly | Gly | Ser | Gly | Tyr | Asp | Pro | Ile | Thr | Pro | Lys | Leu | Val | Ala | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |
|     |     |     | 130 |     |     |     |     |     | 135 |     |     |     |     |     |
| Ser | Leu | Glu | Asp | Gln | Leu | Ser | Tyr | Phe | Glu | Glu | Tyr | Ile | Glu | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |
|     |     |     | 145 |     |     |     |     |     | 150 |     |     |     |     |     |
| Lys | Asn | Ile | Val | Gly | Glu | Ala | Arg | Lys | Asp | Phe | Ile | Val | Ala | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |
| Leu | Phe | Leu | Leu | Val | Ala | Gly | Ser | Asp | Asp | Ile | Ala | Asn | Thr | Tyr |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(1X) FEATURE.  
(A) NAME

(A) NAME/REF: peptide  
(B) LOCATION: 1-356

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2666:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:2000:  
Iys Asp Asp Ser Ser Trp Ser Cys Ser Cys Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Asn | Ser | Ser | Tyr | Ser | Cys | Ser | Cys | Ser | Tyr | Ser | Ser | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ile | Cys | Leu | Leu | Ser | Val | Leu | Phe | Leu | Thr | Glu | Thr | Ile | Thr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Leu | Pro | Pro | Lys | Leu | Ile | Ile | Pro | Ala | Val | Ile | Ala | Phe | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | Ile | Val | Asp | Thr | Gly | Met | Asn | Asn | Asn | Val | Lys | Thr | Val | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Cys | Asp | Phe | Leu | Pro | Tyr | Gly | Ile | Asn | Phe | Gln | Ser | Gly | Val | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Gly | Arg | Phe | Cys | Asp | Gly | Arg | Val | Pro | Ala | Asp | Leu | Leu | Ala | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Leu | Gly | Ile | Lys | Ser | Ile | Val | Pro | Ala | Tyr | Leu | Asp | Pro | Asn | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Ser | Lys | Asp | Leu | Leu | Thr | Gly | Val | Ser | Phe | Ala | Ser | Gly | Gly | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Tyr | Asp | Pro | Ile | Thr | Pro | Lys | Leu | Val | Ala | Val | Ile | Ser | Leu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Gln | Leu | Ser | Tyr | Phe | Glu | Glu | Tyr | Ile | Glu | Lys | Val | Lys | Asn | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Gly | Glu | Ala | Arg | Lys | Asp | Phe | Ile | Val | Ala | Asn | Ser | Leu | Phe | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Val | Ala | Gly | Ser | Asp | Asp | Ile | Ala | Asn | Thr | Tyr | Tyr | Thr | Leu | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Arg | Pro | Glu | Tyr | Asp | Val | Asp | Ser | Tyr | Thr | Thr | Leu | Met | Ser | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Asn | Asn | Val | Lys | Thr | Val | Val | Lys | Cys | Asp | Phe | Leu | Pro | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ile | Asn | Phe | Gln | Ser | Gly | Val | Ala | Thr | Gly | Arg | Phe | Cys | Asp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Pro | Ala | Asp | Leu | Leu | Ala | Glu | Glu | Leu | Gly | Ile | Lys | Ser | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Pro | Ala | Tyr | Leu | Asp | Pro | Asn | Leu | Lys | Ser | Lys | Asp | Leu | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Val | Ser | Phe | Ala | Ser | Gly | Gly | Ser | Gly | Tyr | Asp | Pro | Ile | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Leu | Val | Ala | Val | Ile | Ser | Leu | Glu | Asp | Gln | Leu | Ser | Tyr | Phe | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Tyr | Ile | Glu | Lys | Val | Lys | Asn | Ile | Val | Gly | Glu | Ala | Arg | Lys | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ile | Val | Ala | Asn | Ser | Leu | Phe | Leu | Leu | Val | Ala | Gly | Ser | Asp | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Asn | Thr | Tyr | Tyr | Thr | Leu | Arg | Ala | Arg | Pro | Glu | Tyr | Asp | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ser | Tyr | Thr | Thr | Leu | Met | Ser | Asp | Ser | Ala | Ser | Glu | Phe | Val | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Leu | Tyr | Gly | Tyr | Gly | Val | Arg | Arg | Val | Ala | Val | Phe | Gly | Ala | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ile | Gly | Cys | Val | Pro | Ser | Gln | Arg | Thr | Leu | Gly | Gly | Gly | Ile | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Asp | Cys | Ala | Asp | Asn | Tyr | Asn | Glu | Ala | Ala | Lys | Leu | Phe | Asn | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Leu | Ser | Pro | Lys | Leu | Asp | Ser | Leu | Arg | Lys | Thr | Leu | Pro | Gly | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Pro | Ile | Tyr | Ile | Asn | Ile | Tyr | Asp | Pro | Leu | Phe | Asp | Ile | Ile | Gln |

(2) INFORMATION FOR SEQ ID NO:2668:

(A) LENGTH: 1257 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1257

SEQUENCE DESCRIPTION: SEQ ID NO:2668:

| (A1) SEQUENCE DESCRIPTION FILE |             |             |            |            |             |      |
|--------------------------------|-------------|-------------|------------|------------|-------------|------|
| gtaaatctcaa                    | tcacaaacta  | tttccccctt  | tcgttcacat | aatcctcaag | agaaaaaaaa  | 60   |
| aatccccaaa                     | agcttctctc  | aaaccctaac  | acagatctct | cgatcttctc | cgatctgtct  | 120  |
| ttttctccta                     | tctggtttag  | tttgatttaa  | ttggattgaa | gatgtcagac | gctttgaata  | 180  |
| tgactcttga                     | tgaaattgtg  | aagaagagta  | agagtgaag  | gtctgcagct | gcaagggtctg | 240  |
| gaggtaaagg                     | agtttcccg   | aagagtggac  | gtggacgtgg | tggacctaat | ggtgttgtag  | 300  |
| gagctggaag                     | aggaggtgga  | cctgttcgta  | gaggtctct  | tgctgttaat | actcggccat  | 360  |
| catcatcctt                     | ctccataaac  | aagcttgccc  | gcaGgaagag | gagcttgcca | tggcagaatc  | 420  |
| agaatgattt                     | gtatgaagaa  | acccttagag  | ctgttggggt | gtcaggagtg | gaagtcgga   | 480  |
| ccacagttta                     | tattaccaac  | cttgatcagg  | gagtgacaaa | tgaagatata | agggaactct  | 540  |
| atgctgagat                     | tggagagctG  | Raaagatatg  | caattcacta | tgacaaaaat | gggcgtocaa  | 600  |
| gtggaatcgg                     | tgaagttgtg  | tatatgagaa  | gaagtgatgc | aattcaagct | atgaggaaat  | 660  |
| acaTacaatg                     | tacttttggg  | tgggaaggcct | atgaaactgg | agattctggg | tggaaagtact | 720  |
| gaatctgtct                     | ctgtgcgacg  | ctgtgttaat  | gtgactggat | tgaagtgaag | gatgaagagg  | 780  |
| agtgtcttca                     | ttggacaagg  | agttagagg   | gggagagtag | gaagaggaag | aggttcagg   | 840  |
| ccttctggaa                     | gacgccttc   | agtccaacaa  | aaccaacaag | gtggtcgagg | tggtcgaggc  | 900  |
| ggggtccgtg                     | gtagaggcag  | aggtgctgg   | ggaggcagag | ggaataaaa  | tggtggccga  | 960  |
| ggtggaaaga                     | agccgggtga  | gaagtctgct  | gcgatctcg  | acaaagatct | cgaaagctat  | 1020 |
| catgctgaag                     | ctatgaacat  | ctcttaaagc  | aagactctcg | atcttgtcat | gtacttttgt  | 1080 |
| gttctttatt                     | cgtagctctct | gactaaatat  | gtgccaaagt | ctggtttggt | ttaattacgt  | 1140 |
| ttaggatggc                     | tctactctgc  | tttcgttttc  | ctcttttctt | gtttcacact | ttcacagtca  | 1200 |
| cttttggtta                     | ttgaagttaa  | aaagagattta | gctgtaaatg | agaaagctgt | tcttgtt     |      |

(2) INFORMATION FOR SEQ ID NO:2669:

(A) LENGTH: 186 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asp | Ala | Leu | Asn | Met | Thr | Leu | Asp | Glu | Ile | Val | Lys | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Glu | Arg | Ser | Ala | Ala | Ala | Arg | Ser | Gly | Gly | Lys | Gly | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Lys | Ser | Gly | Arg | Gly | Arg | Gly | Gly | Pro | Asn | Gly | Val | Val | Gly | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Arg | Gly | Gly | Gly | Pro | Val | Arg | Arg | Gly | Pro | Leu | Ala | Val | Asn | Thr |

50 55 60  
Arg Pro Ser Ser Ser Phe Ser Ile Asn Lys Leu Ala Arg Arg Lys Arg  
65 70 75 80  
Ser Leu Pro Trp Gln Asn Gln Asn Asp Leu Tyr Glu Glu Thr Leu Arg  
85 90 95  
Ala Val Gly Val Ser Gly Val Glu Val Gly Thr Thr Val Tyr Ile Thr  
100 105 110  
Asn Leu Asp Gln Gly Val Thr Asn Glu Asp Ile Arg Glu Leu Tyr Ala  
115 120 125  
Glu Ile Gly Glu Leu Xaa Arg Tyr Ala Ile His Tyr Asp Lys Asn Gly  
130 135 140  
Arg Pro Ser Gly Ser Ala Glu Val Val Tyr Met Arg Arg Ser Asp Ala  
145 150 155 160  
Ile Gln Ala Met Arg Lys Tyr Ile Gln Cys Thr Phe Gly Trp Lys Ala  
165 170 175  
Tyr Glu Thr Gly Asp Ser Gly Trp Lys Tyr  
180 185

(2) INFORMATION FOR SEQ ID NO:2670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

Met Thr Leu Asp Glu Ile Val Lys Lys Ser Lys Ser Glu Arg Ser Ala  
1 5 10 15  
Ala Ala Arg Ser Gly Gly Lys Gly Val Ser Arg Lys Ser Gly Arg Gly  
20 25 30  
Arg Gly Gly Pro Asn Gly Val Val Gly Ala Gly Arg Gly Gly Gly Pro  
35 40 45  
Val Arg Arg Gly Pro Leu Ala Val Asn Thr Arg Pro Ser Ser Ser Phe  
50 55 60  
Ser Ile Asn Lys Leu Ala Arg Arg Lys Arg Ser Leu Pro Trp Gln Asn  
65 70 75 80  
Gln Asn Asp Leu Tyr Glu Glu Thr Leu Arg Ala Val Gly Val Ser Gly  
85 90 95  
Val Glu Val Gly Thr Thr Val Tyr Ile Thr Asn Leu Asp Gln Gly Val  
100 105 110  
Thr Asn Glu Asp Ile Arg Glu Leu Tyr Ala Glu Ile Gly Glu Leu Xaa  
115 120 125  
Arg Tyr Ala Ile His Tyr Asp Lys Asn Gly Arg Pro Ser Gly Ser Ala  
130 135 140  
Glu Val Val Tyr Met Arg Arg Ser Asp Ala Ile Gln Ala Met Arg Lys  
145 150 155 160  
Tyr Ile Gln Cys Thr Phe Gly Trp Lys Ala Tyr Glu Thr Gly Asp Ser  
165 170 175  
Gly Trp Lys Tyr  
180

(2) INFORMATION FOR SEQ ID NO:2671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..118  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

Met Lys Leu Glu Ile Leu Gly Gly Ser Thr Glu Ser Ala Pro Val Ala  
1 5 10 15  
Ala Arg Val Asn Val Thr Gly Leu Asn Gly Arg Met Lys Arg Ser Val  
20 25 30  
Phe Ile Gly Gln Gly Val Arg Gly Gly Arg Val Gly Arg Gly Arg Gly  
35 40 45  
Ser Gly Pro Ser Gly Arg Arg Leu Pro Val Gln Gln Asn Gln Gln Gly  
50 55 60  
Gly Arg Gly Gly Arg Gly Gly Val Arg Gly Arg Gly Arg Gly Ala Gly  
65 70 75 80  
Gly Gly Arg Gly Asn Lys Ser Gly Gly Arg Gly Gly Lys Lys Pro Val  
85 90 95  
Glu Lys Ser Ala Ala Asp Leu Asp Lys Asp Leu Glu Ser Tyr His Ala  
100 105 110  
Glu Ala Met Asn Ile Ser  
115

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..600  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

ggatcatata ttgtctgtat gaggcattgtt tcagcacaag gccaaagcaaa gcaggggatg 60  
agcagttgaa cttgttccgt ttccctcttc ttgtagctcc catcaagtgc acgggtttcc 120  
cgcttgttca gaaccaacaa ttcgaggaag cagccaaagt tatttccaag gaactgcct 180  
ctgtcggtat ctcccataag attgacatca ctggtacatc gatagggaag agatatgcga 240  
gaaccgatga gcttgaggatg ccatttgcaa taacagtggga ctcgatataca tcagtgcaca 300  
tcagagaaaag agacagcaaa gatcaagtcc gagtcacctt gaaggaggca gcttccgttg 360  
tgagctcagt ctccagagggg aaaatgacgt ggcaagacgt ctgggcaacc ttccctcacc 420  
attcttctgc ttctgcagac gaggtagctag ctcccttggtt ttttccGgaa ttaaaaacca 480  
aagtgttaaa ttaattgttg ctgaatctac tcatttttaa tgttttgttt cttagtgtca 540  
cgtaaaaagt tcgataccag atttgtagac gaagyggtta taaagtataa actctctgtc 600

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

Ile Ile Tyr Cys Leu Tyr Glu His Cys Phe Ser Thr Arg Pro Ser Lys  
1 5 10 15  
Ala Gly Asp Glu Gln Leu Asn Leu Phe Arg Phe Pro Pro Leu Val Ala  
20 25 30  
Pro Ile Lys Cys Thr Val Phe Pro Leu Val Gln Asn Gln Gln Phe Glu  
35 40 45



Glu Ala Ala Lys Val Ile Ser Lys Glu Leu Ala Ser Val Gly Ile Ser  
50 55 60  
His Lys Ile Asp Ile Thr Gly Thr Ser Ile Gly Lys Arg Tyr Ala Arg  
65 70 75 80  
Thr Asp Glu Leu Gly Val Pro Phe Ala Ile Thr Val Asp Ser Asp Thr  
85 90 95  
Ser Val Thr Ile Arg Glu Arg Asp Ser Lys Asp Gln Val Arg Val Thr  
100 105 110  
Leu Lys Glu Ala Ala Ser Val Val Ser Ser Val Ser Glu Gly Lys Met  
115 120 125  
Thr Trp Gln Asp Val Trp Ala Thr Phe Pro His His Ser Ser Ala Ala  
130 135 140  
Ala Asp Glu  
145

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

|             |            |             |            |            |            |      |
|-------------|------------|-------------|------------|------------|------------|------|
| aattgcaaat  | caaatggatc | gtcttaagct  | ttatttctcc | gttttcgttt | tgtctttctt | 60   |
| tatcgctctg  | gtttcgctgt | ctgatgtcaa  | cgacggcgat | gatctcgtga | tccgtcaggt | 120  |
| ggttggtgga  | gccgagcctc | aggttttgac  | ctcagaggat | cacttttctc | tcttcaagcg | 180  |
| gaagttcggg  | aaggtctacg | cttccaacga  | ggagcatgac | tatagattct | cggtttgagt | 240  |
| tccgtaagaa  | gcacttgagg | gttagaagtg  | gctttaagct | tcctaaagat | gccacaagg  | 300  |
| ctccgattct  | ccctaccgaa | aatctccctg  | aggattttga | ttggagagat | catggcgccg | 360  |
| ttactcccg   | caaaaatcag | ggatcttgcg  | gctcttgctg | gagtttcagc | gccactggag | 420  |
| ctttggaagg  | tgctaacttc | ctcgctaccg  | gcagactcgt | cagcctcagc | gaacaacagc | 480  |
| tcgtcgactg  | tgatcacgag | tgtgatcccc  | aggagGcaga | ttTcctgcga | ctctggttgc | 540  |
| aatggtggGc  | taatgaacac | cgcttttgaa  | tacaccCtca | aaaccggagg | gctcatgaaa | 600  |
| gaagaagact  | atccttacac | cggaaggagc  | ggcaagacct | gcaagctaga | caagtccaag | 660  |
| atcgttgcct  | ctgtctccaa | cttcagtgtt  | atctccattg | atgaagaaca | gattgctgca | 720  |
| aaccttgcca  | agaaaggacc | tcttgctgta  | gccatcaacg | ctggctatat | gcagacttac | 780  |
| attggaggag  | tctcatgccc | ttacatatgc  | accaggaggc | tcaaccacgg | tgtcttattg | 840  |
| gttggtctatg | gagcggcgag | ttacgctccg  | gctaggttca | aggagaagcc | ttactggatc | 900  |
| atcaagaact  | cgtggggaga | gacttggggg  | gaaaatgggt | tctacaaaat | ctgcaaaggc | 960  |
| cgtaacattt  | gtggtgttga | cagtatggtc  | tccactgttg | cagccaccgt | ctcaaccacc | 1020 |
| gcccattaag  | catctcgcca | ataagtttta  | attacttttg | tgatttgtat | gagcgagctc | 1080 |
| tctttgcgct  | gctgactctc | tctattttatc | tctgcttctt | gcttgtaaat | aaaatgcgtt | 1140 |
| ctattg      |            |             |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

Met Pro Thr Arg Leu Arg Phe Ser Leu Pro Lys Ile Ser Leu Arg Ile  
1 5 10 15  
Leu Ile Gly Glu Ile Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Leu | Leu | Pro | Ser | Lys | Ile | Arg | Asp | Leu | Ala | Ala | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Ser | Ala | Pro | Leu | Glu | Leu | Trp | Lys | Val | Leu | Thr | Ser | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ala | Asp | Ser | Ser | Ala | Ser | Ala | Asn | Asn | Ser | Ser | Ser | Thr | Val | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ser | Val | Ile | Pro | Arg | Arg | Gln | Ile | Ser | Cys | Asp | Ser | Gly | Cys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Leu | Met | Asn | Ser | Ala | Phe | Glu | Tyr | Thr | Leu | Lys | Thr | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Met | Lys | Glu | Glu | Asp | Tyr | Pro | Tyr | Thr | Gly | Lys | Asp | Gly | Lys | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Lys | Leu | Asp | Lys | Ser | Lys | Ile | Val | Ala | Ser | Val | Ser | Asn | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ile | Ser | Ile | Asp | Glu | Glu | Gln | Ile | Ala | Ala | Asn | Leu | Val | Lys | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Pro | Leu | Ala | Val | Ala | Ile | Asn | Ala | Gly | Tyr | Met | Gln | Thr | Tyr | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Val | Ser | Cys | Pro | Tyr | Ile | Cys | Thr | Arg | Arg | Leu | Asn | His | Gly |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |

Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe  
165 170 175  
Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp  
180 185 190  
Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly  
195 200 205  
Val Asp Ser Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala  
210 215 220

His  
225

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1573958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly Leu Met Lys  
1 5 10 15  
Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr Cys Lys Leu  
20 25 30  
Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser Val Ile Ser  
35 40 45  
Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn Gly Pro Leu  
50 55 60  
Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile Gly Gly Val  
65 70 75 80  
Ser Cys Pro Tyr Ile Cys Thr Arg Arg Leu Asn His Gly Val Leu Leu  
85 90 95  
Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe Lys Glu Lys  
100 105 110  
Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp Gly Glu Asn  
115 120 125  
Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly Val Asp Ser  
130 135 140  
Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala His  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..883

(D) OTHER INFORMATION: / Ceres Seq. ID 1573960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

aaaaaaaaat catcgtgAaa cgttcgaagg ccattttctt tggacgacca tcggcggttaa 60  
ggagagagct tagatctcgt gccgtcgtgc gacgttggtt tccggcttga tcaaaatggg 120  
gttgctcattc ggaaagttgt tcagcaggct ctttgcgaag aaagagatgc gtattctgat 180  
ggttggtctc gatgctgctg gtaagacgac tatctctac aagctcaaac ttggagagat 240  
cgtcaccact attccaacca ttgggttcaa cgttgagact gttgaataga agaacatcag 300  
cttcaccgtg tgggatgttg ggggtcaaga caagatccgt ccattgtgga gacattactt 360  
ccagaacaca cagggactta tctttgttgt ggacagcaat gatcgtgacc gtgttggtga 420

agccagggac gagcttcaca g gatgctgaa tgaggatgaa ttgagggatg cagttctgct 480  
tgtatttgct aacaagcaag atottoccaa cgcgatgaac gctgctgaga taactgacaa 540  
gcttgggctt cattctcttc gtcaacgaca ctggtacatt cagagcacat gtgccacctc 600  
tgagagaagga ctctatgagg gacttgactg gctctccaac aacatcgcaa gcaaggcata 660  
gatggaatgt tagccagatt cctcttctgc ttgtttgggt taaaaatcaa agacagaggt 720  
ctgtttctct agtactaaaa gatttattat tatattcttc ttctgtcact atctcaaacg 780  
cagatcattt tacactttgt acttccctt caataacttg ttacttctct cgtttgcttc 840  
cgaatttgag tatatcattt ttacatctgc ttttcatcaa agc

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1573961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys  
1 5 10 15  
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
20 25 30  
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
35 40 45  
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr  
50 55 60  
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His  
65 70 75 80  
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp  
85 90 95  
Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn  
100 105 110  
Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln  
115 120 125  
Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly  
130 135 140  
Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala  
145 150 155 160  
Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn  
165 170 175  
Ile Ala Ser Lys Ala  
180

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1573962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile  
1 5 10 15  
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile  
20 25 30  
Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val

(2) INFORMATION FOR SEQ ID NO:2681:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1573963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..771

(D) OTHER INFORMATION: / Ceres Seq. ID 1573964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| acaatccaat | caaaacacac | agagagaaga | aaaactcaga | agaaaagcca  | aagagtgaaa  | 60  |
| caaaaatggc | gtcgacgact | ctctcaatcg | caacaacaat | ccgttcctca  | tcttatccta  | 120 |
| ctctcgcttc | catcaatcac | ttcccttccc | gaaccamcac | catcgaattc  | ccctctcgct  | 180 |
| tcggtggtgg | ttcatcatcc | acattgaccc | accgtgcaac | ccatctccgt  | ccaatcgccg  | 240 |
| ccgtcgaagc | tccggagaaa | atcgagaaga | tcggatccga | aatctcatcc  | ctaaccctcg  | 300 |
| aagaagctcg | tatcctcgtc | gactatctcc | aagacaaatt | cgggtgtctcc | ccactctctt  | 360 |
| tagCccccgc | agcagcGgcg | gttgctgctc | cagccgacgg | tggcgcggcg  | gctgtagtgg  | 420 |
| aagagcaaac | agagttcgat | gtggttatca | atgaagttcc | cagcagttcc  | cgtattgcag  | 480 |
| tgattaaagc | tgttagggct | ttaactagct | tggcgttgaa | ggaagctaag  | gagctaatac  | 540 |
| aaggattacc | aaagaagttt | aaagaaggta | tcactaaaga | tgaagctgaa  | gaagctaaga  | 600 |
| agactcttga | agaagctggg | gctaaagtct | ccattgctta | aggtttttat  | taaaaaaaaaa | 660 |
| aaagaagttg | ttatcttttc | tgggaatttg | ttgggtcttt | gtgttggtta  | gtatagtttg  | 720 |
| cgcttggaat | tgttgagaaa | ttgttgtaat | ttgaatcaca | tttggtttcc  | c           |     |

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1573965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Ile | Lys | Thr | His | Arg | Glu | Lys | Lys | Asn | Ser | Glu | Glu | Lys | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Lys | Ser | Glu | Thr | Lys | Met | Ala | Ser | Thr | Thr | Leu | Ser | Ile | Ala | Thr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Arg | Ser | Ser | Ser | Tyr | Pro | Thr | Leu | Ala | Ser | Ile | Asn | His | Phe | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Arg | Thr | Xaa | Thr | Ile | Glu | Phe | Pro | Ser | Arg | Phe | Gly | Gly | Gly | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Ser | Thr | Leu | Thr | His | Arg | Ala | Thr | His | Leu | Arg | Pro | Ile | Ala | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Glu | Ala | Pro | Glu | Lys | Ile | Glu | Lys | Ile | Gly | Ser | Glu | Ile | Ser | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Thr | Leu | Glu | Glu | Ala | Arg | Ile | Leu | Val | Asp | Tyr | Leu | Gln | Asp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Val | Ser | Pro | Leu | Ser | Leu | Ala | Pro | Ala | Ala | Ala | Ala | Val | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Ala | Asp | Gly | Gly | Ala | Ala | Ala | Val | Val | Glu | Gln | Thr | Glu |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Asp | Val | Val | Ile | Asn | Glu | Val | Pro | Ser | Ser | Ser | Arg | Ile | Ala | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Lys | Ala | Val | Arg | Ala | Leu | Thr | Ser | Leu | Ala | Leu | Lys | Glu | Ala | Lys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Leu | Ile | Glu | Gly | Leu | Pro | Lys | Lys | Phe | Lys | Glu | Gly | Ile | Thr | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Glu | Ala | Glu | Glu | Ala | Lys | Lys | Thr | Leu | Glu | Glu | Ala | Gly | Ala | Lys |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Ser | Ile | Ala |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..191  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573966  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser  
1                    5                    10                    15  
Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro Ser Arg Thr Xaa Thr  
                    20                    25                    30  
Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser Ser Ser Thr Leu Thr  
                    35                    40                    45  
His Arg Ala Thr His Leu Arg Pro Ile Ala Ala Val Glu Ala Pro Glu  
                    50                    55                    60  
Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu  
65                    70                    75                    80  
Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro  
                    85                    90                    95  
Leu Ser Leu Ala Pro Ala Ala Ala Val Ala Ala Pro Ala Asp Gly  
                    100                    105                    110  
Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile  
                    115                    120                    125  
Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg  
                    130                    135                    140  
Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly  
145                    150                    155                    160  
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu  
                    165                    170                    175  
Ala Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala  
                    180                    185                    190

- (2) INFORMATION FOR SEQ ID NO:2685:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 547 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..547  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573980

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ttttccagaa atctctcact atcgccatcg atttttagcag acattgaaga agatgggagt | 60  |
| attcacattc gtatgcaaga atggaggcgg cgcgtggagc gcGaagCaac acgaaggaga  | 120 |
| aottgaatct tcagcttctt ctacctacga gctccagcgt aagCtcgttc aggtatctct  | 180 |
| ctccgctgat tcctccggtg gcgttcagtc ttcgttttct cttgtctccc ctacctccgc  | 240 |
| cgtattccag gtaattggtg gtggtggtgg tggaggagga ttctctgctg gaggagctgc  | 300 |
| ctcaagtgga ggtggtgctg gtgaagctgc agctgccct aaggaagatg agaagaagaa   | 360 |
| agaagaatca gaagaggaag aggagacttc ggattcgatc tcttttggtta agattgaaat | 420 |
| agtatttttg aggtgttggt ttgagctttc catttttgtg tggggtgttt cttccattgt  | 480 |
| caagtgtgat atgctacact gctttcaata atatttcgtg agtaatgaca agtttctctt  | 540 |
| tcgatcc                                                            |     |

- (2) INFORMATION FOR SEQ ID NO:2686:

- (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 152 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1573981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:

Met Gly Val Phe Thr Phe Val Cys Lys Asn Gly Gly Gly Ala Trp Ser  
1 5 10 15  
Ala Lys Gln His Glu Gly Glu Leu Glu Ser Ser Ala Ser Ser Thr Tyr  
20 25 30  
Glu Leu Gln Arg Lys Leu Val Gln Val Ser Leu Ser Ala Asp Ser Ser  
35 40 45  
Gly Gly Val Gln Ser Ser Phe Ser Leu Val Ser Pro Thr Ser Ala Val  
50 55 60  
Phe Gln Val Ile Val Gly Gly Gly Gly Gly Gly Phe Ser Ala Gly  
65 70 75 80  
Gly Ala Ala Ser Ser Gly Gly Gly Ala Gly Glu Ala Ala Ala Ala Pro  
85 90 95  
Lys Glu Asp Glu Lys Lys Lys Glu Glu Ser Glu Glu Glu Glu Glu Thr  
100 105 110  
Ser Asp Ser Ile Ser Leu Val Lys Ile Glu Ile Val Phe Trp Arg Cys  
115 120 125  
Trp Phe Glu Leu Ser Ile Phe Val Trp Gly Val Ser Ser Ile Val Lys  
130 135 140  
Cys Asp Met Leu His Cys Phe Gln  
145 150

(2) INFORMATION FOR SEQ ID NO:2687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..727

(D) OTHER INFORMATION: / Ceres Seq. ID 1573982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:

aacataagtc tctctcttac attttgaaac cctaatttct caaaaaaat gtctgaagtt 60  
gagtaccggt gctttgtcgg cggccttgcc tgggccacca atgatgaaga tcttcaaagg 120  
acgttctcac agttcggcga cgttatcgat tctaagatca ttaacgaccg cgagagtggg 180  
agatcaagg gattcggatt cgtcaccttc aaggacgaga aagccatgag ggatgcgatt 240  
gaagagatga acggtaaaga gctcgatgga cgtgtcatca ccgtgaacga ggctcagtcg 300  
agaggtagcg gcggtggcgg aggaggccgt ggtggaagcg gtggtggtta ccgcagcgga 360  
ggcggtggtg gatactcagg aggcggtggc gccggatact caggaggagg cggtggtggt 420  
tacgagagac gtagcggagg ttacggatct ggtggaggcg gtggtggccg aggatacggg 480  
ggtggtggac gccgtgaggg aggtggctac ggaggcgggt atggtMggaa gttacggcgg 540  
cggtggtggc sgctggtaat caaagataga gttgtttgcg tgctgctgct ctgtttttgg 600  
tttagatttg gatttgtgtc accacttctg gtttggttat cgttcgtttg gtttactttt 660  
ttgatgaaac agtttcggtt aagtcttctt tgtctggatc gaaatgttaa ttcgcgtggt 720  
gtttacc

(2) INFORMATION FOR SEQ ID NO:2688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1573983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

Met Ser Glu Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala Trp Ala

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[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME

(B) LOCATION: 1..167

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2689:

Arg Asp Ala Ile Glu Glu Met Asn Gly Lys Gl

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Val | Ile | Thr | Val | Asn | Glu | Ala | Gln | Ser | Arg | Gly | Ser | Gly | Gly | Gly | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Gly | Gly | Arg | Gly | Gly | Ser | Gly | Gly | Gly | Tyr | Arg | Ser | Gly | Gly | Gly | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Tyr | Ser | Gly | Gly | Gly | Gly | Gly | Gly | Tyr | Ser | Gly | Gly | Gly | Gly | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Tyr | Glu | Arg | Arg | Ser | Gly | Gly | Tyr | Gly | Ser | Gly | Gly | Gly | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Gly | Arg | Gly | Tyr | Gly | Gly | Gly | Gly | Arg | Arg | Glu | Gly | Gly | Gly | Tyr | Gly |
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |
| Gly | Gly | Asp | Gly | Xaa | Lys | Leu | Arg | Arg | Arg | Trp | Trp | Xaa | Leu | Val | Ile |
|     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |     |
| Lys | Asp | Arg | Val | Val | Cys | Val | Leu | Leu | Leu | Cys | Phe | Trp | Phe | Arg | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Gly | Phe | Val | Ser | Pro | Leu | Leu | Val | Trp | Leu | Ser | Phe | Val | Trp | Phe | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Phe | Leu | Met | Lys | Gln | Phe | Arg | Leu | Ser | Leu | Leu | Cys | Leu | Asp | Arg | Asn |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |

Val Asn Ser Arg Val Val Tyr  
165

(2) INFORMATION FOR SEQ ID NO:2690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn Glu Ala  
1 5 10 15  
Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly Arg Gly Gly Ser Gly  
20 25 30  
Gly Gly Tyr Arg Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly  
35 40 45  
Gly Gly Tyr Ser Gly Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly  
50 55 60  
Gly Tyr Gly Ser Gly Gly Gly Gly Gly Arg Gly Tyr Gly Gly Gly  
65 70 75 80  
Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Asp Gly Xaa Lys Leu  
85 90 95  
Arg Arg Arg Trp Trp Xaa Leu Val Ile Lys Asp Arg Val Val Cys Val  
100 105 110  
Leu Leu Leu Cys Phe Trp Phe Arg Phe Gly Phe Val Ser Pro Leu Leu  
115 120 125  
Val Trp Leu Ser Phe Val Trp Phe Thr Phe Leu Met Lys Gln Phe Arg  
130 135 140  
Leu Ser Leu Leu Cys Leu Asp Arg Asn Val Asn Ser Arg Val Val Tyr  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..954
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

aacaaaaaga ttaaacaag agagaagaat atggcgagag ggaagatcca gatcaagagg 60  
atagagaacc agacaaacag acaagtgcgc tattcaaaga gaagaaatgg ttatttcaag 120  
aaagcacatg agctcacggt tttgtgtgat gctagggttt cgattatcat gttctctagc 180  
tccaacaagc ttcattgagta tatcagccct aacaccacaa cgaaggagat cgtagatctg 240  
taccaaaacta tttctgatgt cgatgttttg gccactcaat atgagcgaat gcaagaaacc 300  
aagaggaaac tgttgagagac aaatagaaat ctccggactc agatcaagca gaggctaggt 360  
gagtgttttg acaagcttga cattcaggag ctgcgtcgtc ttgaggatga aatggaaaac 420  
actttcaaac tcgttcgcga gcgcaagttc aaatctcttg ggaatcagat cgagaccacc 480  
aagaaaaaga acaaaagtca acaagacata caaaagaatc tcatacatga gctaactaag 540  
agctgaagat cctcactatg gactagtaga caatggagga gattacgact cagttcttgg 600  
ataccaaatc gaagggtcac gtGcttacgc tcttcgtttc caccagaacc atcaccacta 660  
ttacccaac catggccttc atgcaccctc tgcctctgac atcattacct tccatcttct 720  
tgaataatta aaggctaaaa ggtttgctgg tgccatcatt gtctatctaa ttatttagta 780

actactttaaa acataaggca tgggtgttgct aaaaccttaa actgtcatgt ttcttagtta 840  
tgtatttttaa agcctaaaga aatatggatt gtgtgatcag tagtgcttag gcttattgtg 900  
tgtggaatgt tttcaagact tttatcatgt atcgtattat tatattgacc accc

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

Asn Lys Lys Ile Lys Gln Arg Glu Lys Asn Met Ala Arg Gly Lys Ile  
1 5 10 15  
Gln Ile Lys Arg Ile Glu Asn Gln Thr Asn Arg Gln Val Thr Tyr Ser  
20 25 30  
Lys Arg Arg Asn Gly Leu Phe Lys Lys Ala His Glu Leu Thr Val Leu  
35 40 45  
Cys Asp Ala Arg Val Ser Ile Ile Met Phe Ser Ser Ser Asn Lys Leu  
50 55 60  
His Glu Tyr Ile Ser Pro Asn Thr Thr Thr Lys Glu Ile Val Asp Leu  
65 70 75 80  
Tyr Gln Thr Ile Ser Asp Val Asp Val Trp Ala Thr Gln Tyr Glu Arg  
85 90 95  
Met Gln Glu Thr Lys Arg Lys Leu Leu Glu Thr Asn Arg Asn Leu Arg  
100 105 110  
Thr Gln Ile Lys Lys Gln Arg Leu Gly Glu Cys Leu Asp Lys Leu Asp Ile  
115 120 125  
Gln Glu Leu Arg Arg Leu Glu Asp Glu Met Glu Asn Thr Phe Lys Leu  
130 135 140  
Val Arg Glu Arg Lys Phe Lys Ser Leu Gly Asn Gln Ile Glu Thr Thr  
145 150 155 160  
Lys Lys Lys Asn Lys Ser Gln Gln Asp Ile Gln Lys Asn Leu Ile His  
165 170 175  
Glu Leu Thr Lys Ser  
180

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:

Met Ala Arg Gly Lys Ile Gln Ile Lys Arg Ile Glu Asn Gln Thr Asn  
1 5 10 15  
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Leu Phe Lys Lys Ala  
20 25 30  
His Glu Leu Thr Val Leu Cys Asp Ala Arg Val Ser Ile Ile Met Phe  
35 40 45  
Ser Ser Ser Asn Lys Leu His Glu Tyr Ile Ser Pro Asn Thr Thr Thr  
50 55 60  
Lys Glu Ile Val Asp Leu Tyr Gln Thr Ile Ser Asp Val Asp Val Trp  
65 70 75 80

Ala Thr Gln Tyr Glu Arg Met Gln Glu Thr Lys Arg Lys Leu Leu Glu  
85 90 95  
Thr Asn Arg Asn Leu Arg Thr Gln Ile Lys Gln Arg Leu Gly Glu Cys  
100 105 110  
Leu Asp Lys Leu Asp Ile Gln Glu Leu Arg Arg Leu Glu Asp Glu Met  
115 120 125  
Glu Asn Thr Phe Lys Leu Val Arg Glu Arg Lys Phe Lys Ser Leu Gly  
130 135 140  
Asn Gln Ile Glu Thr Thr Lys Lys Lys Asn Lys Ser Gln Gln Asp Ile  
145 150 155 160  
Gln Lys Asn Leu Ile His Glu Leu Thr Lys Ser  
165 170

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Met Phe Ser Ser Ser Asn Lys Leu His Glu Tyr Ile Ser Pro Asn Thr  
1 5 10 15  
Thr Thr Lys Glu Ile Val Asp Leu Tyr Gln Thr Ile Ser Asp Val Asp  
20 25 30  
Val Trp Ala Thr Gln Tyr Glu Arg Met Gln Glu Thr Lys Arg Lys Leu  
35 40 45  
Leu Glu Thr Asn Arg Asn Leu Arg Thr Gln Ile Lys Gln Arg Leu Gly  
50 55 60  
Glu Cys Leu Asp Lys Leu Asp Ile Gln Glu Leu Arg Arg Leu Glu Asp  
65 70 75 80  
Glu Met Glu Asn Thr Phe Lys Leu Val Arg Glu Arg Lys Phe Lys Ser  
85 90 95  
Leu Gly Asn Gln Ile Glu Thr Thr Lys Lys Asn Lys Ser Gln Gln  
100 105 110  
Asp Ile Gln Lys Asn Leu Ile His Glu Leu Thr Lys Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ataccaataa gcaatttgct cattagagaa cagagaaaaa aaaaaaaciaa tggcaactca | 60  |
| agccgcgggg atcttcaact ccgccataac aaccgcccga acctccggcg tcaagaaact  | 120 |
| ccactttttc tcaacaaccc accgtcccaa atccctctcc ttcacaaaaa ccgcaatccg  | 180 |
| cgccgagaaa acagattcct ccgcccgcgc tgctgcagcc cccgccacga aagaagctcc  | 240 |
| cgtgggattc acgccaccgc agctagacc aaacacaccg tctccgatct tcgctggaag   | 300 |
| caccggtggt cttctacgta aagcgcaagt ggaagagttc tacgttatca cgtggaactc  | 360 |
| accgaaagaa cagatctttg agatgccgac aggaggagca gcatcatga gagaaggccc   | 420 |
| gaatcttctg aagctagcga ggaaagagca gtgttttagct ttggggacaa ggcttagatc | 480 |
| caagtacaag atcaattacc agttttacag agtgtttcct aacggtgagg ttcaatatct  | 540 |

tcatacctaaa gatggtgttt atccagagaa ggccaatcca ggaagagaag gtgttggtct 600  
caacatgaga tctattggga aaaatgttag tccattgaa gtttaagttta ctggcaaaca 660  
aagttatgat ttgtaagatc tgtaaactaa aaaaaAccaa aaactatgtg catgtggtga 720  
tgattatgac tatgtttcat gtTaattttt aatggatttt gKttttg

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:

Ile Pro Ile Ser Asn Leu Leu Ile Arg Glu Gln Arg Lys Lys Lys Asn  
1 5 10 15  
Asn Gly Asn Ser Ser Arg Arg Asp Leu Gln Leu Arg His Asn Asn Arg  
20 25 30  
Arg Asn Leu Arg Arg Gln Glu Thr Pro Leu Phe Leu Asn Asn Pro Pro  
35 40 45  
Ser Gln Ile Pro Leu Leu His Gln Asn Arg Asn Pro Arg Arg Glu Asn  
50 55 60  
Arg Phe Leu Arg Arg Arg Cys Cys Ser Pro Arg His Glu Arg Ser Ser  
65 70 75 80  
Arg Gly Ile His Ala Thr Ala Ala Arg Pro Lys His Thr Val Ser Asp  
85 90 95  
Leu Arg Trp Lys His Arg Trp Ser Ser Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:2697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala  
1 5 10 15  
Ala Thr Ser Gly Val Lys Lys Leu His Phe Phe Ser Thr Thr His Arg  
20 25 30  
Pro Lys Ser Leu Ser Phe Thr Lys Thr Ala Ile Arg Ala Glu Lys Thr  
35 40 45  
Asp Ser Ser Ala Ala Ala Ala Ala Ala Pro Ala Thr Lys Glu Ala Pro  
50 55 60  
Val Gly Phe Thr Pro Pro Gln Leu Asp Pro Asn Thr Pro Ser Pro Ile  
65 70 75 80  
Phe Ala Gly Ser Thr Gly Gly Leu Leu Arg Lys Ala Gln Val Glu Glu  
85 90 95  
Phe Tyr Val Ile Thr Trp Asn Ser Pro Lys Glu Gln Ile Phe Glu Met  
100 105 110  
Pro Thr Gly Gly Ala Ala Ile Met Arg Glu Gly Pro Asn Leu Leu Lys  
115 120 125  
Leu Ala Arg Lys Glu Gln Cys Leu Ala Leu Gly Thr Arg Leu Arg Ser  
130 135 140  
Lys Tyr Lys Ile Thr Tyr Gln Phe Tyr Arg Val Phe Pro Asn Gly Glu

145 150 155 160  
Val Gln Tyr Leu His Pro Lys Asp Gly Val Tyr Pro Glu Lys Ala Asn  
165 170 175  
Pro Gly Arg Glu Gly Val Gly Leu Asn Met Arg Ser Ile Gly Lys Asn  
180 185 190  
Val Ser Pro Ile Glu Val Lys Phe Thr Gly Lys Gln Ser Tyr Asp Leu  
195 200 205

(2) INFORMATION FOR SEQ ID NO:2698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..800
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

taatttagga gaagagcaac cggtgaaacg tacggcgagt ggtgggtggtg gtgtctcgac 60  
tggtctgtat atgagtcctcg gaagtcctac gggatctgac gtcagcgagc aatctagtgg 120  
tggtgcacac gtgttttaaac caacgggttag atctgaggtt acagcgatcat cgtctggtga 180  
agatcctcca acttatctta gtttgtctct tccttggaact gacgagacgg ttcgagtcaa 240  
cgagccgggtt caacttaacc agaatacggg tatggacggg ggttatacgg cggaGctggt 300  
tccgggttaga aaggaagagc aagtggaaagt agaagaagaa gaagcgaaaag ggatatctgg 360  
tggtatcggt ggtgagttca tgacgggtggt tcaggagatg ataaggacgg aggtgaggag 420  
ttacatggcg gatttacagc gaggaaacgt cggtggtagt agttctggcg gcggaggtgg 480  
cggttcgtgt atgccacaaa gtgtaaacag ccgtcgtgtt gggtttagag agtttatagt 540  
gaaccagatc ggaattggga agatggagta gagtgataag aacaagtttt ccctctgttt 600  
ctcgggaaaa taaaagtttc aggccttttca tgtatagagc cagtagtaga gacgacgaaa 660  
ggaggaagcg aaatcaaaaa atgttttggt atcatcatca tatgatcttc ttctgtgatt 720  
caattaaaag caaagcaaga tcatttatta acaatttaca caaacttgaa gaagaaaagt 780  
caaaaacact tctcaaactc

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

Asn Leu Gly Glu Glu Gln Pro Leu Lys Arg Thr Ala Ser Gly Gly Gly  
1 5 10 15  
Gly Val Ser Thr Gly Leu Tyr Met Ser Pro Gly Ser Pro Ser Gly Ser  
20 25 30  
Asp Val Ser Glu Gln Ser Ser Gly Ala His Val Phe Lys Pro Thr  
35 40 45  
Val Arg Ser Glu Val Thr Ala Ser Ser Ser Gly Glu Asp Pro Pro Thr  
50 55 60  
Tyr Leu Ser Leu Ser Leu Pro Trp Thr Asp Glu Thr Val Arg Val Asn  
65 70 75 80  
Glu Pro Val Gln Leu Asn Gln Asn Thr Val Met Asp Gly Gly Tyr Thr  
85 90 95  
Ala Glu Leu Phe Pro Val Arg Lys Glu Glu Gln Val Glu Val Glu Glu  
100 105 110

Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe Gly Gly Glu Phe Met Thr  
115 120 125  
Val Val Gln Glu Met Ile Arg Thr Glu Val Arg Ser Tyr Met Ala Asp  
130 135 140  
Leu Gln Arg Gly Asn Val Gly Gly Ser Ser Ser Gly Gly Gly Gly Gly  
145 150 155 160  
Gly Ser Cys Met Pro Gln Ser Val Asn Ser Arg Arg Val Gly Phe Arg  
165 170 175  
Glu Phe Ile Val Asn Gln Ile Gly Ile Gly Lys Met Glu  
180 185

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

Met Ser Pro Gly Ser Pro Ser Gly Ser Asp Val Ser Glu Gln Ser Ser  
1 5 10 15  
Gly Gly Ala His Val Phe Lys Pro Thr Val Arg Ser Glu Val Thr Ala  
20 25 30  
Ser Ser Ser Gly Glu Asp Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro  
35 40 45  
Trp Thr Asp Glu Thr Val Arg Val Asn Glu Pro Val Gln Leu Asn Gln  
50 55 60  
Asn Thr Val Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg  
65 70 75 80  
Lys Glu Glu Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser  
85 90 95  
Gly Gly Phe Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg  
100 105 110  
Thr Glu Val Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly  
115 120 125  
Gly Ser Ser Ser Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser  
130 135 140  
Val Asn Ser Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile  
145 150 155 160  
Gly Ile Gly Lys Met Glu  
165

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1573998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys Glu Glu  
1 5 10 15  
Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe  
20 25 30  
Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg Thr Glu Val

35 40 45  
Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly Ser Ser  
50 55 60  
Ser Gly Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val Asn Ser  
65 70 75 80  
Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly Ile Gly  
85 90 95  
Lys Met Glu

(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

aaaaaagaaa aaaaaactca gagcagagga gatcgagaga gacaaagaga gacaaagaga 60  
gagagagaga gagagagaga gagagagaga gagagatctt caacaagcaa tgtctatatc 120  
catggcggtta ttctctccgc cgatctcttc ctcaactcaa aaccctaata tcatcccca 180  
gatctcaacc tctcttctct ccaccaaacg tttctctcta atctccgtcc ctgagagcttc 240  
ctcogacaat ggtacgactt cccccgtcgt gaaaattccg aagcctgcgt ctgtagctgt 300  
agaggaagtt ccggttaaat ctccggcgga aagctcctcc gcttctgaaa acggcgccgt 360  
tggaggtgaa gcgactgatt cgagtactga gacggaatc aaatatcaaa atgcgaagtg 420  
ggtaaatgga acttgggata tgaaacagtt cgagaaagat ggcaaaactg attgggattc 480  
tgttatcggt tctgaggcaa agaggagaaa atggcttgaa gataaccccg aaacaacgag 540  
taacgaagag cttgttgtct tcgatacttc gattattcca tgggtgggcat ggatgaagag 600  
ataccatcta cctgaagctg aacttctcaa tggctcgtgt gcgatgatag ggttcttcat 660  
ggcttacttt gttgatagtc ttaccggagt aggacttggt gatcaaatgg ggaatttctt 720  
ctgcaaaaca ctcttggttg tggctgtagc tggagttctc ttcatccgta agaatgaaga 780  
tttagacaaa ctttaaggatc tgttcgatga gactacgta tatgacaaac aatggcaagc 840  
tgcattggaaa gagccagatt catcaGacag tttcttcaaa gaagtgaaca agttcttaca 900  
atctttcatt ttcttttttt tgttatgcaa taatctgtga atcagtgaat gtttatctct 960  
actgaactac tgatcttcag attttgtaat ctttctgctt taaaaatctc tatgaagtag 1020  
tctcaaagat aatgtatcga aggtctttga cttgtaaagc agacctatct cggttttgacg 1080  
cttgataatt taatcaataa gagatttttt tttt

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

Lys Lys Lys Lys Lys Leu Arg Ala Glu Glu Ile Glu Arg Asp Lys Glu  
1 5 10 15  
Arg Gln Arg Glu Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp  
20 25 30  
Leu Gln Gln Ala Met Ser Ile Ser Met Ala Leu Phe Ser Pro Pro Ile  
35 40 45  
Ser Ser Ser Leu Gln Asn Pro Asn Leu Ile Pro Lys Ile Ser Thr Ser  
50 55 60  
Leu Leu Ser Thr Lys Arg Phe Ser Leu Ile Ser Val Pro Arg Ala Ser



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65 70 75 80
Ser Asp Asn Gly Thr Thr Ser Pro Val Val Lys Ile Pro Lys Pro Ala
85 90 95
Ser Val Ala Val Glu Glu Val Pro Val Lys Ser Pro Ala Glu Ser Ser
100 105 110
Ser Ala Ser Glu Asn Gly Ala Val Gly Gly Glu Ala Thr Asp Ser Ser
115 120 125
Thr Glu Thr Val Ile Lys Tyr Gln Asn Ala Lys Trp Val Asn Gly Thr
130 135 140
Trp Asp Leu Lys Gln Phe Glu Lys Asp Gly Lys Thr Asp Trp Asp Ser
145 150 155 160
Val Ile Val Ser Glu Ala Lys Arg Arg Lys Trp Leu Glu Asp Asn Pro
165 170 175
Glu Thr Thr Ser Asn Asp Glu Leu Val Val Phe Asp Thr Ser Ile Ile
180 185 190
Pro Trp Trp Ala Trp Met Lys Arg Tyr His Leu Pro Glu Ala Glu Leu
195 200 205
Leu Asn Gly Arg Ala Ala Met Ile Gly Phe Phe Met Ala Tyr Phe Val
210 215 220
Asp Ser Leu Thr Gly Val Gly Leu Val Asp Gln Met Gly Asn Phe Phe
225 230 235 240
Cys Lys Thr Leu Leu Phe Val Ala Val Ala Gly Val Leu Phe Ile Arg
245 250 255
Lys Asn Glu Asp Leu Asp Lys Leu Lys Asp Leu Phe Asp Glu Thr Thr
260 265 270
Leu Tyr Asp Lys Gln Trp Gln Ala Ala Trp Lys Glu Pro Asp Ser Ser
275 280 285
Asp Ser Phe Phe Lys Glu Val Asn Lys Phe Leu Gln Ser Phe Ile Phe
290 295 300
Leu Phe Leu Leu Cys Asn Asn Leu
305 310

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(2) INFORMATION FOR SEQ ID NO:2704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

```

Met Ser Ile Ser Met Ala Leu Phe Ser Pro Pro Ile Ser Ser Ser Leu
1 5 10 15
Gln Asn Pro Asn Leu Ile Pro Lys Ile Ser Thr Ser Leu Leu Ser Thr
20 25 30
Lys Arg Phe Ser Leu Ile Ser Val Pro Arg Ala Ser Ser Asp Asn Gly
35 40 45
Thr Thr Ser Pro Val Val Lys Ile Pro Lys Pro Ala Ser Val Ala Val
50 55 60
Glu Glu Val Pro Val Lys Ser Pro Ala Glu Ser Ser Ser Ala Ser Glu
65 70 75 80
Asn Gly Ala Val Gly Gly Glu Ala Thr Asp Ser Ser Thr Glu Thr Val
85 90 95
Ile Lys Tyr Gln Asn Ala Lys Trp Val Asn Gly Thr Trp Asp Leu Lys
100 105 110
Gln Phe Glu Lys Asp Gly Lys Thr Asp Trp Asp Ser Val Ile Val Ser
115 120 125
Glu Ala Lys Arg Arg Lys Trp Leu Glu Asp Asn Pro Glu Thr Thr Ser
130 135 140

```

SEQUENCE: 2704

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Phe | Ser | Pro | Pro | Ile | Ser | Ser | Ser | Leu | Gln | Asn | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ile | Pro | Lys | Ile | Ser | Thr | Ser | Leu | Leu | Ser | Thr | Lys | Arg | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ile | Ser | Val | Pro | Arg | Ala | Ser | Ser | Asp | Asn | Gly | Thr | Thr | Ser | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Val | Lys | Ile | Pro | Lys | Pro | Ala | Ser | Val | Ala | Val | Glu | Glu | Val | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Ser | Pro | Ala | Glu | Ser | Ser | Ser | Ala | Ser | Glu | Asn | Gly | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Gly | Glu | Ala | Thr | Asp | Ser | Ser | Thr | Glu | Thr | Val | Ile | Lys | Tyr | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Ala | Lys | Trp | Val | Asn | Gly | Thr | Trp | Asp | Leu | Lys | Gln | Phe | Glu | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Gly | Lys | Thr | Asp | Trp | Asp | Ser | Val | Ile | Val | Ser | Glu | Ala | Lys | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Lys | Trp | Leu | Glu | Asp | Asn | Pro | Glu | Thr | Thr | Ser | Asn | Asp | Glu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Val | Phe | Asp | Thr | Ser | Ile | Ile | Pro | Trp | Trp | Ala | Trp | Met | Lys | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | His | Leu | Pro | Glu | Ala | Glu | Leu | Leu | Asn | Gly | Arg | Ala | Ala | Met | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Phe | Phe | Met | Ala | Tyr | Phe | Val | Asp | Ser | Leu | Thr | Gly | Val | Gly | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Asp | Gln | Met | Gly | Asn | Phe | Phe | Cys | Lys | Thr | Leu | Leu | Phe | Val | Ala |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ala | Gly | Val | Leu | Phe | Ile | Arg | Lys | Asn | Glu | Asp | Leu | Asp | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Asp | Leu | Phe | Asp | Glu | Thr | Thr | Leu | Tyr | Asp | Lys | Gln | Trp | Gln | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Trp | Lys | Glu | Pro | Asp | Ser | Ser | Asp | Ser | Phe | Phe | Lys | Glu | Val | Asn |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |
| Lys | Phe | Leu | Gln | Ser | Phe | Ile | Phe | Leu | Leu | Cys | Asn | Asn | Leu |
|     | 260 |     |     |     |     |     |     | 265 |     |     |     | 270 |     |

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..551
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| ataaacaaaa | agaatttgaa | ccaacaaagc  | aaaacatgaa | aggcacattc | actaacttgc | 60  |
| ttgtgctcct | cctcattgca | cttgtttggtg | ccaatgtcgg | tgctaggaaa | gttatctccg | 120 |
| aagataccca | attcaaggat | gaaaaatctt  | tcctcggagg | cagtggcagc | ggtgatggct | 180 |
| tagggcttgg | ccttggtgga | ggagctgggc  | ttggtgggct | tgggattggg | gctgggatcg | 240 |
| gcgcgggagc | cggactaggg | ttaggtggag  | gcggtggggg | aggagccggg | ggcggactcg | 300 |
| ttggccttcc | ttgaacgtat | tgacaagtgt  | gcgtgtgaga | gctgattctc | agcttattac | 360 |
| taattaatta | agttactttc | attctcttaa  | taaaatctag | agggtttgaa | tttcggattt | 420 |
| cttcagcttt | aatttaaact | tcaatatttg  | aaccaaaaaa | ggtcttagct | actagaggta | 480 |
| atgctcgtaa | tcgtattatg | tgtaAcgccg  | gttctgatat | tcttatgtgc | aAgtgtggaa | 540 |
| cgtttctctt | t          |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Lys | Glu | Phe | Glu | Pro | Thr | Lys | Gln | Asn | Met | Lys | Gly | Thr | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asn | Leu | Leu | Val | Leu | Leu | Leu | Ile | Ala | Leu | Val | Cys | Ala | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Arg | Lys | Val | Ile | Ser | Glu | Asp | Thr | Gln | Phe | Lys | Asp | Glu | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Phe | Leu | Gly | Gly | Ser | Gly | Ser | Gly | Asp | Gly | Leu | Gly | Leu | Gly | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Gly | Ala | Gly | Leu | Gly | Gly | Leu | Gly | Ile | Gly | Ala | Gly | Ile | Gly |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Ala | Gly | Leu | Gly | Leu | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Ala | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Gly | Leu | Val | Gly | Leu | Pro |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

(2) INFORMATION FOR SEQ ID NO:2709:

(A) LENGTH: 1005 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1005

(D) OTHER INFORMATION: / Ceres Seq. ID 1574009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

| (X1) SEQUENCE | DESCRIPTION | SEQ ID NO  | LENGTH     |            |             |     |
|---------------|-------------|------------|------------|------------|-------------|-----|
| aaaaacaac     | aaaaaatca   | gtgttcggct | ctaacacgct | cgacgaccat | ggcggctctcg | 60  |
| tttaataca     | cgcttcacca  | gccttctctg | agtccacgct | gtagcatcaa | gctttattct  | 120 |
| gggttaaagc    | ctcaatctgc  | aagctttttg | gcaagtgggt | atcagaattt | gaataaggag  | 180 |
| ttctatggaa    | gagttcataa  | gagttctgaa | tctgggactg | gcaaagcgag | caggtcacgg  | 240 |
| gtaaagatga    | tgccaatagg  | aacaccgaga | gtgccctaca | gaaaccgtga | agaaggcact  | 300 |
| tggcaaKggg    | ttgatatatg  | gaatgccctt | tatcgagagc | gtgtaattct | tattggacaa  | 360 |
| aacattgatg    | aagagctttg  | caaccagata | ttagcaacca | tgttgtacct | cgatactctt  | 420 |
| gatgactcga    | ggaggattta  | tatgtaccta | aatggctcgg | gtggtgatct | tactccaagt  | 480 |
| ctagcactct    | atgatacaat  | gaagagcttg | aaaagtccgg | ttgggacaca | ttgcgttggg  | 540 |
| cttgcttaca    | accttgccag  | ttttcttctt | gcggctggag | aaaagggtca | ccgatttgcg  | 600 |
| atgccattgt    | caagaatcgc  | cctccaatca | ccagctgggt | cagcccgtag | ccaggetgat  | 660 |
| gatatccaaa    | atgaagcaaa  | agagctttca | aggataagag | actacctctt | caatgaacta  | 720 |
| gccaaagaata   | caggccagcc  | tgcggaagg  | gtcttcaaag | acttgagccg | ggtgaaaagg  | 780 |
| ttcaatgcag    | aggaagcaat  | cgagtatgga | cttattgata | agattgttag | accaccgcgc  | 840 |
| atcaaagaag    | acgctcctcg  | ccaagacgaa | agcgcagggc | taggctagtc | ttttttgttt  | 900 |
| gtttgttatg    | tcaaaagttt  | taatctttat | gttattgtga | tttgtattgt | tacctaaaaa  | 960 |
| aatcactgat    | tattgttttt  | tcattccacc | gattttctga | tttct      |             |     |

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1574010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

| (xi) SEQUENCE DESCRIPTION: SH-1 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys                             | Asn | Lys | Gln | Lys | Asn | Gln | Cys | Ser | Ala | Leu | Thr | Arg | Ser | Thr | Thr |
| 1                               |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met                             | Ala | Val | Ser | Phe | Asn | Thr | Thr | Leu | His | Gln | Pro | Ser | Leu | Ser | Pro |
|                                 |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser  
35 40 45  
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg  
50 55 60  
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg  
65 70 75 80  
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg  
85 90 95  
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg  
100 105 110  
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn  
115 120 125  
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg  
130 135 140  
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser  
145 150 155 160  
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr  
165 170 175  
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala  
180 185 190  
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu  
195 200 205  
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn  
210 215 220  
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu  
225 230 235 240  
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser  
245 250 255  
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile  
260 265 270  
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln  
275 280 285  
Asp Glu Ser Ala Gly Leu Gly  
290 295

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1574011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

Met Ala Val Ser Phe Asn Thr Thr Leu His Gln Pro Ser Leu Ser Pro  
1 5 10 15  
Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser  
20 25 30  
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg  
35 40 45  
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg  
50 55 60  
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg  
65 70 75 80  
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg  
85 90 95  
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn  
100 105 110  
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

(2) INFORMATION FOR SEQ ID NO:2714:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

(2) INFORMATION FOR SEQ ID NO:2715:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1574015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

```
Met Glu Leu Ala Leu Thr Ala Arg Arg Phe Ser Gly Gly Glu Ala Lys
1 5 10 15
Asp Leu Gly Leu Val Ser Lys Val Phe Gly Ser Lys Ser Glu Leu Asp
 20 25 30
Asn Gly Val Ser Thr Ile Ala Glu Gly Ile Gly Gly Lys Ser Pro Leu
 35 40 45
Ala Val Thr Gly Thr Lys Ala Val Leu Leu Arg Ser Arg Glu Val Ser
 50 55 60
Val Glu Gln Gly Leu Asp Tyr Val Ala Thr Trp Asn Ser Ala Met Leu
65 70 75 80
Ile Ser Asp Asp Leu Asn Glu Ala Val Ser Ala Gln Met Met Lys Thr
 85 90 95
Lys Pro Arg Phe Ala Lys Leu
 100
```

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2259 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2259

(D) OTHER INFORMATION: / Ceres Seq. ID 1574021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

```
gctgcggtct cgccgtgctg cccacaacaa tctccgactt cgtcttctct atctatcctc 60
gtcgtcgtca accctatttta tctcttaatt tatcattaaa accaaaaaac caaaaaaaaaa 120
gccttagctt tcgtttcttc aatcccagca aaaaaaatgg ctcagggttc agctccttct 180
tcacattctc ctctctctcc tgctgttggt aacgacgggg ctgcgacggc ttctgctacc 240
cctggaatcg gcgtcggcgg cggtgagac ggagtcactc acggtgctct ttgttctctc 300
tatgtcggag atctggattt caatgtcacc gattctcagc tttatgacta ttccaccgag 360
gtgtgtcagg ttgtatctgt tcgtgtttgt cgtgatgctg ctaccaatac ttctcttggt 420
tatggttatg tcaactacag caacaccgac gatgcggaga aggcaatgca gaagttgaac 480
tacagttatc tcaatgggaa gatgattcgg attacttact cttctcgtga ctcttctgcc 540
cgtagaagtg gggttgggaa tttgtttgta aagaatttgg ataagtcagt tgacaacaaa 600
accctgcacg aggcgttttc cgggtgtggg actattgtgt cctgtaaggt tgctactgat 660
cacatgggtc agtctagagg atatgggttt gtgcagtttg aactaagga ttcagctaag 720
aatgctattg agaagctgaa cgggaaagtg ttgaatgaca aacagatttt tggtggacct 780
tttcttcgta aggaggaaag agagtctgct gctgataaga tgaagtttac taatgtttat 840
gtgaagaatc tttcggaggc gactactgac gatgagttga agactacttt tggtcagtat 900
ggtagttatc cgagcgctgt agttatgagg gatggagatg ggaaatccag gtgttttgga 960
tttgtcaact ttgagaatcc tgaagatgca gctcgtgctg ttgaagctct caatggaaaag 1020
aagtttgatg ataaggagtg gtatgtgggt aaagctcagS aagaaatctg agagggaact 1080
tgagttgagc cggagatatg aacaaggctc aagtgatggt ggaaacaaat ttgatgggtt 1140
gaatttatat gttaagaacc ttgatgatac cgtcaccgat gagaagttgc gcgagttggt 1200
tgccgaattt ggtacaatca cctcttgcaa gggtatgcgg gaccctagtg gtactagcaa 1260
aggatcagga tttgttgct tctctgctgc cagtgaagct tcaagagtgc tgaatgaaat 1320
gaatggtaaa atggttggtg gcaaaccgtt gtatgttgct cttgcacaga ggaaagaaga 1380
aaggagggtc aagctgcagg cacagttttc tcaaagtga cctgctttta tccccggtgt 1440
gggtcctcga atgccaatat ttacaggttg tgctccaggt cttggacaac agatttttta 1500
cgggtcaagga cctccacca tcatccctca ccagcctgga tttggatac agcctcagct 1560
ggttcctgga atgaggcgg ccttttttgg tggaccgatg atgcagccag gtcagcaagg 1620
tccacaccag gtggcagacg gtcaggtgat ggacccatgc gccatcagca tcagcagcca 1680
atgccttaca tgcagccaca gatgatgcca agaggacgag ggtaccggtc cccttctggt 1740
ggtagaaaca tgctgacgg tccaatgcca ggaggaaatg ttccagttgc ttatgacatg 1800
aatgtaatgc cgtatagtc gctatgtcc gctgggtcaat tggctacttc ccttgctaata 1860
gctacacctg ctcaacagag aacacttctt ggtgagagtc tatatccatt agtggaccag 1920
```



atagagagtg agcacgctgc gaaagtgact ggtatgcttc tggaaatgga tcagaccgag 1980  
gttttgcacg tgcctgagtc accagaggct ctaaagtcca aagtttcaga ggcattagat 2040  
gtgttgagaa acgtgaatca gccatcttca cagggaagtg aaggcaacaa aagtggaagt 2100  
ccaagtgatc tcttggcttc actttccatc aatgatcact tatgagaagc ttttgttcga 2160  
gttttttttt ttttactttg actctcttcc tctctatctc tctctctgat tgacaaattt 2220  
ttgcgggaat ctatttgctg ttttagactt tttttgctc

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1574022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met Ala Gln Val Gln Ala Pro Ser Ser His Ser Pro Pro Pro Pro Ala  
1 5 10 15  
Val Val Asn Asp Gly Ala Ala Thr Ala Ser Ala Thr Pro Gly Ile Gly  
20 25 30  
Val Gly Gly Gly Gly Asp Gly Val Thr His Gly Ala Leu Cys Ser Leu  
35 40 45  
Tyr Val Gly Asp Leu Asp Phe Asn Val Thr Asp Ser Gln Leu Tyr Asp  
50 55 60  
Tyr Phe Thr Glu Val Cys Gln Val Val Ser Val Arg Val Cys Arg Asp  
65 70 75 80  
Ala Ala Thr Asn Thr Ser Leu Gly Tyr Gly Tyr Val Asn Tyr Ser Asn  
85 90 95  
Thr Asp Asp Ala Glu Lys Ala Met Gln Lys Leu Asn Tyr Ser Tyr Leu  
100 105 110  
Asn Gly Lys Met Ile Arg Ile Thr Tyr Ser Ser Arg Asp Ser Ser Ala  
115 120 125  
Arg Arg Ser Gly Val Gly Asn Leu Phe Val Lys Asn Leu Asp Lys Ser  
130 135 140  
Val Asp Asn Lys Thr Leu His Glu Ala Phe Ser Gly Cys Gly Thr Ile  
145 150 155 160  
Val Ser Cys Lys Val Ala Thr Asp His Met Gly Gln Ser Arg Gly Tyr  
165 170 175  
Gly Phe Val Gln Phe Asp Thr Lys Asp Ser Ala Lys Asn Ala Ile Glu  
180 185 190  
Lys Leu Asn Gly Lys Val Leu Asn Asp Lys Gln Ile Phe Val Gly Pro  
195 200 205  
Phe Leu Arg Lys Glu Glu Arg Glu Ser Ala Ala Asp Lys Met Lys Phe  
210 215 220  
Thr Asn Val Tyr Val Lys Asn Leu Ser Glu Ala Thr Thr Asp Asp Glu  
225 230 235 240  
Leu Lys Thr Thr Phe Gly Gln Tyr Gly Ser Ile Ser Ser Ala Val Val  
245 250 255  
Met Arg Asp Gly Asp Gly Lys Ser Arg Cys Phe Gly Phe Val Asn Phe  
260 265 270  
Glu Asn Pro Glu Asp Ala Ala Arg Ala Val Glu Ala Leu Asn Gly Lys  
275 280 285  
Lys Phe Asp Asp Lys Glu Trp Tyr Val Gly Lys Ala Gln Xaa Glu Ile  
290 295 300

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..257  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574023  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

Met Glu Met Gly Asn Pro Gly Val Leu Asp Leu Ser Thr Leu Arg Ile  
1                   5                   10                   15  
Leu Lys Met Gln Leu Val Leu Leu Lys Leu Ser Met Glu Arg Ser Leu  
                  20                   25                   30  
Met Ile Arg Ser Gly Met Trp Val Lys Leu Xaa Lys Lys Ser Glu Arg  
                  35                   40                   45  
Glu Leu Glu Leu Ser Arg Arg Tyr Glu Gln Gly Ser Ser Asp Gly Gly  
50                   55                   60  
Asn Lys Phe Asp Gly Leu Asn Leu Tyr Val Lys Asn Leu Asp Asp Thr  
65                   70                   75                   80  
Val Thr Asp Glu Lys Leu Arg Glu Leu Phe Ala Glu Phe Gly Thr Ile  
                  85                   90                   95  
Thr Ser Cys Lys Val Met Arg Asp Pro Ser Gly Thr Ser Lys Gly Ser  
                  100                   105                   110  
Gly Phe Val Ala Phe Ser Ala Ala Ser Glu Ala Ser Arg Val Leu Asn  
                  115                   120                   125  
Glu Met Asn Gly Lys Met Val Gly Gly Lys Pro Leu Tyr Val Ala Leu  
130                   135                   140  
Ala Gln Arg Lys Glu Glu Arg Arg Ala Lys Leu Gln Ala Gln Phe Ser  
145                   150                   155                   160  
Gln Met Arg Pro Ala Phe Ile Pro Gly Val Gly Pro Arg Met Pro Ile  
                  165                   170                   175  
Phe Thr Gly Gly Ala Pro Gly Leu Gly Gln Gln Ile Phe Tyr Gly Gln  
                  180                   185                   190  
Gly Pro Pro Pro Ile Ile Pro His Gln Pro Gly Phe Gly Tyr Gln Pro  
                  195                   200                   205  
Gln Leu Val Pro Gly Met Arg Pro Ala Phe Phe Gly Gly Pro Met Met  
210                   215                   220  
Gln Pro Gly Gln Gln Gly Pro His Gln Val Ala Asp Gly Gln Val Met  
225                   230                   235                   240  
Asp Pro Cys Ala Ile Ser Ile Ser Ser Gln Cys Leu Thr Cys Ser His  
                  245                   250                   255  
Arg

(2) INFORMATION FOR SEQ ID NO:2719:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 255 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..255  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574024  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

Met Gly Asn Pro Gly Val Leu Asp Leu Ser Thr Leu Arg Ile Leu Lys  
1                   5                   10                   15  
Met Gln Leu Val Leu Leu Lys Leu Ser Met Glu Arg Ser Leu Met Ile  
                  20                   25                   30  
Arg Ser Gly Met Trp Val Lys Leu Xaa Lys Lys Ser Glu Arg Glu Leu  
35                   40                   45

Glu Leu Ser Arg Arg Tyr Glu Gln Gly Ser Ser Asp Gly Gly Asn Lys  
50 55 60  
Phe Asp Gly Leu Asn Leu Tyr Val Lys Asn Leu Asp Asp Thr Val Thr  
65 70 75 80  
Asp Glu Lys Leu Arg Glu Leu Phe Ala Glu Phe Gly Thr Ile Thr Ser  
85 90 95  
Cys Lys Val Met Arg Asp Pro Ser Gly Thr Ser Lys Gly Ser Gly Phe  
100 105 110  
Val Ala Phe Ser Ala Ala Ser Glu Ala Ser Arg Val Leu Asn Glu Met  
115 120 125  
Asn Gly Lys Met Val Gly Gly Lys Pro Leu Tyr Val Ala Leu Ala Gln  
130 135 140  
Arg Lys Glu Glu Arg Arg Ala Lys Leu Gln Ala Gln Phe Ser Gln Met  
145 150 155 160  
Arg Pro Ala Phe Ile Pro Gly Val Gly Pro Arg Met Pro Ile Phe Thr  
165 170 175  
Gly Gly Ala Pro Gly Leu Gly Gln Gln Ile Phe Tyr Gly Gln Gly Pro  
180 185 190  
Pro Pro Ile Ile Pro His Gln Pro Gly Phe Gly Tyr Gln Pro Gln Leu  
195 200 205  
Val Pro Gly Met Arg Pro Ala Phe Phe Gly Gly Pro Met Met Gln Pro  
210 215 220  
Gly Gln Gln Gly Pro His Gln Val Ala Asp Gly Gln Val Met Asp Pro  
225 230 235 240  
Cys Ala Ile Ser Ile Ser Ser Gln Cys Leu Thr Cys Ser His Arg  
245 250 255

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..927
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| attttttcatt cttctaagcc cttagctcaaa gctttctctc tcaaataccgc catgactaaa | 60  |
| cagcacgcga actggtctcc ttacgataac aatggaggaa catgtgtggc catcgctgga    | 120 |
| tcggtattact gtgttatcgc cgccgatact cggatgtcta ctggttacag tattcttagt   | 180 |
| cgcgattact ccaaaatcca taaactagcg gacagacctg ttttgtcttc ctctggcttc    | 240 |
| caggctgatg tgaaagcttt gcagaagggt ctcaaatcca gacacttgat ctatcaacat    | 300 |
| cagcataaca agcagatgag ctgtcctgca atggcccagc ttctctccaa cacgctttat    | 360 |
| ttcaagcggg ttttccccta ctatgccttt aatgttctag gagggcttga cgaggaagga    | 420 |
| aaaggggtgtg tctttactta cgacgctgtt ggctcatagc agagagttgg atacggtgct   | 480 |
| caaggttctg gttccacact catcatgcct ttccttgaca atcagctcaa gtctccaagt    | 540 |
| cctcttttgc tacctaaaca ggattcaaac acgCcccttt ccgaagctga agcagttgac    | 600 |
| ttggttAaaa ctgttttctgc atctgccaca Tgagagggat atctacactg gagacaagct   | 660 |
| tgagattatg atacttaagg ccgacggtat caagaccgaa ctcatggacc tgaggaaaga    | 720 |
| ctaagctcct ttagtgcat tagccaacct tatcggtttg ttatttcaact tcaacatcga    | 780 |
| gcttcctgag ttgtagaact cgtatgaaat gctactgggt ttgatatttt acagttaaaa    | 840 |
| tcatgactcg tgtttgaagt ttctccaaaa ctgtttcctt atgtatgaga atcactcgaa    | 900 |
| tccttgtctt aaatcaatgt ttctccc                                        |     |

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1574026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

Met Thr Lys Gln His Ala Asn Trp Ser Pro Tyr Asp Asn Asn Gly Gly  
1 5 10 15  
Thr Cys Val Ala Ile Ala Gly Ser Asp Tyr Cys Val Ile Ala Ala Asp  
20 25 30  
Thr Arg Met Ser Thr Gly Tyr Ser Ile Leu Ser Arg Asp Tyr Ser Lys  
35 40 45  
Ile His Lys Leu Ala Asp Arg Pro Val Leu Ser Ser Ser Gly Phe Gln  
50 55 60  
Ala Asp Val Lys Ala Leu Gln Lys Val Leu Lys Ser Arg His Leu Ile  
65 70 75 80  
Tyr Gln His Gln His Asn Lys Gln Met Ser Cys Pro Ala Met Ala Gln  
85 90 95  
Leu Leu Ser Asn Thr Leu Tyr Phe Lys Arg Phe Phe Pro Tyr Tyr Ala  
100 105 110  
Phe Asn Val Leu Gly Gly Leu Asp Glu Glu Gly Lys Gly Cys Val Phe  
115 120 125  
Thr Tyr Asp Ala Val Gly Ser Tyr Glu Arg Val Gly Tyr Gly Ala Gln  
130 135 140  
Gly Ser Gly Ser Thr Leu Ile Met Pro Phe Leu Asp Asn Gln Leu Lys  
145 150 155 160  
Ser Pro Ser Pro Leu Leu Leu Pro Lys Gln Asp Ser Asn Thr Pro Leu  
165 170 175  
Ser Glu Ala Glu Ala Val Asp Leu Val Lys Thr Val Phe Ala Ser Ala  
180 185 190  
Thr

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1574027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

Met Ser Thr Gly Tyr Ser Ile Leu Ser Arg Asp Tyr Ser Lys Ile His  
1 5 10 15  
Lys Leu Ala Asp Arg Pro Val Leu Ser Ser Ser Gly Phe Gln Ala Asp  
20 25 30  
Val Lys Ala Leu Gln Lys Val Leu Lys Ser Arg His Leu Ile Tyr Gln  
35 40 45  
His Gln His Asn Lys Gln Met Ser Cys Pro Ala Met Ala Gln Leu Leu  
50 55 60  
Ser Asn Thr Leu Tyr Phe Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn  
65 70 75 80  
Val Leu Gly Gly Leu Asp Glu Glu Gly Lys Gly Cys Val Phe Thr Tyr  
85 90 95  
Asp Ala Val Gly Ser Tyr Glu Arg Val Gly Tyr Gly Ala Gln Gly Ser  
100 105 110  
Gly Ser Thr Leu Ile Met Pro Phe Leu Asp Asn Gln Leu Lys Ser Pro  
115 120 125  
Ser Pro Leu Leu Leu Pro Lys Gln Asp Ser Asn Thr Pro Leu Ser Glu  
130 135 140

Ala Glu Ala Val Asp Leu Val Lys Thr Val Phe Ala Ser Ala Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

Met Ser Cys Pro Ala Met Ala Gln Leu Leu Ser Asn Thr Leu Tyr Phe  
1 5 10 15  
Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn Val Leu Gly Gly Leu Asp  
20 25 30  
Glu Glu Gly Lys Gly Cys Val Phe Thr Tyr Asp Ala Val Gly Ser Tyr  
35 40 45  
Glu Arg Val Gly Tyr Gly Ala Gln Gly Ser Gly Ser Thr Leu Ile Met  
50 55 60  
Pro Phe Leu Asp Asn Gln Leu Lys Ser Pro Ser Pro Leu Leu Leu Pro  
65 70 75 80  
Lys Gln Asp Ser Asn Thr Pro Leu Ser Glu Ala Glu Ala Val Asp Leu  
85 90 95  
Val Lys Thr Val Phe Ala Ser Ala Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

tttgatgact ggttacgata caatgtcact atccatcgaa atcctggaag ttgagttcgg 60  
tgaagctgcg gatattggcg aagaagcaat ctattataga catttcaaac cggatgatctt 120  
gtggaggcctt caaaactgga ttggtattgg gcttgagagg aagatgagaa cagctttggc 180  
cactgtcaat cgtatgtttg cgaagatcat atcttcaaga agaaaaggag agataagtcg 240  
cgccaaaacg gagccatatt ccaaggacgc gttgacgtat tatatgaatg tggacacgag 300  
caaataataag ctcttgaaac ctaataaaga taagtttata agagatgta tttttagtct 360  
agtgttagca ggaagggaca ccacaagctc agttctcact tggttctttt ggcttctttc 420  
taagcatcct caagttatgg ccaagctcag acatgagatc aacacaaagt ttgataatga 480  
agatctagag aagctcgtgt atctgcatgc tgcattgtcc gaatcaatga gactctaccc 540  
gccacttccc ttcaaccaca agtctCctgc gaaGccagat gtacttccaa gcgggcacaa 600  
agttgatgca aattcaaaga tcgtgatatg tatctatgca ttggggagga tgagatctgt 660  
atggggagaa gacgcattgg atttcaaacc agagagatgg atttcagaca atggaggctc 720  
aagacatgaa ccttcataca agttcatggc ttttaattct ggtccgagaa cttgcttggg 780  
taaaaatcta gctctcttgc agatgaagat ggtagctctg gagatcatat gaaactatga 840  
ctttaaggctc attgaaggct acaaggctga accaattcct tctatccttc tccgtatgaa 900  
acatggctctt aaagtcacag tcacaaagaa gatatgatta ttatgcttgc ttggcttcta 960  
cggcaactat tactatttcc ttattttaa gtgttactta ctagtttgtt cccacgttat 1020  
aactacttgt attacgtact aagtacgggtg tttgtccac gtcagtctca taaattaatt 1080  
aatatcgtca ataaagtatt agagcatcct cgtccat

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..311  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574030  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:

Leu Met Thr Gly Tyr Asp Pro Met Ser Leu Ser Ile Glu Ile Leu Glu  
1                  5                  10                  15  
Val Glu Phe Gly Glu Ala Ala Asp Ile Gly Glu Glu Ala Ile Tyr Tyr  
                  20                  25                  30  
Arg His Phe Lys Pro Val Ile Leu Trp Arg Leu Gln Asn Trp Ile Gly  
                  35                  40                  45  
Ile Gly Leu Glu Arg Lys Met Arg Thr Ala Leu Ala Thr Val Asn Arg  
                  50                  55                  60  
Met Phe Ala Lys Ile Ile Ser Ser Arg Arg Lys Glu Glu Ile Ser Arg  
65                  70                  75                  80  
Ala Lys Thr Glu Pro Tyr Ser Lys Asp Ala Leu Thr Tyr Tyr Met Asn  
                  85                  90                  95  
Val Asp Thr Ser Lys Tyr Lys Leu Leu Lys Pro Asn Lys Asp Lys Phe  
                  100                  105                  110  
Ile Arg Asp Val Ile Phe Ser Leu Val Leu Ala Gly Arg Asp Thr Thr  
                  115                  120                  125  
Ser Ser Val Leu Thr Trp Phe Phe Trp Leu Leu Ser Lys His Pro Gln  
130                  135                  140  
Val Met Ala Lys Leu Arg His Glu Ile Asn Thr Lys Phe Asp Asn Glu  
145                  150                  155                  160  
Asp Leu Glu Lys Leu Val Tyr Leu His Ala Ala Leu Ser Glu Ser Met  
                  165                  170                  175  
Arg Leu Tyr Pro Pro Leu Pro Phe Asn His Lys Ser Pro Ala Lys Pro  
                  180                  185                  190  
Asp Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Val  
                  195                  200                  205  
Ile Cys Ile Tyr Ala Leu Gly Arg Met Arg Ser Val Trp Gly Glu Asp  
210                  215                  220  
Ala Leu Asp Phe Lys Pro Glu Arg Trp Ile Ser Asp Asn Gly Gly Leu  
225                  230                  235                  240  
Arg His Glu Pro Ser Tyr Lys Phe Met Ala Phe Asn Ser Gly Pro Arg  
                  245                  250                  255  
Thr Cys Leu Gly Lys Asn Leu Ala Leu Leu Gln Met Lys Met Val Ala  
                  260                  265                  270  
Leu Glu Ile Ile Arg Asn Tyr Asp Phe Lys Val Ile Glu Gly His Lys  
275                  280                  285  
Val Glu Pro Ile Pro Ser Ile Leu Leu Arg Met Lys His Gly Leu Lys  
290                  295                  300  
Val Thr Val Thr Lys Lys Ile  
305                  310

(2) INFORMATION FOR SEQ ID NO:2726:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 310 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..310  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

Met Thr Gly Tyr Asp Pro Met Ser Leu Ser Ile Glu Ile Leu Glu Val  
1 5 10 15  
Glu Phe Gly Glu Ala Ala Asp Ile Gly Glu Glu Ala Ile Tyr Tyr Arg  
20 25 30  
His Phe Lys Pro Val Ile Leu Trp Arg Leu Gln Asn Trp Ile Gly Ile  
35 40 45  
Gly Leu Glu Arg Lys Met Arg Thr Ala Leu Ala Thr Val Asn Arg Met  
50 55 60  
Phe Ala Lys Ile Ile Ser Ser Arg Arg Lys Glu Ile Ser Arg Ala  
65 70 75 80  
Lys Thr Glu Pro Tyr Ser Lys Asp Ala Leu Thr Tyr Tyr Met Asn Val  
85 90 95  
Asp Thr Ser Lys Tyr Lys Leu Leu Lys Pro Asn Lys Asp Lys Phe Ile  
100 105 110  
Arg Asp Val Ile Phe Ser Leu Val Leu Ala Gly Arg Asp Thr Thr Ser  
115 120 125  
Ser Val Leu Thr Trp Phe Phe Trp Leu Leu Ser Lys His Pro Gln Val  
130 135 140  
Met Ala Lys Leu Arg His Glu Ile Asn Thr Lys Phe Asp Asn Glu Asp  
145 150 155 160  
Leu Glu Lys Leu Val Tyr Leu His Ala Ala Leu Ser Glu Ser Met Arg  
165 170 175  
Leu Tyr Pro Pro Leu Pro Phe Asn His Lys Ser Pro Ala Lys Pro Asp  
180 185 190  
Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Val Ile  
195 200 205  
Cys Ile Tyr Ala Leu Gly Arg Met Arg Ser Val Trp Gly Glu Asp Ala  
210 215 220  
Leu Asp Phe Lys Pro Glu Arg Trp Ile Ser Asp Asn Gly Gly Leu Arg  
225 230 235 240  
His Glu Pro Ser Tyr Lys Phe Met Ala Phe Asn Ser Gly Pro Arg Thr  
245 250 255  
Cys Leu Gly Lys Asn Leu Ala Leu Leu Gln Met Lys Met Val Ala Leu  
260 265 270  
Glu Ile Ile Arg Asn Tyr Asp Phe Lys Val Ile Glu Gly His Lys Val  
275 280 285  
Glu Pro Ile Pro Ser Ile Leu Leu Arg Met Lys His Gly Leu Lys Val  
290 295 300  
Thr Val Thr Lys Lys Ile  
305 310

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1574032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:

Met Ser Leu Ser Ile Glu Ile Leu Glu Val Glu Phe Gly Glu Ala Ala  
1 5 10 15  
Asp Ile Gly Glu Glu Ala Ile Tyr Tyr Arg His Phe Lys Pro Val Ile  
20 25 30  
Leu Trp Arg Leu Gln Asn Trp Ile Gly Ile Gly Leu Glu Arg Lys Met  
35 40 45  
Arg Thr Ala Leu Ala Thr Val Asn Arg Met Phe Ala Lys Ile Ile Ser  
50 55 60

| Variable                                                                                      | Mean         | SD   | Min  | Max  |
|-----------------------------------------------------------------------------------------------|--------------|------|------|------|
| Age                                                                                           | 34.5         | 10.2 | 21   | 55   |
| Gender                                                                                        | Male         |      |      |      |
| Marital status                                                                                | Married      |      |      |      |
| Education                                                                                     | High school  |      |      |      |
| Occupation                                                                                    | Teacher      |      |      |      |
| Income                                                                                        | 1500         | 500  | 1000 | 2000 |
| Health status                                                                                 | Good         |      |      |      |
| Stress level                                                                                  | Low          |      |      |      |
| Life satisfaction                                                                             | High         |      |      |      |
| Family size                                                                                   | 3            | 1    | 2    | 4    |
| Religion                                                                                      | Islam        |      |      |      |
| Political views                                                                               | Conservative |      |      |      |
| Environmental concerns                                                                        | High         |      |      |      |
| Technology use                                                                                | High         |      |      |      |
| Travel frequency                                                                              | Low          |      |      |      |
| Exercise frequency                                                                            | Low          |      |      |      |
| Dietary habits                                                                                | Traditional  |      |      |      |
| Work-life balance                                                                             | Low          |      |      |      |
| Community involvement                                                                         | Low          |      |      |      |
| Artistic interests                                                                            | Low          |      |      |      |
| Reading habits                                                                                | Low          |      |      |      |
| Gardening interests                                                                           | Low          |      |      |      |
| Volunteering frequency                                                                        | Low          |      |      |      |
| Charitable donations                                                                          | Low          |      |      |      |
| Political participation                                                                       | Low          |      |      |      |
| Environmental activism                                                                        | Low          |      |      |      |
| Technology adoption                                                                           | High         |      |      |      |
| Travel preferences                                                                            | Domestic     |      |      |      |
| Exercise preferences                                                                          | Walking      |      |      |      |
| Dietary preferences                                                                           | Halal        |      |      |      |
| Work-life balance preferences                                                                 | Flexibility  |      |      |      |
| Community involvement preferences                                                             | Local        |      |      |      |
| Artistic interests preferences                                                                | Traditional  |      |      |      |
| Reading preferences                                                                           | Non-fiction  |      |      |      |
| Gardening preferences                                                                         | Vegetables   |      |      |      |
| Volunteering preferences                                                                      | Education    |      |      |      |
| Charitable donations preferences                                                              | Religious    |      |      |      |
| Political participation preferences                                                           | Local        |      |      |      |
| Environmental activism preferences                                                            | Local        |      |      |      |
| Technology adoption preferences                                                               | High         |      |      |      |
| Travel preferences preferences                                                                | Domestic     |      |      |      |
| Exercise preferences preferences                                                              | Walking      |      |      |      |
| Dietary preferences preferences                                                               | Halal        |      |      |      |
| Work-life balance preferences preferences                                                     | Flexibility  |      |      |      |
| Community involvement preferences preferences                                                 | Local        |      |      |      |
| Artistic interests preferences preferences                                                    | Traditional  |      |      |      |
| Reading preferences preferences                                                               | Non-fiction  |      |      |      |
| Gardening preferences preferences                                                             | Vegetables   |      |      |      |
| Volunteering preferences preferences                                                          | Education    |      |      |      |
| Charitable donations preferences preferences                                                  | Religious    |      |      |      |
| Political participation preferences preferences                                               | Local        |      |      |      |
| Environmental activism preferences preferences                                                | Local        |      |      |      |
| Technology adoption preferences preferences                                                   | High         |      |      |      |
| Travel preferences preferences preferences                                                    | Domestic     |      |      |      |
| Exercise preferences preferences preferences                                                  | Walking      |      |      |      |
| Dietary preferences preferences preferences                                                   | Halal        |      |      |      |
| Work-life balance preferences preferences preferences                                         | Flexibility  |      |      |      |
| Community involvement preferences preferences preferences                                     | Local        |      |      |      |
| Artistic interests preferences preferences preferences                                        | Traditional  |      |      |      |
| Reading preferences preferences preferences                                                   | Non-fiction  |      |      |      |
| Gardening preferences preferences preferences                                                 | Vegetables   |      |      |      |
| Volunteering preferences preferences preferences                                              | Education    |      |      |      |
| Charitable donations preferences preferences preferences                                      | Religious    |      |      |      |
| Political participation preferences preferences preferences                                   | Local        |      |      |      |
| Environmental activism preferences preferences preferences                                    | Local        |      |      |      |
| Technology adoption preferences preferences preferences                                       | High         |      |      |      |
| Travel preferences preferences preferences preferences                                        | Domestic     |      |      |      |
| Exercise preferences preferences preferences preferences                                      | Walking      |      |      |      |
| Dietary preferences preferences preferences preferences                                       | Halal        |      |      |      |
| Work-life balance preferences preferences preferences preferences                             | Flexibility  |      |      |      |
| Community involvement preferences preferences preferences preferences                         | Local        |      |      |      |
| Artistic interests preferences preferences preferences preferences                            | Traditional  |      |      |      |
| Reading preferences preferences preferences preferences                                       | Non-fiction  |      |      |      |
| Gardening preferences preferences preferences preferences                                     | Vegetables   |      |      |      |
| Volunteering preferences preferences preferences preferences                                  | Education    |      |      |      |
| Charitable donations preferences preferences preferences preferences                          | Religious    |      |      |      |
| Political participation preferences preferences preferences preferences                       | Local        |      |      |      |
| Environmental activism preferences preferences preferences preferences                        | Local        |      |      |      |
| Technology adoption preferences preferences preferences preferences                           | High         |      |      |      |
| Travel preferences preferences preferences preferences preferences                            | Domestic     |      |      |      |
| Exercise preferences preferences preferences preferences preferences                          | Walking      |      |      |      |
| Dietary preferences preferences preferences preferences preferences                           | Halal        |      |      |      |
| Work-life balance preferences preferences preferences preferences preferences                 | Flexibility  |      |      |      |
| Community involvement preferences preferences preferences preferences preferences             | Local        |      |      |      |
| Artistic interests preferences preferences preferences preferences preferences                | Traditional  |      |      |      |
| Reading preferences preferences preferences preferences preferences                           | Non-fiction  |      |      |      |
| Gardening preferences preferences preferences preferences preferences                         | Vegetables   |      |      |      |
| Volunteering preferences preferences preferences preferences preferences                      | Education    |      |      |      |
| Charitable donations preferences preferences preferences preferences preferences              | Religious    |      |      |      |
| Political participation preferences preferences preferences preferences preferences           | Local        |      |      |      |
| Environmental activism preferences preferences preferences preferences preferences            | Local        |      |      |      |
| Technology adoption preferences preferences preferences preferences preferences               | High         |      |      |      |
| Travel preferences preferences preferences preferences preferences preferences                | Domestic     |      |      |      |
| Exercise preferences preferences preferences preferences preferences preferences              | Walking      |      |      |      |
| Dietary preferences preferences preferences preferences preferences preferences               | Halal        |      |      |      |
| Work-life balance preferences preferences preferences preferences preferences preferences     | Flexibility  |      |      |      |
| Community involvement preferences preferences preferences preferences preferences preferences | Local        |      |      |      |
| Artistic interests preferences preferences preferences preferences preferences preferences    | Traditional  |      |      |      |
| Reading preferences preferences preferences preferences preferences preferences               | Non-fiction  |      |      |      |
| Gardening preferences preferences preferences preferences preferences preferences             | Vegetables   |      |      |      |
|                                                                                               |              |      |      |      |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (q

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..923

(D) OTHER INFORMATION: / Ceres Seq. ID 1574038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

| (A1) SEQUENCE ALIGNMENT |             |            |            |            |            |     |
|-------------------------|-------------|------------|------------|------------|------------|-----|
| aggtccgaga              | aagataaaca  | aaatggcggc | aatcagaacg | atgacgaaca | tgattctacg | 60  |
| cgagttcatc              | catcatccac  | ttctccttca | ctcttcacgc | aaatcgtgtc | aatctcTttt | 120 |
| taccatgtct              | ccgtctcact  | cccctaattt | ctccaattca | ccctaattcc | cggttcgtat | 180 |
| ccgtccgatg              | tgcggcatcg  | acctccggtg | gaagcgggtg | tgatcggaaa | gtctcttcac | 240 |
| ggttgtcgca              | ggtgcaacag  | atgcttcacg | aagccgaaga | gagagctagt | tccgttggca | 300 |
| atgagcctac              | tcctcaaate  | actctagaca | atgttacact | taactttgct | agaagtggcg | 360 |
| gtctctggag              | ccagaatgtg  | aacaaattga | ataccaaagt | agatatgcgc | ttcaatgtta | 420 |
| agaacgcgta              | ttggctgagt  | gacaggatca | gagagaaaat | cttactgacg | gagaagaatc | 480 |
| ggatcaacaa              | ggatgggtgaa | cttgtgatat | cttcaaccaa | aaccagaacg | cagaaaggca | 540 |
| acatcgacga              | tgcacttgaa  | aaactacagg | cgatcattga | tgcggtctct | tatgttccac | 600 |
| ctccaccatc              | agaagaacag  | aagaagaaaa | tagtaaagct | ggctgcgaaa | gctgacaata | 660 |
| aacgacttaa              | aagcaaaaaa  | gttctgtcag | acaagaaatc | tgcgagaaga | agccgcggta | 720 |
| gttacgatga              | ttaaaacttaa | aaccatacaa | tggagtccag | gttgattcta | aagcttttaa | 780 |
| cttaaaatga              | ttgttatttt  | cttggaaatt | aatgtaacac | aacaatcaaa | tcattcaata | 840 |
| aaaattgcag              | tataattggat | tttatgtaca | aaccactctt | atacaaatta | tgaacaaaaa | 900 |
| aagtatcaaa              | cataacattc  | ctc        |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2729:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 157 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..157  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

Met Leu His Glu Ala Glu Glu Arg Ala Ser Ser Ala Gly Asn Glu Pro  
1                    5                    10                    15  
Thr Pro Gln Ile Thr Leu Asp Asn Val Thr Leu Asn Phe Ala Arg Ser  
                    20                    25                    30  
Gly Gly Pro Gly Gly Gln Asn Val Asn Lys Leu Asn Thr Lys Val Asp  
                    35                    40                    45  
Met Arg Phe Asn Val Lys Asn Ala Tyr Trp Leu Ser Asp Arg Ile Arg  
50                    55                    60  
Glu Lys Ile Leu Leu Thr Glu Lys Asn Arg Ile Asn Lys Asp Gly Glu  
65                    70                    75                    80  
Leu Val Ile Ser Ser Thr Lys Thr Arg Thr Gln Lys Gly Asn Ile Asp  
                    85                    90                    95  
Asp Ala Leu Glu Lys Leu Gln Ala Ile Ile Asp Ala Ala Ser Tyr Val  
                    100                    105                    110  
Pro Pro Pro Pro Ser Glu Glu Gln Lys Lys Lys Ile Val Lys Leu Ala  
                    115                    120                    125  
Ala Lys Ala Asp Asn Lys Arg Leu Lys Ser Lys Lys Val Leu Ser Asp  
130                    135                    140  
Lys Lys Ser Ala Arg Arg Ser Arg Gly Ser Tyr Asp Asp  
145                    150                    155

(2) INFORMATION FOR SEQ ID NO:2730:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 109 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

Met Arg Phe Asn Val Lys Asn Ala Tyr Trp Leu Ser Asp Arg Ile Arg  
1                    5                    10                    15  
Glu Lys Ile Leu Leu Thr Glu Lys Asn Arg Ile Asn Lys Asp Gly Glu  
                    20                    25                    30  
Leu Val Ile Ser Ser Thr Lys Thr Arg Thr Gln Lys Gly Asn Ile Asp  
                    35                    40                    45  
Asp Ala Leu Glu Lys Leu Gln Ala Ile Ile Asp Ala Ala Ser Tyr Val  
50                    55                    60  
Pro Pro Pro Pro Ser Glu Glu Gln Lys Lys Lys Ile Val Lys Leu Ala  
65                    70                    75                    80  
Ala Lys Ala Asp Asn Lys Arg Leu Lys Ser Lys Lys Val Leu Ser Asp  
                    85                    90                    95  
Lys Lys Ser Ala Arg Arg Ser Arg Gly Ser Tyr Asp Asp  
100                    105

(2) INFORMATION FOR SEQ ID NO:2731:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 506 base pairs  
    (B) TYPE: nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

(2) INFORMATION FOR SEQ ID NO:2732:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

(2) INFORMATION FOR SEQ ID NO:2733:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

| Met | Asp | Glu | Asn | Ala | Ser | Lys | Ile | Ile | Ser | Ala | Gly | Arg | Ala | Lys | Arg |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met Ile Leu Asp Val Leu Arg Thr Phe Ser Thr Arg Thr Arg Asn Leu  
1 5 10 15  
Pro Ser Ser Gly Phe Tyr Ser Ile Ser Thr Ser Ile Met Arg Asp Ile  
20 25 30  
Lys Val Lys Ser Asp Ser Lys Glu Phe Leu Thr Ser Ser Asp Glu Glu  
35 40 45  
Glu Glu Ser Val Ser Ile Arg Val Ser Ser Ser Ser Ser Leu Ser Ser  
50 55 60  
Val Lys Ser Thr Pro Glu Ile Glu Lys Lys Tyr Val His Arg Val Tyr  
65 70 75 80  
Asp Ala Ile Ala Pro His Phe Ser Ser Thr Arg Phe Ala Lys Trp Pro  
85 90 95  
Lys Val Ala Ala Phe Leu Glu Ser Leu Pro Ser Gly Ser Val Ile Leu  
100 105 110  
Asp Ala Gly Cys Gly Asn Gly Lys Tyr Leu Gly Leu Asn Pro Ser Cys  
115 120 125  
Phe Phe Ile Gly Cys Asp Ile Ser His Pro Leu Ile Lys Ile Cys Ser  
130 135 140  
Asp Lys Gly Gln Glu Val Leu Val Ala Asp Ala Val Asn Xaa Xaa Tyr  
145 150 155 160  
Arg Glu Glu Phe Gly Asp Ala Ala Ile Ser Ile Ala Val Leu His His  
165 170 175  
Leu Ser Thr Glu Asn Arg Arg Lys Lys Ala Ile Glu Glu Leu Val Arg  
180 185 190  
Val Val Lys Pro Gly Gly Phe Val Leu Ile Thr Val Trp Ala Ala Glu  
195 200 205  
Gln Glu Asp Thr Ser Leu Leu Thr Lys Trp Thr Pro Leu Ser Ala Lys  
210 215 220  
Tyr Val Glu Glu Trp Val Gly Pro Gly Ser Pro Met Asn Ser Pro Arg  
225 230 235 240  
Val Arg Asn Asn Pro Phe Phe Ser Leu Glu Ser Ile Pro Glu Thr Glu  
245 250 255  
Val Ser Thr Lys Glu Gln Lys Val Glu Asn Ser Gln Phe Ile Gly Leu  
260 265 270  
Glu Ser Ile Pro Glu Ser Glu Glu Ser Xaa Arg Glu Gln Lys Gly Glu  
275 280 285  
Ser Ile Ile Pro Glu Thr Lys Ala Ser Ile Val Glu Gln Arg Met Arg  
290 295 300  
Asn Leu Leu Arg Ser His Trp Arg Leu  
305 310

(2) INFORMATION FOR SEQ ID NO:2736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736:

Met Arg Asp Ile Lys Val Lys Ser Asp Ser Lys Glu Phe Leu Thr Ser  
1 5 10 15  
Ser Asp Glu Glu Glu Ser Val Ser Ile Arg Val Ser Ser Ser Ser  
20 25 30  
Ser Leu Ser Ser Val Lys Ser Thr Pro Glu Ile Glu Lys Lys Tyr Val  
35 40 45  
His Arg Val Tyr Asp Ala Ile Ala Pro His Phe Ser Ser Thr Arg Phe  
50 55 60  
Ala Lys Trp Pro Lys Val Ala Ala Phe Leu Glu Ser Leu Pro Ser Gly

65 70 75 80  
Ser Val Ile Leu Asp Ala Gly Cys Gly Asn Gly Lys Tyr Leu Gly Leu  
85 90 95  
Asn Pro Ser Cys Phe Phe Ile Gly Cys Asp Ile Ser His Pro Leu Ile  
100 105 110  
Lys Ile Cys Ser Asp Lys Gly Gln Glu Val Leu Val Ala Asp Ala Val  
115 120 125  
Asn Xaa Xaa Tyr Arg Glu Glu Phe Gly Asp Ala Ala Ile Ser Ile Ala  
130 135 140  
Val Leu His His Leu Ser Thr Glu Asn Arg Arg Lys Lys Ala Ile Glu  
145 150 155 160  
Glu Leu Val Arg Val Val Lys Pro Gly Gly Phe Val Leu Ile Thr Val  
165 170 175  
Trp Ala Ala Glu Gln Glu Asp Thr Ser Leu Leu Thr Lys Trp Thr Pro  
180 185 190  
Leu Ser Ala Lys Tyr Val Glu Glu Trp Val Gly Pro Gly Ser Pro Met  
195 200 205  
Asn Ser Pro Arg Val Arg Asn Asn Pro Phe Phe Ser Leu Glu Ser Ile  
210 215 220  
Pro Glu Thr Glu Val Ser Thr Lys Glu Gln Lys Val Glu Asn Ser Gln  
225 230 235 240  
Phe Ile Gly Leu Glu Ser Ile Pro Glu Ser Glu Ser Xaa Arg Glu  
245 250 255  
Gln Lys Gly Glu Ser Ile Ile Pro Glu Thr Lys Ala Ser Ile Val Glu  
260 265 270  
Gln Arg Met Arg Asn Leu Leu Arg Ser His Trp Arg Leu  
275 280 285

(2) INFORMATION FOR SEQ ID NO:2737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2737:

atttgtttgc cttcttcttt ctttctgact caaaccccta aatcaattct cgcgattaag 60  
caaaacccta gatttattct actcttcgaa gtcgatttca atggaagggt cctcgtcagc 120  
catcgcgagg aagacatggg agctagagaa caacattctc ccagtggaac caaccgattc 180  
agcctccgac agtatattcc actacgacga cgcttcacaa gccaaaatcc agcaggagaa 240  
gccatgggccc tccgatccta actacttcaa gcgcgttcac atctcagccc ttgctcttct 300  
caagatgggtg gttcacgctc gtcccggttg cacaatcgag atcatgggtc ttatgcaggg 360  
taaaaccgag ggtgatacaa tcatcgttat ggatgctttt gctttgcctg ttgaaggtag 420  
tgagactagg gttaatgctc agtctgatgc ctatgagtat atggttgaat actctcagac 480  
cagcaagctg gctgggaggt tggagaacgt tgttggtggt tatcactctc accctgggta 540  
tggatgttgg ctctcgggta ttgatgtttc gacacagatg cttaaccaac agtatcagga 600  
gccattotta gctgttggtt ttgatccaac aaggactgtt tcggctggtg aggttgagat 660  
tggggcattc agaacatatc cagagggaca taagatctcg gatgatcatg tttctgagta 720  
tcagactatc cctcttaaca agattgagga ctttggtgta cattgcaaac agtactactc 780  
attggacatc acttatttca agtcatctct cgatagtcac cttctggatc tCcttcggaa 840  
caagtactgg gtgaacaactc tttcttcttc ccactgtttg ggcaatggag actatgtttg 900  
cgggcaaata tcagacttgg ctgagaagct cgagcaagcg gagagtcagc tcgctaactc 960  
ccggtatgga ggaattgcgc cagccggtca ccaaaggagg aaagaggatg agcctcaact 1020  
cgcgaagata actcgggata gtgcaaagat aactgtcgag caggtccatg gactaatgtc 1080  
acaggttatc aaagacatct tgttcaattc cgctcgtcag tccaagaagt ctgctgacga 1140  
ctcatcagat ccagagccca tgattacatc gtgaagttgg tctattcttt tgttttttgg 1200  
ctgcggaaat tgactatcgg tttgacccag tttatgaggc aatgccatt gttccctata 1260  
tctctagtgt agtatctgct tcagacaaag atctttgggt tattaatga cattaacata 1320

aatcgatcat tatgtttttg tg

(2) INFORMATION FOR SEQ ID NO:2738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..357

(D) OTHER INFORMATION: / Ceres Seq. ID 1574048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2738:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Gly | Ser | Ser | Ser | Ala | Ile | Ala | Arg | Lys | Thr | Trp | Glu | Leu | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Asn | Ile | Leu | Pro | Val | Glu | Pro | Thr | Asp | Ser | Ala | Ser | Asp | Ser | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | His | Tyr | Asp | Asp | Ala | Ser | Gln | Ala | Lys | Ile | Gln | Gln | Glu | Lys | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Trp | Ala | Ser | Asp | Pro | Asn | Tyr | Phe | Lys | Arg | Val | His | Ile | Ser | Ala | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Leu | Leu | Lys | Met | Val | Val | His | Ala | Arg | Ser | Gly | Gly | Thr | Ile | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Ile | Met | Gly | Leu | Met | Gln | Gly | Lys | Thr | Glu | Gly | Asp | Thr | Ile | Ile | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Met | Asp | Ala | Phe | Ala | Leu | Pro | Val | Glu | Gly | Thr | Glu | Thr | Arg | Val | Asn |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Gln | Ser | Asp | Ala | Tyr | Glu | Tyr | Met | Val | Glu | Tyr | Ser | Gln | Thr | Ser |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Lys | Leu | Ala | Gly | Arg | Leu | Glu | Asn | Val | Val | Gly | Trp | Tyr | His | Ser | His |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Gly | Tyr | Gly | Cys | Trp | Leu | Ser | Gly | Ile | Asp | Val | Ser | Thr | Gln | Met |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Leu | Asn | Gln | Gln | Tyr | Gln | Glu | Pro | Phe | Leu | Ala | Val | Val | Ile | Asp | Pro |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Thr | Arg | Thr | Val | Ser | Ala | Gly | Lys | Val | Glu | Ile | Gly | Ala | Phe | Arg | Thr |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Tyr | Pro | Glu | Gly | His | Lys | Ile | Ser | Asp | Asp | His | Val | Ser | Glu | Tyr | Gln |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Thr | Ile | Pro | Leu | Asn | Lys | Ile | Glu | Asp | Phe | Gly | Val | His | Cys | Lys | Gln |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Tyr | Tyr | Ser | Leu | Asp | Ile | Thr | Tyr | Phe | Lys | Ser | Ser | Leu | Asp | Ser | His |  |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |  |
| Leu | Leu | Asp | Leu | Leu | Arg | Asn | Lys | Tyr | Trp | Val | Asn | Thr | Leu | Ser | Ser |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ser | Pro | Leu | Leu | Gly | Asn | Gly | Asp | Tyr | Val | Ala | Gly | Gln | Ile | Ser | Asp |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Ala | Glu | Lys | Leu | Glu | Gln | Ala | Glu | Ser | Gln | Leu | Ala | Asn | Ser | Arg |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Tyr | Gly | Gly | Ile | Ala | Pro | Ala | Gly | His | Gln | Arg | Arg | Lys | Glu | Asp | Glu |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Pro | Gln | Leu | Ala | Lys | Ile | Thr | Arg | Asp | Ser | Ala | Lys | Ile | Thr | Val | Glu |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gln | Val | His | Gly | Leu | Met | Ser | Gln | Val | Ile | Lys | Asp | Ile | Leu | Phe | Asn |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Ser | Ala | Arg | Gln | Ser | Lys | Lys | Ser | Ala | Asp | Asp | Ser | Ser | Asp | Pro | Glu |  |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Pro | Met | Ile | Thr | Ser |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 355 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..289  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574049  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2739:

Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu  
1 5 10 15  
Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met Asp Ala Phe  
20 25 30  
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ser Asp  
35 40 45  
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys Leu Ala Gly  
50 55 60  
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly  
65 70 75 80  
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln  
85 90 95  
Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val  
100 105 110  
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Pro Glu Gly  
115 120 125  
His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr Ile Pro Leu  
130 135 140  
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu  
145 150 155 160  
Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu  
165 170 175  
Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu  
180 185 190  
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys  
195 200 205  
Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr Gly Gly Ile  
210 215 220  
Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu Pro Gln Leu Ala  
225 230 235 240  
Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln Val His Gly  
245 250 255  
Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn Ser Ala Arg Gln  
260 265 270  
Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu Pro Met Ile Thr  
275 280 285  
Ser

(2) INFORMATION FOR SEQ ID NO:2740:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 276 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..276  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574050  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740:

Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met

1 5 10 15  
Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala  
20 25 30  
Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys  
35 40 45  
Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro  
50 55 60  
Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu  
65 70 75 80  
Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr  
85 90 95  
Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr  
100 105 110  
Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr  
115 120 125  
Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr  
130 135 140  
Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu  
145 150 155 160  
Leu Asp Leu Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser  
165 170 175  
Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu  
180 185 190  
Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr  
195 200 205  
Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu Pro  
210 215 220  
Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln  
225 230 235 240  
Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn Ser  
245 250 255  
Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu Pro  
260 265 270  
Met Ile Thr Ser  
275

(2) INFORMATION FOR SEQ ID NO:2741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1950
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| aacagagtgcg | cacacactaa | aatggcggttc | cgcgttttgc | tcctcttctc  | actcaccgca | 60  |
| cttctcatct  | tctccgccgt | ttctccttct  | ttcgccgctt | cttctccga   | cgacgttgac | 120 |
| gatgaggatc  | tcagcttctc | cgaagatctc  | aaagaagacg | acgttcccgg  | cgctgactca | 180 |
| ctctcttctc  | caactggatt | tgacgaattc  | gaaggaggag | aagaagaaga  | tcccgatatg | 240 |
| tacaacgacg  | atgacgatga | agaaggagat  | ttttccgata | taggtaatcc  | ggattccgat | 300 |
| ccgttaccga  | cgccggagat | tgatgagaaa  | gacgttgttg | ttatcaagga  | gcgtaacttc | 360 |
| actgatgtga  | ttgagaataa | tcaatacgtt  | ttggttgagt | tttatgctcc  | gtggtgtggt | 420 |
| cattgtcagt  | ctcttgctcc | tgagtatgct  | gctgctgcca | cggagcttaa  | ggaagatggt | 480 |
| ggtgttttgg  | ctaagattga | tgcgacggag  | gagaatgagt | tagctcagga  | gtatcgtggt | 540 |
| cagggttttc  | cgacgcttct | tttcttcgtt  | gatggtgagc | acaagcctta  | cactggagga | 600 |
| aggactaaag  | aaacaattgt | gacatgggtg  | aagaagaaga | ttggtcctgg  | tgtgtataat | 660 |
| ctaactacat  | tagatgatgc | tgagaaagtg  | ttgacttctg | ggaacaaaagt | tggtttggga | 720 |
| tacttgaact  | ccttggtggg | tggtgagcac  | gatcagctta | atgctgcttc  | caaagctgaa | 780 |
| gacgatgtga  | acttttatca | aacagtgaat  | cctgatgttg | caaagatggt  | tcaccttgat | 840 |



ccggagtcta aaaggcctgc tcttgtccta gttagaagg aagaggagaa aattagccat 900  
tttgatggag aatttggttaa gtctgtccta gttagttttg tgtctgccaa caagcttgct 960  
ttgggtctctg ttttcaccag agagactgct ccggaaattt ttgagagtgc aatcaagaaa 1020  
cagttgttgt tgtttgtaac caaaaatgaa tctgaaaagg ttcttacgga atttcaagaa 1080  
gcagcgaaat cattcaaagg aaagctcatc tttgtatctg tggatctgga taatgaggat 1140  
tatgggaagc cagtcgctga atacttttgg gtgtctggaa atggctcctaa acttattggc 1200  
tacacagga atgaagacca taaaaaatat tttttcgatg gcgagatcca gtcagataaa 1260  
attaagatat ttgggggagga tttcctgaac gacaagttaa agccttttcta taagtcagac 1320  
cccattcctg aaaagaacga tgaagatgtg aaaatagtgg ttggagataa ctttgatgaa 1380  
attgttcttg acgattctaa agatgtgctt ctcgaggtct acgcaccatg gtgtggccat 1440  
tgccaagccc ttgagccaat gtataacaaa cttgccaagc atttacgaag tattgattct 1500  
ctcgtcataa ccaagatgga tggaacaacc aatgaacatc ccaaggcaaa ggctgagggG 1560  
ttccctacca ttctcttctt ccCtgcgggc aacaagactt cagagccgat tactgtagat 1620  
acagaccgca ctgTggttgc attttacaag ttcttaagga aacacgcaac gatcccatc 1680  
aaactggaga aacctgcac aaccgaatca cctaaaactg cagagtccac accaaaagta 1740  
gaaactaccg agaccaaaga atcaccgat agcagacaaa agagtagcca aagtgactcg 1800  
aaggacgaat tgtgatcaga aaagggata atatatatta catgtctcct taagttgtta 1860  
tatgtatgat cagaattgtc acatcatgag tttggactag ataaagatgg gaattaaagt 1920  
aattttagtt ttgagaaaaga caatttcttc

(2) INFORMATION FOR SEQ ID NO:2742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Arg | Val | Ala | His | Thr | Lys | Met | Ala | Phe | Arg | Val | Leu | Leu | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Thr | Ala | Leu | Leu | Ile | Phe | Ser | Ala | Val | Ser | Pro | Ser | Phe | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Ser | Ser | Asp | Asp | Val | Asp | Asp | Glu | Asp | Leu | Ser | Phe | Leu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Leu | Lys | Glu | Asp | Asp | Val | Pro | Gly | Ala | Asp | Ser | Leu | Ser | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gly | Phe | Asp | Glu | Phe | Glu | Gly | Gly | Glu | Glu | Glu | Asp | Pro | Asp | Met |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Asn | Asp | Asp | Asp | Asp | Glu | Glu | Gly | Asp | Phe | Ser | Asp | Leu | Gly | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asp | Ser | Asp | Pro | Leu | Pro | Thr | Pro | Glu | Ile | Asp | Glu | Lys | Asp | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Val | Ile | Lys | Glu | Arg | Asn | Phe | Thr | Asp | Val | Ile | Glu | Asn | Asn | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Val | Leu | Val | Glu | Phe | Tyr | Ala | Pro | Trp | Cys | Gly | His | Cys | Gln | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ala | Pro | Glu | Tyr | Ala | Ala | Ala | Ala | Thr | Glu | Leu | Lys | Glu | Asp | Gly |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Val | Leu | Ala | Lys | Ile | Asp | Ala | Thr | Glu | Glu | Asn | Glu | Leu | Ala | Gln |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Tyr | Arg | Val | Gln | Gly | Phe | Pro | Thr | Leu | Leu | Phe | Phe | Val | Asp | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | His | Lys | Pro | Tyr | Thr | Gly | Gly | Arg | Thr | Lys | Glu | Thr | Ile | Val | Thr |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Trp | Val | Lys | Lys | Lys | Ile | Gly | Pro | Gly | Val | Tyr | Asn | Leu | Thr | Thr | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Asp | Ala | Glu | Lys | Val | Leu | Thr | Ser | Gly | Asn | Lys | Val | Val | Leu | Gly |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |

Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln Leu Asn Ala Ala  
245 250 255  
Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr Val Asn Pro Asp  
260 265 270  
Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala Leu  
275 280 285  
Val Leu Val Lys Lys Glu Glu Glu Lys Ile Ser His Phe Asp Gly Glu  
290 295 300  
Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu Ala  
305 310 315 320  
Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu Ser  
325 330 335  
Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser Glu  
340 345 350  
Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly Lys  
355 360 365  
Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys Pro  
370 375 380  
Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile Gly  
385 390 395 400  
Tyr Thr Gly Asn Glu Asp His Lys Lys Tyr Phe Phe Asp Gly Glu Ile  
405 410 415  
Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp Lys  
420 425 430  
Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp Glu  
435 440 445  
Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu Asp  
450 455 460  
Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly His  
465 470 475 480  
Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu Arg  
485 490 495  
Ser Ile Asp Ser Leu Val Ile Thr Lys Met Asp Gly Thr Thr Asn Glu  
500 505 510  
His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe Pro  
515 520 525  
Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg Thr  
530 535 540  
Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro Phe  
545 550 555 560  
Lys Leu Glu Lys Pro Ala Ser Thr Glu Ser Pro Lys Thr Ala Glu Ser  
565 570 575  
Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser Thr  
580 585 590  
Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu  
595 600

(2) INFORMATION FOR SEQ ID NO:2743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..597

(D) OTHER INFORMATION: / Ceres Seq. ID 1574061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743:

Met Ala Phe Arg Val Leu Leu Leu Phe Ser Leu Thr Ala Leu Leu Ile  
1 5 10 15  
Phe Ser Ala Val Ser Pro Ser Phe Ala Ala Ser Ser Ser Asp Asp Val

SEQUENCE CHARACTERISTICS

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|--|
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |    |  |
| Asp | Asp | Glu | Asp | Leu | Ser | Phe | Leu | Glu | Asp | Leu | Lys | Glu | Asp | Asp | Val |    |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |    |  |
| Pro | Gly | Ala | Asp | Ser | Leu | Ser | Ser | Ser | Thr | Gly | Phe | Asp | Glu | Phe | Glu |    |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |    |  |
| Gly | Gly | Glu | Glu | Glu | Asp | Pro | Asp | Met | Tyr | Asn | Asp | Asp | Asp | Asp | Glu |    |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80 |  |
| Glu | Gly | Asp | Phe | Ser | Asp | Leu | Gly | Asn | Pro | Asp | Ser | Asp | Pro | Leu | Pro |    |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |    |  |
| Thr | Pro | Glu | Ile | Asp | Glu | Lys | Asp | Val | Val | Val | Ile | Lys | Glu | Arg | Asn |    |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |    |  |
| Phe | Thr | Asp | Val | Ile | Glu | Asn | Asn | Gln | Tyr | Val | Leu | Val | Glu | Phe | Tyr |    |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 | -   |     |     |    |  |
| Ala | Pro | Trp | Cys | Gly | His | Cys | Gln | Ser | Leu | Ala | Pro | Glu | Tyr | Ala | Ala |    |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |    |  |
| Ala | Ala | Thr | Glu | Leu | Lys | Glu | Asp | Gly | Val | Val | Leu | Ala | Lys | Ile | Asp |    |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |    |  |
| Ala | Thr | Glu | Glu | Asn | Glu | Leu | Ala | Gln | Glu | Tyr | Arg | Val | Gln | Gly | Phe |    |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |    |  |
| Pro | Thr | Leu | Leu | Phe | Phe | Val | Asp | Gly | Glu | His | Lys | Pro | Tyr | Thr | Gly |    |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |    |  |
| Gly | Arg | Thr | Lys | Glu | Thr | Ile | Val | Thr | Trp | Val | Lys | Lys | Lys | Ile | Gly |    |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |    |  |
| Pro | Gly | Val | Tyr | Asn | Leu | Thr | Thr | Leu | Asp | Asp | Ala | Glu | Lys | Val | Leu |    |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |    |  |
| Thr | Ser | Gly | Asn | Lys | Val | Val | Leu | Gly | Tyr | Leu | Asn | Ser | Leu | Val | Gly |    |  |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |    |  |
| Val | Glu | His | Asp | Gln | Leu | Asn | Ala | Ala | Ser | Lys | Ala | Glu | Asp | Asp | Val |    |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |    |  |
| Asn | Phe | Tyr | Gln | Thr | Val | Asn | Pro | Asp | Val | Ala | Lys | Met | Phe | His | Leu |    |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |    |  |
| Asp | Pro | Glu | Ser | Lys | Arg | Pro | Ala | Leu | Val | Leu | Val | Lys | Lys | Glu | Glu |    |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |    |  |
| Glu | Lys | Ile | Ser | His | Phe | Asp | Gly | Glu | Phe | Val | Lys | Ser | Ala | Leu | Val |    |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |    |  |
| Ser | Phe | Val | Ser | Ala | Asn | Lys | Leu | Ala | Leu | Val | Ser | Val | Phe | Thr | Arg |    |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |    |  |
| Glu | Thr | Ala | Pro | Glu | Ile | Phe | Glu | Ser | Ala | Ile | Lys | Lys | Gln | Leu | Leu |    |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |    |  |
| Leu | Phe | Val | Thr | Lys | Asn | Glu | Ser | Glu | Lys | Val | Leu | Thr | Glu | Phe | Gln |    |  |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |    |  |
| Glu | Ala | Ala | Lys | Ser | Phe | Lys | Gly | Lys | Leu | Ile | Phe | Val | Ser | Val | Asp |    |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |    |  |

(2) INFORMATION FOR SEQ ID NO:2744:

(A) LENGTH: 525 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1574062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Asn | Asp | Asp | Asp | Glu | Glu | Gly | Asp | Phe | Ser | Asp | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Pro | Asp | Ser | Asp | Pro | Leu | Pro | Thr | Pro | Glu | Ile | Asp | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Val | Val | Val | Ile | Lys | Glu | Arg | Asn | Phe | Thr | Asp | Val | Ile | Glu | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gln | Tyr | Val | Leu | Val | Glu | Phe | Tyr | Ala | Pro | Trp | Cys | Gly | His | Cys |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ser | Leu | Ala | Pro | Glu | Tyr | Ala | Ala | Ala | Ala | Thr | Glu | Leu | Lys | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Gly | Val | Val | Leu | Ala | Lys | Ile | Asp | Ala | Thr | Glu | Glu | Asn | Glu | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |
| Gln | Glu | Tyr | Arg | Val | Gln | Gly | Phe | Pro | Thr | Leu | Leu | Phe | Phe | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Gly | Glu | His | Lys | Pro | Tyr | Thr | Gly | Gly | Arg | Thr | Lys | Glu | Thr | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | Trp | Val | Lys | Lys | Lys | Ile | Gly | Pro | Gly | Val | Tyr | Asn | Leu | Thr |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Asp | Asp | Ala | Glu | Lys | Val | Leu | Thr | Ser | Gly | Asn | Lys | Val | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Tyr | Leu | Asn | Ser | Leu | Val | Gly | Val | Glu | His | Asp | Gln | Leu | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Ala | Ser | Lys | Ala | Glu | Asp | Asp | Val | Asn | Phe | Tyr | Gln | Thr | Val | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Asp | Val | Ala | Lys | Met | Phe | His | Leu | Asp | Pro | Glu | Ser | Lys | Arg | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Leu | Val | Leu | Val | Lys | Lys | Glu | Glu | Lys | Ile | Ser | His | Phe | Asp | Gly |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Glu | Phe | Val | Lys | Ser | Ala | Leu | Val | Ser | Phe | Val | Ser | Ala | Asn | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ala | Leu | Val | Ser | Val | Phe | Thr | Arg | Glu | Thr | Ala | Pro | Glu | Ile | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Ser | Ala | Ile | Lys | Lys | Gln | Leu | Leu | Leu | Phe | Val | Thr | Lys | Asn | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Glu | Lys | Val | Leu | Thr | Glu | Phe | Gln | Glu | Ala | Ala | Lys | Ser | Phe | Lys |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Lys | Leu | Ile | Phe | Val | Ser | Val | Asp | Leu | Asp | Asn | Glu | Asp | Tyr | Gly |

290 295 300  
Pro Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile  
305 310 315 320  
Gly Tyr Thr Gly Asn Glu Asp His Lys Lys Tyr Phe Phe Asp Gly Glu  
325 330 335  
Ile Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp  
340 345 350  
Lys Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp  
355 360 365  
Glu Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu  
370 375 380  
Asp Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly  
385 390 395 400  
His Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu  
405 410 415  
Arg Ser Ile Asp Ser Leu Val Ile Thr Lys Met Asp Gly Thr Thr Asn  
420 425 430  
Glu His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe  
435 440 445  
Pro Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg  
450 455 460  
Thr Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro  
465 470 475 480  
Phe Lys Leu Glu Lys Pro Ala Ser Thr Glu Ser Pro Lys Thr Ala Glu  
485 490 495  
Ser Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser  
500 505 510  
Thr Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu  
515 520 525

(2) INFORMATION FOR SEQ ID NO:2745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2745:

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| atcagtcact | tattcagact | gttggaaatta | caaagatggg  | tgtgtatggt | gaagccagta | 60  |
| ctggctttgg | gcaatctcct | gagagtattc  | atactcacta  | tgggattatg | tcgaacaaga | 120 |
| atgaattggt | ttccaccatt | cctgcaaagc  | agagaagacc  | agaagcaacg | caagcttaca | 180 |
| tcacaagaaa | caaataccaa | cttcacgaag  | cattcaatgg  | aagtttcatc | ttggagaaac | 240 |
| ttgcttacc  | gatctctaga | gggcatttga  | gcttgggtcaa | cacaaatggt | gatgacaacc | 300 |
| cttcagtcac | cttcaattac | tttaaacacc  | cgggtggatct | ccaacgctgt | gttgaagcca | 360 |
| ttcgtcttgt | ttccaaagtg | gtgacgtcta  | agcgtttctt  | aaactacacg | cagKtgGaca | 420 |
| agcaaaacgt | acacaagatg | cttagcttaa  | gcgtcaaggc  | aaacatcaat | ctaaggccaa | 480 |
| agcaactgaa | cgataccaaa | tcaatggctc  | agttctgcaa  | agacactggt | gtcacaatct | 540 |
| ggcactacca | tgggtgatgt | cttgtgggta  | aagttgtgag  | ccctaaccgc | aaagttcctg | 600 |
| gtgtcgacag | gcttagagtt | attgatgggt  | caacgtttga  | cgagtctcca | ggaaccaacc | 660 |
| cgcaagctac | tatgatgatg | atgggaagat  | acatgggagt  | caagattcct | cgggagagac | 720 |
| ttggaacaaa | agctggtggt | tagtttgcag  | attgagcttt  | tatggtagac | aaattcgtag | 780 |
| cagataattc | tgatgtggaa | ttgtgttgga  | gaatatctct  | ctctgtctcc | ttctctgtta | 840 |
| tttgatattc | gattcattga | agtataggat  | catattgtct  | aatgaactgt | gtaaccctct | 900 |
| attgggcaat | cggctctgtt | gcttattagc  | ttgtgtgaaa  | agttaatcac | gttttctgtt | 960 |
| tcaatactct | tacaatcg   |             |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..246
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2746:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Leu | Ile | Gln | Thr | Val | Gly | Ile | Thr | Lys | Met | Gly | Val | Tyr | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Ala | Ser | Thr | Gly | Phe | Gly | Gln | Ser | Pro | Glu | Ser | Ile | His | Thr | His |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Tyr | Gly | Ile | Met | Ser | Asn | Lys | Asn | Glu | Leu | Phe | Ser | Thr | Ile | Pro | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gln | Arg | Arg | Pro | Glu | Ala | Thr | Gln | Ala | Tyr | Ile | Thr | Arg | Asn | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Tyr | Gln | Leu | His | Glu | Ala | Phe | Asn | Gly | Ser | Phe | Ile | Leu | Glu | Lys | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Tyr | Pro | Ile | Ser | Arg | Gly | His | Leu | Ser | Leu | Val | Asn | Thr | Asn | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Asp | Asn | Pro | Ser | Val | Thr | Phe | Asn | Tyr | Phe | Lys | His | Pro | Val | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gln | Arg | Cys | Val | Glu | Ala | Ile | Arg | Leu | Val | Ser | Lys | Val | Val | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Lys | Arg | Phe | Leu | Asn | Tyr | Thr | Gln | Xaa | Asp | Lys | Gln | Asn | Val | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Met | Leu | Ser | Leu | Ser | Val | Lys | Ala | Asn | Ile | Asn | Leu | Arg | Pro | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Leu | Asn | Asp | Thr | Lys | Ser | Met | Ala | Gln | Phe | Cys | Lys | Asp | Thr | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Thr | Ile | Trp | His | Tyr | His | Gly | Gly | Cys | Leu | Val | Gly | Lys | Val | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Pro | Asn | Arg | Lys | Val | Leu | Gly | Val | Asp | Arg | Leu | Arg | Val | Ile | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ser | Thr | Phe | Asp | Glu | Ser | Pro | Gly | Thr | Asn | Pro | Gln | Ala | Thr | Met |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Met | Met | Gly | Arg | Tyr | Met | Gly | Val | Lys | Ile | Leu | Arg | Glu | Arg | Leu |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Asn | Lys | Ala | Gly | Val |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2747:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 235 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..235
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2747:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Val | Tyr | Val | Glu | Ala | Ser | Thr | Gly | Phe | Gly | Gln | Ser | Pro | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ile | His | Thr | His | Tyr | Gly | Ile | Met | Ser | Asn | Lys | Asn | Glu | Leu | Phe |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Thr | Ile | Pro | Ala | Lys | Gln | Arg | Arg | Pro | Glu | Ala | Thr | Gln | Ala | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Thr | Arg | Asn | Lys | Tyr | Gln | Leu | His | Glu | Ala | Phe | Asn | Gly | Ser | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Ile Leu Glu Lys Leu Ala Tyr Pro Ile Ser Arg Gly His Leu Ser Leu  
65 70 75 80  
Val Asn Thr Asn Val Asp Asp Asn Pro Ser Val Thr Phe Asn Tyr Phe  
85 90 95  
Lys His Pro Val Asp Leu Gln Arg Cys Val Glu Ala Ile Arg Leu Val  
100 105 110  
Ser Lys Val Val Thr Ser Lys Arg Phe Leu Asn Tyr Thr Gln Xaa Asp  
115 120 125  
Lys Gln Asn Val His Lys Met Leu Ser Leu Ser Val Lys Ala Asn Ile  
130 135 140  
Asn Leu Arg Pro Lys Gln Leu Asn Asp Thr Lys Ser Met Ala Gln Phe  
145 150 155 160  
Cys Lys Asp Thr Val Val Thr Ile Trp His Tyr His Gly Gly Cys Leu  
165 170 175  
Val Gly Lys Val Val Ser Pro Asn Arg Lys Val Leu Gly Val Asp Arg  
180 185 190  
Leu Arg Val Ile Asp Gly Ser Thr Phe Asp Glu Ser Pro Gly Thr Asn  
195 200 205  
Pro Gln Ala Thr Met Met Met Met Gly Arg Tyr Met Gly Val Lys Ile  
210 215 220  
Leu Arg Glu Arg Leu Gly Asn Lys Ala Gly Val  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1574069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2748:

Met Ser Asn Lys Asn Glu Leu Phe Ser Thr Ile Pro Ala Lys Gln Arg  
1 5 10 15  
Arg Pro Glu Ala Thr Gln Ala Tyr Ile Thr Arg Asn Lys Tyr Gln Leu  
20 25 30  
His Glu Ala Phe Asn Gly Ser Phe Ile Leu Glu Lys Leu Ala Tyr Pro  
35 40 45  
Ile Ser Arg Gly His Leu Ser Leu Val Asn Thr Asn Val Asp Asp Asn  
50 55 60  
Pro Ser Val Thr Phe Asn Tyr Phe Lys His Pro Val Asp Leu Gln Arg  
65 70 75 80  
Cys Val Glu Ala Ile Arg Leu Val Ser Lys Val Val Thr Ser Lys Arg  
85 90 95  
Phe Leu Asn Tyr Thr Gln Xaa Asp Lys Gln Asn Val His Lys Met Leu  
100 105 110  
Ser Leu Ser Val Lys Ala Asn Ile Asn Leu Arg Pro Lys Gln Leu Asn  
115 120 125  
Asp Thr Lys Ser Met Ala Gln Phe Cys Lys Asp Thr Val Val Thr Ile  
130 135 140  
Trp His Tyr His Gly Gly Cys Leu Val Gly Lys Val Val Ser Pro Asn  
145 150 155 160  
Arg Lys Val Leu Gly Val Asp Arg Leu Arg Val Ile Asp Gly Ser Thr  
165 170 175  
Phe Asp Glu Ser Pro Gly Thr Asn Pro Gln Ala Thr Met Met Met Met  
180 185 190  
Gly Arg Tyr Met Gly Val Lys Ile Leu Arg Glu Arg Leu Gly Asn Lys  
195 200 205  
Ala Gly Val

210

(2) INFORMATION FOR SEQ ID NO:2749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..827
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2749:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tgattccgaa ttgtttgttt cgtgttggtg gttcggcgat tttgttgtcg aacaagggga  | 60  |
| aagatcgtag acggtctaag tataagcttg ttcataccgt taggactcat aaaggagctg  | 120 |
| ttgagaaggc tttcaactgt gtttaccaag agcaagatga taatgggaag accgggggtt  | 180 |
| cgttgtcgaa agatccttat gctatagctg gtgaagctct taaggcgaat atcactactt  | 240 |
| taggtccttt ggttcttccct ataagtgagc agattctggt tttcatgact ttggttacga | 300 |
| agaaactggt taactcgaag ctgaagccgt atattccgga tttcaagctt gcgtttgatc  | 360 |
| atttctgtat ccattgctggt ggtagagctg tgattgatga gcttgagaag aatctgcagc | 420 |
| tttcgcagac tcattgctgag gcatcgagaa tgacactgca tagatttgga aacacttctt | 480 |
| cgagctcgat ttggtatgaa ctggcctaca tagaggctaa aggtaggatg aagaaaggaa  | 540 |
| accggggttg gcagattgct tttggaagtg ggtttaagtg taacagtgcg gtttggtatg  | 600 |
| ctctaaacaa tgtcaagcCt tcggttagta gtccgtggga aactgcacg gaccgatatc   | 660 |
| cggttaagct cgacttctga tttaatgaaa aaccatttgt ttggttagtc ctagtcttac  | 720 |
| tagactctgc cttgtttatt tttcttcttt tctggttaag ctcttgtagt cttaatgtga  | 780 |
| cgcttcttga ttattactct cgcgttttat gctatggcat cttttatc               |     |

(2) INFORMATION FOR SEQ ID NO:2750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2750:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Pro Asn Cys Leu Phe Arg Val Gly Gly Ser Ala Ile Leu Leu Ser |  |
| 1 5 10 15                                                       |  |
| Asn Lys Gly Lys Asp Arg Arg Arg Ser Lys Tyr Lys Leu Val His Thr |  |
| 20 25 30                                                        |  |
| Val Arg Thr His Lys Gly Ala Val Glu Lys Ala Phe Asn Cys Val Tyr |  |
| 35 40 45                                                        |  |
| Gln Glu Gln Asp Asp Asn Gly Lys Thr Gly Val Ser Leu Ser Lys Asp |  |
| 50 55 60                                                        |  |
| Leu Met Ala Ile Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Leu |  |
| 65 70 75 80                                                     |  |
| Gly Pro Leu Val Leu Pro Ile Ser Glu Gln Ile Leu Phe Phe Met Thr |  |
| 85 90 95                                                        |  |
| Leu Val Thr Lys Lys Leu Phe Asn Ser Lys Leu Lys Pro Tyr Ile Pro |  |
| 100 105 110                                                     |  |
| Asp Phe Lys Leu Ala Phe Asp His Phe Cys Ile His Ala Gly Gly Arg |  |
| 115 120 125                                                     |  |
| Ala Val Ile Asp Glu Leu Glu Lys Asn Leu Gln Leu Ser Gln Thr His |  |
| 130 135 140                                                     |  |
| Val Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser |  |
| 145 150 155 160                                                 |  |
| Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met |  |
| 165 170 175                                                     |  |



Lys Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys  
180 185 190  
Cys Asn Ser Ala Val Trp Met Ala Leu Asn Asn Val Lys Pro Ser Val  
195 200 205  
Ser Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Leu Asp  
210 215 220

Phe  
225

(2) INFORMATION FOR SEQ ID NO:2751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1574076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751:

Met Ala Ile Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Leu Gly  
1 5 10 15  
Pro Leu Val Leu Pro Ile Ser Glu Gln Ile Leu Phe Phe Met Thr Leu  
20 25 30  
Val Thr Lys Lys Leu Phe Asn Ser Lys Leu Lys Pro Tyr Ile Pro Asp  
35 40 45  
Phe Lys Leu Ala Phe Asp His Phe Cys Ile His Ala Gly Gly Arg Ala  
50 55 60  
Val Ile Asp Glu Leu Glu Lys Asn Leu Gln Leu Ser Gln Thr His Val  
65 70 75 80  
Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser  
85 90 95  
Ser Ile Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys  
100 105 110  
Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys  
115 120 125  
Asn Ser Ala Val Trp Met Ala Leu Asn Asn Val Lys Pro Ser Val Ser  
130 135 140  
Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Leu Asp Phe  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:2752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1574077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752:

Met Thr Leu Val Thr Lys Lys Leu Phe Asn Ser Lys Leu Lys Pro Tyr  
1 5 10 15  
Ile Pro Asp Phe Lys Leu Ala Phe Asp His Phe Cys Ile His Ala Gly  
20 25 30  
Gly Arg Ala Val Ile Asp Glu Leu Glu Lys Asn Leu Gln Leu Ser Gln  
35 40 45  
Thr His Val Glu Ala Ser Arg Met Thr Leu His Arg Phe Gly Asn Thr

50 55 60  
Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile Glu Ala Lys Gly  
65 70 75 80  
Arg Met Lys Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly  
85 90 95  
Phe Lys Cys Asn Ser Ala Val Trp Met Ala Leu Asn Asn Val Lys Pro  
100 105 110  
Ser Val Ser Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys  
115 120 125  
Leu Asp Phe  
130

(2) INFORMATION FOR SEQ ID NO:2753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2753:

aaatccttat gtcaggagat cccattctct agtgaattgc cctttctact tcaagattgg 60  
cgcttgccgt catggtgacc ggtgctcgcg tcttcacaac cGtcctacca tctccccaac 120  
actccttctt tcaaacatgt accaaaggcc tgacatgatt acccctggtg ttgacgctca 180  
gggccaaacca ctcgacccgc gtaagattca ggagcacttt gaggatttct ttgaggatct 240  
ttttgaggag cttggaaagt ttggcgagat agagagcctc aacattttgtg acaaccttgc 300  
tgaccacatg attggcaacg tatatgttca gtttaaggaa gaggatcagg ctgcagctgc 360  
tttgacggct ctgcaaggta ggttctattc aggacgtccc atcattgctg atttctctcc 420  
tgtgacggat ttccgcgaag ccacgtgtag gcagtatgaa gaaaacaact gcaaccgtgg 480  
tgggtactgt aatttcatgc atgtgaagct tgtttcgagg gaactaagga gaaaactcct 540  
tgggagatat cggcgatcat accgcagagg aagtagaagc aggagcagaa gcaggagtat 600  
tagccccagg aacaagagag ataatgaccg acgtgatcct tctcacaggg aattcagtca 660  
tcgggacaga gatcgcgagt tttaccgtca tgggaagtga aaaaggagca gtgagagggtc 720  
ggagaggcaa gagagggacg gttcaagggg taggagacaa gcaagcccta aacgaggagg 780  
gagcccgggt ggccgggaggg aaggaagtga ggagaggagg gcaaggattg agcaatggaa 840  
cagagaacgg gaggagaagg aagagggagg agcataaaaa cagttgttta ctcaaatcac 900  
aattgctgct atgtggtttc tgcgtctgct tctctgcgtt tattctgaaa tcggtaaaat 960  
ctgggtactgg atttttcatt tggctgttct aatttggaaac ttgaaatgag tggaaatcaac 1020  
ttcttttagat tataaaatgt ttggggttac tttctttagt ttttgattag gaaaaaccgc 1080  
tctgtccctt tgttattgat tttaccaggt gttctttaga actttgtact atcttctggt 1140  
ggttaaaact taaaagagtt ctagttt

(2) INFORMATION FOR SEQ ID NO:2754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2754:

Asn Pro Tyr Val Arg Arg Ser His Ser Leu Val Asn Cys Pro Phe Tyr  
1 5 10 15  
Phe Lys Ile Gly Ala Cys Arg His Gly Asp Arg Cys Ser Arg Leu His  
20 25 30  
Asn Arg Pro Thr Ile Ser Pro Thr Leu Leu Leu Ser Asn Met Tyr Gln  
35 40 45

Arg Pro Asp Met Ile Thr Pro Gly Val Asp Ala Gln Gly Gln Pro Leu  
50 55 60  
Asp Pro Arg Lys Ile Gln Glu His Phe Glu Asp Phe Phe Glu Asp Leu  
65 70 75 80  
Phe Glu Glu Leu Gly Lys Phe Gly Glu Ile Glu Ser Leu Asn Ile Cys  
85 90 95  
Asp Asn Leu Ala Asp His Met Ile Gly Asn Val Tyr Val Gln Phe Lys  
100 105 110  
Glu Glu Asp Gln Ala Ala Ala Ala Leu Gln Ala Leu Gln Gly Arg Phe  
115 120 125  
Tyr Ser Gly Arg Pro Ile Ile Ala Asp Phe Ser Pro Val Thr Asp Phe  
130 135 140  
Arg Glu Ala Thr Cys Arg Gln Tyr Glu Glu Asn Asn Cys Asn Arg Gly  
145 150 155 160  
Gly Tyr Cys Asn Phe Met His Val Lys Leu Val Ser Arg Glu Leu Arg  
165 170 175  
Arg Lys Leu Phe Gly Arg Tyr Arg Arg Ser Tyr Arg Arg Gly Ser Arg  
180 185 190  
Ser Arg Ser Arg Ser Arg Ser Ile Ser Pro Arg Asn Lys Arg Asp Asn  
195 200 205  
Asp Arg Arg Asp Pro Ser His Arg Glu Phe Ser His Arg Asp Arg Asp  
210 215 220  
Arg Glu Phe Tyr Arg His Gly Ser Gly Lys Arg Ser Ser Glu Arg Ser  
225 230 235 240  
Glu Arg Gln Glu Arg Asp Gly Ser Arg Gly Arg Arg Gln Ala Ser Pro  
245 250 255  
Lys Arg Gly Gly Ser Pro Gly Gly Gly Arg Glu Gly Ser Glu Glu Arg  
260 265 270  
Arg Ala Arg Ile Glu Gln Trp Asn Arg Glu Arg Glu Glu Lys Glu Glu  
275 280 285  
Gly Gly Ala  
290

(2) INFORMATION FOR SEQ ID NO:2755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2755:

Met Tyr Gln Arg Pro Asp Met Ile Thr Pro Gly Val Asp Ala Gln Gly  
1 5 10 15  
Gln Pro Leu Asp Pro Arg Lys Ile Gln Glu His Phe Glu Asp Phe Phe  
20 25 30  
Glu Asp Leu Phe Glu Glu Leu Gly Lys Phe Gly Glu Ile Glu Ser Leu  
35 40 45  
Asn Ile Cys Asp Asn Leu Ala Asp His Met Ile Gly Asn Val Tyr Val  
50 55 60  
Gln Phe Lys Glu Glu Asp Gln Ala Ala Ala Ala Leu Gln Ala Leu Gln  
65 70 75 80  
Gly Arg Phe Tyr Ser Gly Arg Pro Ile Ile Ala Asp Phe Ser Pro Val  
85 90 95  
Thr Asp Phe Arg Glu Ala Thr Cys Arg Gln Tyr Glu Glu Asn Asn Cys  
100 105 110  
Asn Arg Gly Gly Tyr Cys Asn Phe Met His Val Lys Leu Val Ser Arg  
115 120 125  
Glu Leu Arg Arg Lys Leu Phe Gly Arg Tyr Arg Arg Ser Tyr Arg Arg

130 135 140  
Gly Ser Arg Ser Arg Ser Arg Ser Ile Ser Pro Arg Asn Lys  
145 150 155 160  
Arg Asp Asn Asp Arg Arg Asp Pro Ser His Arg Glu Phe Ser His Arg  
165 170 175  
Asp Arg Asp Arg Glu Phe Tyr Arg His Gly Ser Gly Lys Arg Ser Ser  
180 185 190  
Glu Arg Ser Glu Arg Gln Glu Arg Asp Gly Ser Arg Gly Arg Arg Gln  
195 200 205  
Ala Ser Pro Lys Arg Gly Gly Ser Pro Gly Gly Gly Arg Glu Gly Ser  
210 215 220  
Glu Glu Arg Arg Ala Arg Ile Glu Gln Trp Asn Arg Glu Arg Glu Glu  
225 230 235 240  
Lys Glu Glu Gly Gly Ala  
245

(2) INFORMATION FOR SEQ ID NO:2756:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1574089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2756:

Met Ile Thr Pro Gly Val Asp Ala Gln Gly Gln Pro Leu Asp Pro Arg  
1 5 10 15  
Lys Ile Gln Glu His Phe Glu Asp Phe Phe Glu Asp Leu Phe Glu Glu  
20 25 30  
Leu Gly Lys Phe Gly Glu Ile Glu Ser Leu Asn Ile Cys Asp Asn Leu  
35 40 45  
Ala Asp His Met Ile Gly Asn Val Tyr Val Gln Phe Lys Glu Glu Asp  
50 55 60  
Gln Ala Ala Ala Ala Leu Gln Ala Leu Gln Gly Arg Phe Tyr Ser Gly  
65 70 75 80  
Arg Pro Ile Ile Ala Asp Phe Ser Pro Val Thr Asp Phe Arg Glu Ala  
85 90 95  
Thr Cys Arg Gln Tyr Glu Glu Asn Asn Cys Asn Arg Gly Gly Tyr Cys  
100 105 110  
Asn Phe Met His Val Lys Leu Val Ser Arg Glu Leu Arg Arg Lys Leu  
115 120 125  
Phe Gly Arg Tyr Arg Arg Ser Tyr Arg Arg Gly Ser Arg Ser Arg Ser  
130 135 140  
Arg Ser Arg Ser Ile Ser Pro Arg Asn Lys Arg Asp Asn Asp Arg Arg  
145 150 155 160  
Asp Pro Ser His Arg Glu Phe Ser His Arg Asp Arg Asp Arg Glu Phe  
165 170 175  
Tyr Arg His Gly Ser Gly Lys Arg Ser Ser Glu Arg Ser Glu Arg Gln  
180 185 190  
Glu Arg Asp Gly Ser Arg Gly Arg Gln Ala Ser Pro Lys Arg Gly  
195 200 205  
Gly Ser Pro Gly Gly Gly Arg Glu Gly Ser Glu Glu Arg Arg Ala Arg  
210 215 220  
Ile Glu Gln Trp Asn Arg Glu Arg Glu Glu Lys Glu Glu Gly Gly Ala  
225 230 235 240

(2) INFORMATION FOR SEQ ID NO:2757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..662
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574093
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2757:

```
atttttttctt tctctctctc ctccctaagc aaaactaaaa caagctatgg ctggtatgct 60
tcccggaggtt gagtgtgcaa ggaggcggcg cttccacggt ggtgctcctc cgattgaatc 120
ctogaacaca gcttctgtgg cggctgcggc gggacacgtc tggacacggc gaccatcggt 180
ctctcttttac actaccaatc atgagagcca ccaggcccat gtctccttct cggagagaag 240
tgtttaggaat aaatcttatg gagaagacaa cgatgagaaa cttgacggag cagccaaaga 300
ggcaaagcag aggcttaaca agcggctgag aatcccacca cgtacaagtt caggcaaaat 360
ggtaaagaca aaggggaataa attggagcaa ggaaagggtt aacctctcgg ggacttacgg 420
accgaggtgg Gtcgggttaa agaagagccg aggaagggtg atggaatggt tcaagcggcg 480
agttagggaa caacaagatt gtgctatatg tctagaccgg ttcaagaagg gtgagacctt 540
ggtacaccta ccatgtgccc ataagtttca ctccatatgc ttattgcctt ggctagacac 600
taatgtttat tgcccatatt gtagaactga tatttggaat taaatgttat atttttgatg 660
tc
```

(2) INFORMATION FOR SEQ ID NO:2758:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 198 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..198
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574094
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2758:

```
Met Ala Gly Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Arg Phe
1 5 10 15
His Gly Gly Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala
20 25 30
Ala Ala Ala Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr
35 40 45
Thr Thr Asn His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg
50 55 60
Ser Val Arg Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp
65 70 75 80
Gly Ala Ala Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile
85 90 95
Pro Pro Arg Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn
100 105 110
Trp Ser Lys Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp
115 120 125
Val Gly Leu Lys Lys Ser Arg Gly Arg Leu Met Glu Trp Phe Lys Arg
130 135 140
Arg Val Arg Glu Gln Gln Asp Cys Ala Ile Cys Leu Asp Arg Phe Lys
145 150 155 160
Lys Gly Glu Thr Leu Val His Leu Pro Cys Ala His Lys Phe His Ser
165 170 175
Ile Cys Leu Leu Pro Trp Leu Asp Thr Asn Val Tyr Cys Pro Tyr Cys
180 185 190
Arg Thr Asp Ile Trp Asn
195
```

(2) INFORMATION FOR SEQ ID NO:2759:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 195 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..195  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574095  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759:

Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Phe His Gly Gly  
1                  5                  10                  15  
Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala Ala Ala Ala  
                  20                  25                  30  
Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr Thr Thr Asn  
                  35                  40                  45  
His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg Ser Val Arg  
                  50                  55                  60  
Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp Gly Ala Ala  
65                  70                  75                  80  
Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile Pro Pro Arg  
                  85                  90                  95  
Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn Trp Ser Lys  
                  100                 105                 110  
Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp Val Gly Leu  
                 115                 120                 125  
Lys Lys Ser Arg Gly Arg Leu Met Glu Trp Phe Lys Arg Arg Val Arg  
                 130                 135                 140  
Glu Gln Gln Asp Cys Ala Ile Cys Leu Asp Arg Phe Lys Lys Gly Glu  
145                 150                 155                 160  
Thr Leu Val His Leu Pro Cys Ala His Lys Phe His Ser Ile Cys Leu  
                 165                 170                 175  
Leu Pro Trp Leu Asp Thr Asn Val Tyr Cys Pro Tyr Cys Arg Thr Asp  
                 180                 185                 190  
Ile Trp Asn  
                 195

(2) INFORMATION FOR SEQ ID NO:2760:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1396 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1396  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574100  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760:

aaagatgaaa agtaataccc ttctctctctt gccctttttg ctggtctggg tgaaacatag 60  
aaaagtttct cttgctcaag ttaatgataa aaggttggtg taggatttgt tgctctggct 120  
ctggtggtag gtctatgaaa tcaaccata tctgtaatgg actgcaacat ggtatcttcg 180  
tcccagtggtg attgggagca tttgatcatg tccaatccgt caaggactga agatgacagc 240  
aaacagctac ctactgagtg ggaaattgaa aaaggtgaag gaattgaatc tatagttcca 300  
catttctcag gccttgagag agtcagtaGg tggctctgcc accagcttct ggcacactgc 360  
tgtatcgaaa agctcacagt cgacctctat caactcatca tctcccgaag ccaaacgatg 420  
caagcttgca tcagaaagtt cccctggaga ttcttgcagc aacatagact ttgtccaggt 480  
gaaggctccc acagctctcg aggtatccgt tgccctcagct gaatcagatc tttgtttaaa 540  
actaggaaaag cggacatact ctgaagaata ctggggtaga aacaataatg aaatttcagc 600  
ggtttctatg aagttgttaa ctccatctgt tgtcgctggg aaatccaaat tgtgtggtca 660  
gagcatgccca gtcccgcgtt gccaaattga tggctgtgaa ctggatctct catctgctaa 720

gggttatcat cgtaagcaca aagtctgcga aaagcattca aagtgcccaa aagtttagcgt 780  
gagtggcctg gaacgtcggg tctgccaaca gtgtagcagg ttccatgctg tctctgaatt 840  
tgatgagaag aaacgaagct gccgaaaacg tctttctcat cataatgcga ggcgtcgtaa 900  
gccacaagga gtatttttcaa tgaatcccga gaggggtgtat gatcgaagac agcatacaaa 960  
tatgttgtgg aatgggggtgt cccttaacgc gagatctgaa gaaatgtatg aatggggtaa 1020  
taacacttat gatacaaagc ctagacaaac ggaaaaaagc tttactctga gcttccagag 1080  
aggtaatggc tctgaggacc agctgggtgc tagtagcagc cgtatgttCc tctacatctc 1140  
aaacctcagg tgggttccca gcaggaaagt ccaagtttca acttcatggc gaagatgtgg 1200  
gagaatactc aggagtcctc catgaatctc aagatatcca ccgtgctctc tctcttctgt 1260  
caacctcttc ggatcccctg gcccaaccac atgtgcagcc attttctcta ctctgttcat 1320  
atgatgttgt accaaaatag atgagtaagt aatgtgtaat ttgtaaacct gttactcagt 1380  
agggtgatac ttttcc

(2) INFORMATION FOR SEQ ID NO:2761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1574101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2761:

Met Asp Cys Asn Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu  
1 5 10 15  
Ile Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro  
20 25 30  
Thr Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro  
35 40 45  
His Phe Ser Gly Leu Glu Arg Val Ser Arg Trp Leu Cys His Gln Leu  
50 55 60  
Leu Ala His Cys Cys Ile Glu Lys Leu Thr Val Asp Leu Tyr Gln Leu  
65 70 75 80  
Ile Ile Ser Arg Ser Gln Thr Met Gln Ala Cys Ile Arg Lys Phe Pro  
85 90 95  
Trp Arg Phe Leu Gln Gln His Arg Leu Cys Pro Gly Glu Gly Ser His  
100 105 110  
Ser Ser Arg Gly Ile Arg Cys Leu Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:2762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1574102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2762:

Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys Leu Cys  
1 5 10 15  
Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu  
20 25 30  
Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu  
35 40 45  
Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg  
50 55 60  
Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu

(2) INFORMATION FOR SEQ ID NO:2763:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1574103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2763:

(2) INFORMATION FOR SEQ ID NO:2764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1454 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:



(A) NAME/KEY: -

(B) LOCATION: 1..1454

(D) OTHER INFORMATION: / Ceres Seq. ID 1574104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764:

|            |             |            |             |            |             |      |
|------------|-------------|------------|-------------|------------|-------------|------|
| ctgggtgaaa | catagaaaag  | tttctcttgc | tcaagttaat  | gataaaaagg | tgagagcaat  | 60   |
| aaacgctgat | aagccttgtc  | tggtccttgg | aattttgaat  | tttctttttc | tatcttactt  | 120  |
| atagtattgg | tagttgaggg  | tgctcgtcgt | aagttgttgt  | aggatttggt | gctctggctc  | 180  |
| tggtggtagg | tctatgaaat  | caacccatat | cgtgaatgga  | ctgcaacatg | gtatcttcgt  | 240  |
| cccagtgga  | ttgggagcat  | ttgatcatgt | ccaatccgtc  | aaggactgaa | gatgacagca  | 300  |
| aacagctacc | tactgagtgg  | gaaattgaaa | aaggtgaagg  | aattgaatct | atagttccac  | 360  |
| atttctcagg | ccttgagaga  | gtcagtagtg | gctctgCcac  | cagcttctgg | cacactgctg  | 420  |
| tatcgaaaag | ctcacagtcg  | acctctatca | actcatcatc  | tcccgaagcc | aaacgatgca  | 480  |
| agcttgcatc | agaaagttcc  | cctggagatt | cttgacagcaa | catagacttt | gtccaggtga  | 540  |
| aggctccac  | agctctcgag  | gtatccgttg | cctcagctga  | atcagatctt | tgtttaaaac  | 600  |
| taggaaagcg | gacatactct  | gaagaatact | ggggtagaaa  | caataatgaa | atttcagcgg  | 660  |
| tttctatgaa | gttggttaact | ccatctgttg | tcgctgggaa  | atccaaattg | tgtgggtcaga | 720  |
| gcatgccagt | cccgcgttgc  | caaattgatg | gctgtgaact  | ggatctctca | tctgctaagg  | 780  |
| gttatcatcg | taagcacaaa  | gtctgcgaaa | agcattcaaa  | gtgcccgaaa | gttagcgtga  | 840  |
| gtggcctgga | acgtcggttc  | tgccaacagt | gtagcaggtt  | ccatgctgtc | tctgaatttg  | 900  |
| atgagaagaa | acgaagctgc  | cgaaaacgtc | tttctcatca  | taatgcgagg | cgtcgtgaagc | 960  |
| cacaaggagt | attttcaatg  | aatcccagga | gggtgtatga  | tcgaagacag | catacaaaata | 1020 |
| tggtgtggaa | tgggggtgtcc | cttaacgcga | gatctgAaag  | aaatgtatga | atggggtaaat | 1080 |
| aacacttatg | atacaaagcc  | tagacaaacg | gaaaaaagct  | ttactctgag | cttccagaga  | 1140 |
| ggtaatggct | ctgaggacca  | gctgggttgc | agtagcagcc  | gtatgttctc | tacatctcaa  | 1200 |
| acctcaggtg | ggttcccagc  | aggaaagtcc | aagtttcaac  | ttcatggcga | agatgtggga  | 1260 |
| gaatactcag | gagtcctcca  | tgaatctcaa | gatatccacc  | gtgctctctc | tcttctgtca  | 1320 |
| acctcttcgg | atcccctggc  | ccaaccacat | gtgcagccat  | tttctctact | ctgttcatat  | 1380 |
| gatgttgtac | caaaaatagat | gagtaagtaa | tgtgtaattt  | gtaaacctgt | tactcagttg  | 1440 |
| gtggatactt | ttcc        |            |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1574105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Cys | Asn | Met | Val | Ser | Ser | Ser | Gln | Trp | Asp | Trp | Glu | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Ser | Asn | Pro | Ser | Arg | Thr | Glu | Asp | Asp | Ser | Lys | Gln | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Trp | Glu | Ile | Glu | Lys | Gly | Glu | Gly | Ile | Glu | Ser | Ile | Val | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Phe | Ser | Gly | Leu | Glu | Arg | Val | Ser | Ser | Gly | Ser | Ala | Thr | Ser | Phe |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | His | Thr | Ala | Val | Ser | Lys | Ser | Ser | Gln | Ser | Thr | Ser | Ile | Asn | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ser | Pro | Glu | Ala | Lys | Arg | Cys | Lys | Leu | Ala | Ser | Glu | Ser | Ser | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Asp | Ser | Cys | Ser | Asn | Ile | Asp | Phe | Val | Gln | Val | Lys | Ala | Pro | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Glu | Val | Ser | Val | Ala | Ser | Ala | Glu | Ser | Asp | Leu | Cys | Leu | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Lys | Arg | Thr | Tyr | Ser | Glu | Glu | Tyr | Trp | Gly | Arg | Asn | Asn | Asn |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Glu | Ile | Ser | Ala | Val | Ser | Met | Lys | Leu | Leu | Thr | Pro | Ser | Val | Val | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Gly Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln  
165 170 175  
Ile Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg  
180 185 190  
Lys His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val  
195 200 205  
Ser Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala  
210 215 220  
Val Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser  
225 230 235 240  
His His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn  
245 250 255  
Pro Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn  
260 265 270  
Gly Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val  
275 280

(2) INFORMATION FOR SEQ ID NO:2766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1574106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2766:

Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu Ile Met Ser Asn  
1 5 10 15  
Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr Glu Trp Glu  
20 25 30  
Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His Phe Ser Gly  
35 40 45  
Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp His Thr Ala  
50 55 60  
Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser Ser Pro Glu  
65 70 75 80  
Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly Asp Ser Cys  
85 90 95  
Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala Leu Glu Val  
100 105 110  
Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu Gly Lys Arg  
115 120 125  
Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu Ile Ser Ala  
130 135 140  
Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys  
145 150 155 160  
Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys  
165 170 175  
Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val  
180 185 190  
Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu  
195 200 205  
Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe  
210 215 220  
Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His His Asn Ala  
225 230 235 240  
Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val  
245 250 255  
Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly Val Ser Leu

260 265 270  
Asn Ala Arg Ser Glu Arg Asn Val  
275 280  
(2) INFORMATION FOR SEQ ID NO:2767:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 267 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..267  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574107  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2767:  
Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr  
1 5 10 15  
Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His  
20 25 30  
Phe Ser Gly Leu Glu Arg Val Ser Gly Ser Ala Thr Ser Phe Trp  
35 40 45  
His Thr Ala Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser  
50 55 60  
Ser Pro Glu Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly  
65 70 75 80  
Asp Ser Cys Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala  
85 90 95  
Leu Glu Val Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu  
100 105 110  
Gly Lys Arg Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu  
115 120 125  
Ile Ser Ala Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly  
130 135 140  
Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile  
145 150 155 160  
Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys  
165 170 175  
His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser  
180 185 190  
Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val  
195 200 205  
Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His  
210 215 220  
His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro  
225 230 235 240  
Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly  
245 250 255  
Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val  
260 265

(2) INFORMATION FOR SEQ ID NO:2768:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1658 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1658  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574122  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768:

aattttctcaa taacgctctc agagagacca tttgatgaag cttctcgcctt ctggaatttg 60  
aaaaggaact tggtatggag ataatctcac tgaacgttgt gcccagtgct tctgtgggta 120  
cttgagtagt taaattagca acgaaaagat tgggtccaaa tcggtcaagt ttgttattct 180  
caggggtcaa aaaatccaga cttgtgattc gaagtggaaa ttccgatggt tatgttgttg 240  
gtgagaatga tgacttgggt cgtatagcca gaagaggaga atcaacgtca aagggttttg 300  
ttcctgggtt gcctgatgaa tcaaatgggt aaattgctgc tcgaatcagt cattctcact 360  
gcgagtggaa gcccagctt agagtacatt atgagaaagc cggttgtgac aatctcgatg 420  
ctcctgcggt gttgtttctt cctggctttg gcgttggttc atttcactat gagaagcagc 480  
ttaccgattt ggggaaggat tatcgagtat gggctattga ttttcttga caggggttat 540  
ctctccctac tgaagatcct actaccatga ctgaagaaac cagttcctcg gaagataagg 600  
aaccattttg gggatttggg gacaaaactg aaccgtgggc tgatcaactt gtattctctc 660  
tggtatctct gagggatcaa gttcagttt ttgtagaaga ggttatcggt gagcctgtgt 720  
acattgcttg gaactcactt ggagggtatg tagctctcta ctttgacgca acccatcctc 780  
acctgggtta ggggtgttacc ttgcttaatg caacacctt ctgggggtttc ttccctaata 840  
cagtaagatc cccaaagcta gcacgtctct ttccatggcc cggagcattc cctctgccgg 900  
aaagagttaa aaaaatcaca gaattgggtg ggcaaaagat aagtgtcctt gaaagcatag 960  
ctgagatact taaacagggtc tacacagacc attctaccaa tgtggataaa gtattctcac 1020  
gtattgtgga ggtcacacag catccggctg ctgcagcatc gtttgcttca attatgcttg 1080  
ctcctgggtg agagctatct ttctccgaag ctttatctag gtgtaaggaa aacaatgttc 1140  
agatatgtct catgtatgga agagaagatc catgggtgag accgttatgg ggaaagaaga 1200  
taaagaagga aatccccaac gctccatact acgagatcag cccagcgggt cactgcccac 1260  
acgatgaagt cctgaggtg gtgaactatc tgatgcgcgg gtggatcaag cacctggagt 1320  
ctggtgggtt tgaaNgcgct cccgcttttg gaggacactg aagaagattg ggaggagtcc 1380  
aggattggta gagaaattga gttcccgaga gatggttga aaaaagcagt gaatctgtgg 1440  
ttatatgggt caaactatac gtactggaga ggagttagag aatctttcag atccagtttt 1500  
ataaggtgtt ttggagggaa gtctgcatag aagaagcatg gaacagtcgt ctagtgtaaa 1560  
ttaattgtaa tctatgttgc atccgatgct agctatataa tgttgtctgt agaatacaag 1620  
ttctaaaatg ttcaaaagga aaagttagaa aaatatcc

(2) INFORMATION FOR SEQ ID NO:2769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769:

Met Glu Ile Ile Ser Leu Asn Val Val Pro Gln Cys Ser Val Val Thr  
1 5 10 15  
Trp Ser Ser Lys Leu Ala Thr Lys Arg Leu Val Pro Asn Arg Ser Ser  
20 25 30  
Leu Leu Phe Ser Gly Val Lys Lys Ser Arg Leu Val Ile Arg Ser Gly  
35 40 45  
Asn Ser Asp Gly Tyr Val Val Gly Glu Asn Asp Asp Leu Gly Arg Ile  
50 55 60  
Ala Arg Arg Gly Glu Ser Thr Ser Lys Val Leu Ile Pro Gly Leu Pro  
65 70 75 80  
Asp Glu Ser Asn Gly Glu Ile Ala Ala Arg Ile Ser His Ser His Cys  
85 90 95  
Glu Trp Lys Pro Lys Leu Arg Val His Tyr Glu Lys Ala Gly Cys Asp  
100 105 110  
Asn Leu Asp Ala Pro Ala Val Leu Phe Leu Pro Gly Phe Gly Val Gly  
115 120 125  
Ser Phe His Tyr Glu Lys Gln Leu Thr Asp Leu Gly Arg Asp Tyr Arg  
130 135 140  
Val Trp Ala Ile Asp Phe Leu Gly Gln Gly Leu Ser Leu Pro Thr Glu  
145 150 155 160  
Asp Pro Thr Thr Met Thr Glu Glu Thr Ser Ser Ser Glu Asp Lys Glu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Phe | Trp | Gly | 165 | Phe | Gly | Asp | Lys | Thr | Glu | Pro | Trp | Ala | Asp | 175 | Gln | Leu |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Val | Phe | Ser | Leu | Asp | Leu | Trp | Arg | Asp | Gln | Val | Gln | Tyr | Phe | Val | Glu |     |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| Glu | Val | Ile | Gly | Glu | Pro | Val | Tyr | Ile | Ala | Gly | Asn | Ser | Leu | Gly | Gly |     |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |     |
| Tyr | Val | Ala | Leu | Tyr | Phe | Ala | Ala | Thr | His | Pro | His | Leu | Val | Lys | Gly |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |     |
| Val | Thr | Leu | Leu | Asn | Ala | Thr | Pro | Phe | Trp | Gly | Phe | Phe | Pro | Asn | Pro |     |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |     |
| Val | Arg | Ser | Pro | Lys | Leu | Ala | Arg | Leu | Phe | Pro | Trp | Pro | Gly | Ala | Phe |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |
| Pro | Leu | Pro | Glu | Arg | Val | Lys | Lys | Ile | Thr | Glu | Leu | Val | Trp | Gln | Lys |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |     |
| Ile | Ser | Asp | Pro | Glu | Ser | Ile | Ala | Glu | Ile | Leu | Lys | Gln | Val | Tyr | Thr |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |     |
| Asp | His | Ser | Thr | Asn | Val | Asp | Lys | Val | Phe | Ser | Arg | Ile | Val | Glu | Val |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |     |
| Thr | Gln | His | Pro | Ala | Ala | Ala | Ala | Ser | Phe | Ala | Ser | Ile | Met | Leu | Ala |     |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |     |
| Pro | Gly | Gly | Glu | Leu | Ser | Phe | Ser | Glu | Ala | Leu | Ser | Arg | Cys | Lys | Glu |     |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |     |
| Asn | Asn | Val | Gln | Ile | Cys | Leu | Met | Tyr | Gly | Arg | Glu | Asp | Pro | Trp | Val |     |     |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |     |
| Arg | Pro | Leu | Trp | Gly | Lys | Lys | Ile | Lys | Lys | Glu | Ile | Pro | Asn | Ala | Pro |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |     |
| Tyr | Tyr | Glu | Ile | Ser | Pro | Ala | Gly | His | Cys | Pro | His | Asp | Glu | Val | Pro |     |     |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |     |
| Glu | Val | Val | Asn | Tyr | Leu | Met | Arg | Gly | Trp | Ile | Lys | His | Leu | Glu | Ser |     |     |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |     | 415 |     |     |     |
| Gly | Gly | Phe | Glu | Xaa | Ala | Pro | Ala | Phe | Gly | Gly | His |     |     |     |     |     |     |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..264

(D) OTHER INFORMATION: / Ceres Seq. ID 1574124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2770:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Thr | Glu | Glu | Thr | Ser | Ser | Ser | Glu | Asp | Lys | Glu | Pro | Phe | Trp | Gly |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |  |
| Phe | Gly | Asp | Lys | Thr | Glu | Pro | Trp | Ala | Asp | Gln | Leu | Val | Phe | Ser | Leu |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |
| Asp | Leu | Trp | Arg | Asp | Gln | Val | Gln | Tyr | Phe | Val | Glu | Glu | Val | Ile | Gly |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Glu | Pro | Val | Tyr | Ile | Ala | Gly | Asn | Ser | Leu | Gly | Gly | Tyr | Val | Ala | Leu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Tyr | Phe | Ala | Ala | Thr | His | Pro | His | Leu | Val | Lys | Gly | Val | Thr | Leu | Leu |  |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Asn | Ala | Thr | Pro | Phe | Trp | Gly | Phe | Phe | Pro | Asn | Pro | Val | Arg | Ser | Pro |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Lys | Leu | Ala | Arg | Leu | Phe | Pro | Trp | Pro | Gly | Ala | Phe | Pro | Leu | Pro | Glu |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Arg | Val | Lys | Lys | Ile | Thr | Glu | Leu | Val | Trp | Gln | Lys | Ile | Ser | Asp | Pro |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |

Glu Ser Ile Ala Glu Ile Leu Lys Gln Val Tyr Thr Asp His Ser Thr  
130 135 140  
Asn Val Asp Lys Val Phe Ser Arg Ile Val Glu Val Thr Gln His Pro  
145 150 155 160  
Ala Ala Ala Ala Ser Phe Ala Ser Ile Met Leu Ala Pro Gly Gly Glu  
165 170 175  
Leu Ser Phe Ser Glu Ala Leu Ser Arg Cys Lys Glu Asn Asn Val Gln  
180 185 190  
Ile Cys Leu Met Tyr Gly Arg Glu Asp Pro Trp Val Arg Pro Leu Trp  
195 200 205  
Gly Lys Lys Ile Lys Lys Glu Ile Pro Asn Ala Pro Tyr Tyr Glu Ile  
210 215 220  
Ser Pro Ala Gly His Cys Pro His Asp Glu Val Pro Glu Val Val Asn  
225 230 235 240  
Tyr Leu Met Arg Gly Trp Ile Lys His Leu Glu Ser Gly Gly Phe Glu  
245 250 255  
Xaa Ala Pro Ala Phe Gly Gly His  
260

(2) INFORMATION FOR SEQ ID NO:2771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| acccatcaca caatcctcaa aacagagtaa cccaaaaaac agagcaatct ctaaaaaaatc | 60   |
| tcaagaaacc tactaaaaat gggttcaacg gcggagacac aattaactcc ggtgcaagtc  | 120  |
| accgacgacg aagctgccct ctccgccatg caactagcca gtgcttccgt tcttYccgat  | 180  |
| ggctttaaaa tccgccttag agcttgacct tcttgagatt atggccaaga atggttctcc  | 240  |
| catgtctcct accgagatcg cttctaaact tccgaccaa aaccctgaag ctccgggtcat  | 300  |
| gctcgaccgt atcctccgtc ttcttacgtc ttactccgtc ttaacctgct ccaaccgtaa  | 360  |
| actttccggg gatggcggtt aacggattta cgggcttggt ccggtttgca agtatttgac  | 420  |
| caagaacgaa gatggtgttt ccattgctgc tctttgtctt atgaaccaag acaaggttct  | 480  |
| catggaaagc tggtagcatt tgaaggatgc aattcttgat ggtgggattc cattcaacaa  | 540  |
| ggcttatgga atgagcgctg tcgagtacca cgggactgac cctagattca acaaggctct  | 600  |
| taacaatgga atgtctaacc attccacaat caccatgaag aagattcttg agacctataa  | 660  |
| gggttttgaa ggattgactt ctttggttga tgttggtggt ggcattggtg ctacactcaa  | 720  |
| aatgattgtc tccaagtacc ctaatcttaa aggcataaac tttgatctcc cacatgtcat  | 780  |
| tgaagatgct ccttctcatc ctggtattga gcatgttgga ggagatatgt ttgtaagtgt  | 840  |
| ccctaaagggt gatgccatat tcatgaagtg gatatgtcat gactggagtg acgaacattg | 900  |
| cgtgaaattc ttgaaaaact gctacgagtc acttccagag gatggaaaag tgatattagc  | 960  |
| agagtgtata cttccagaga caccagactc aagcctctca accaaacaag tagtccatgt  | 1020 |
| cgattgcatt atgttggtc acaatcccgg aggcaaagaa cgaaccgaga aagagtttga   | 1080 |
| ggcattagcc aaagcatcag gcttcaaggg catcaaagtt Gtctgcgacg cttttggtgt  | 1140 |
| taaccttatt gagttactca agaagctcta aaaacaaaca atgttcctat gaagatgatt  | 1200 |
| tatatgtaaa cattatctca tatctccttc cacggttcca aaactatgct gtttaataat  | 1260 |
| gggttttt                                                           |      |

(2) INFORMATION FOR SEQ ID NO:2772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1574134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772:

Met Ala Leu Lys Ser Ala Leu Glu Leu Asp Leu Leu Glu Ile Met Ala  
1 5 10 15  
Lys Asn Gly Ser Pro Met Ser Pro Thr Glu Ile Ala Ser Lys Leu Pro  
20 25 30  
Thr Lys Asn Pro Glu Ala Pro Val Met Leu Asp Arg Ile Leu Arg Leu  
35 40 45  
Leu Thr Ser Tyr Ser Val Leu Thr Cys Ser Asn Arg Lys Leu Ser Gly  
50 55 60  
Asp Gly Val Glu Arg Ile Tyr Gly Leu Gly Pro Val Cys Lys Tyr Leu  
65 70 75 80  
Thr Lys Asn Glu Asp Gly Val Ser Ile Ala Ala Leu Cys Leu Met Asn  
85 90 95  
Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His Leu Lys Asp Ala Ile  
100 105 110  
Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe  
115 120 125  
Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Lys Val Phe Asn Asn Gly  
130 135 140  
Met Ser Asn His Ser Thr Ile Thr Met Lys Lys Ile Leu Glu Thr Tyr  
145 150 155 160  
Lys Gly Phe Glu Gly Leu Thr Ser Leu Val Asp Val Gly Gly Gly Ile  
165 170 175  
Gly Ala Thr Leu Lys Met Ile Val Ser Lys Tyr Pro Asn Leu Lys Gly  
180 185 190  
Ile Asn Phe Asp Leu Pro His Val Ile Glu Asp Ala Pro Ser His Pro  
195 200 205  
Gly Ile Glu His Val Gly Gly Asp Met Phe Val Ser Val Pro Lys Gly  
210 215 220  
Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp Trp Ser Asp Glu His  
225 230 235 240  
Cys Val Lys Phe Leu Lys Asn Cys Tyr Glu Ser Leu Pro Glu Asp Gly  
245 250 255  
Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Glu Thr Pro Asp Ser Ser  
260 265 270  
Leu Ser Thr Lys Gln Val Val His Val Asp Cys Ile Met Leu Ala His  
275 280 285  
Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu Phe Glu Ala Leu Ala  
290 295 300  
Lys Ala Ser Gly Phe Lys Gly Ile Lys Val Val Cys Asp Ala Phe Gly  
305 310 315 320  
Val Asn Leu Ile Glu Leu Leu Lys Lys Leu  
325 330

(2) INFORMATION FOR SEQ ID NO:2773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1574135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773:

Met Ala Lys Asn Gly Ser Pro Met Ser Pro Thr Glu Ile Ala Ser Lys  
1 5 10 15  
Leu Pro Thr Lys Asn Pro Glu Ala Pro Val Met Leu Asp Arg Ile Leu  
20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Leu | Thr | Ser | Tyr | Ser | Val | Leu | Thr | Cys | Ser | Asn | Arg | Lys | Leu | 35  | 40  | 45  |
| Ser | Gly | Asp | Gly | Val | Glu | Arg | Ile | Tyr | Gly | Leu | Gly | Pro | Val | Cys | Lys | 50  | 55  | 60  |
| Tyr | Leu | Thr | Lys | Asn | Glu | Asp | Gly | Val | Ser | Ile | Ala | Ala | Leu | Cys | Leu | 65  | 70  | 75  |
| Met | Asn | Gln | Asp | Lys | Val | Leu | Met | Glu | Ser | Trp | Tyr | His | Leu | Lys | Asp | 85  | 90  | 95  |
| Ala | Ile | Leu | Asp | Gly | Gly | Ile | Pro | Phe | Asn | Lys | Ala | Tyr | Gly | Met | Ser | 100 | 105 | 110 |
| Ala | Phe | Glu | Tyr | His | Gly | Thr | Asp | Pro | Arg | Phe | Asn | Lys | Val | Phe | Asn | 115 | 120 | 125 |
| Asn | Gly | Met | Ser | Asn | His | Ser | Thr | Ile | Thr | Met | Lys | Lys | Ile | Leu | Glu | 130 | 135 | 140 |
| Thr | Tyr | Lys | Gly | Phe | Glu | Gly | Leu | Thr | Ser | Leu | Val | Asp | Val | Gly | Gly | 145 | 150 | 155 |
| Gly | Ile | Gly | Ala | Thr | Leu | Lys | Met | Ile | Val | Ser | Lys | Tyr | Pro | Asn | Leu | 165 | 170 | 175 |
| Lys | Gly | Ile | Asn | Phe | Asp | Leu | Pro | His | Val | Ile | Glu | Asp | Ala | Pro | Ser | 180 | 185 | 190 |
| His | Pro | Gly | Ile | Glu | His | Val | Gly | Asp | Met | Phe | Val | Ser | Val | Pro |     | 195 | 200 | 205 |
| Lys | Gly | Asp | Ala | Ile | Phe | Met | Lys | Trp | Ile | Cys | His | Asp | Trp | Ser | Asp | 210 | 215 | 220 |
| Glu | His | Cys | Val | Lys | Phe | Leu | Lys | Asn | Cys | Tyr | Glu | Ser | Leu | Pro | Glu | 225 | 230 | 235 |
| Asp | Gly | Lys | Val | Ile | Leu | Ala | Glu | Cys | Ile | Leu | Pro | Glu | Thr | Pro | Asp | 245 | 250 | 255 |
| Ser | Ser | Leu | Ser | Thr | Lys | Gln | Val | Val | His | Val | Asp | Cys | Ile | Met | Leu | 260 | 265 | 270 |
| Ala | His | Asn | Pro | Gly | Gly | Lys | Glu | Arg | Thr | Glu | Lys | Glu | Phe | Glu | Ala | 275 | 280 | 285 |
| Leu | Ala | Lys | Ala | Ser | Gly | Phe | Lys | Gly | Ile | Lys | Val | Val | Cys | Asp | Ala | 290 | 295 | 300 |
| Phe | Gly | Val | Asn | Leu | Ile | Glu | Leu | Leu | Lys | Lys | Leu |     |     |     |     | 305 | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:2774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1574136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Ser | Pro | Thr | Glu | Ile | Ala | Ser | Lys | Leu | Pro | Thr | Lys | Asn | Pro | Glu | 1  | 5  | 10 | 15 |
| Ala | Pro | Val | Met | Leu | Asp | Arg | Ile | Leu | Arg | Leu | Leu | Thr | Ser | Tyr | Ser | 20 | 25 | 30 |    |
| Val | Leu | Thr | Cys | Ser | Asn | Arg | Lys | Leu | Ser | Gly | Asp | Gly | Val | Glu | Arg | 35 | 40 | 45 |    |
| Ile | Tyr | Gly | Leu | Gly | Pro | Val | Cys | Lys | Tyr | Leu | Thr | Lys | Asn | Glu | Asp | 50 | 55 | 60 |    |
| Gly | Val | Ser | Ile | Ala | Ala | Leu | Cys | Leu | Met | Asn | Gln | Asp | Lys | Val | Leu | 65 | 70 | 75 | 80 |
| Met | Glu | Ser | Trp | Tyr | His | Leu | Lys | Asp | Ala | Ile | Leu | Asp | Gly | Gly | Ile | 85 | 90 | 95 |    |
| Pro | Phe | Asn | Lys | Ala | Tyr | Gly | Met | Ser | Ala | Phe | Glu | Tyr | His | Gly | Thr |    |    |    |    |



100 105 110  
Asp Pro Arg Phe Asn Lys Val Phe Asn Asn Gly Met Ser Asn His Ser  
115 120 125  
Thr Ile Thr Met Lys Lys Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly  
130 135 140  
Leu Thr Ser Leu Val Asp Val Gly Gly Gly Ile Gly Ala Thr Leu Lys  
145 150 155 160  
Met Ile Val Ser Lys Tyr Pro Asn Leu Lys Gly Ile Asn Phe Asp Leu  
165 170 175  
Pro His Val Ile Glu Asp Ala Pro Ser His Pro Gly Ile Glu His Val  
180 185 190  
Gly Gly Asp Met Phe Val Ser Val Pro Lys Gly Asp Ala Ile Phe Met  
195 200 205  
Lys Trp Ile Cys His Asp Trp Ser Asp Glu His Cys Val Lys Phe Leu  
210 215 220  
Lys Asn Cys Tyr Glu Ser Leu Pro Glu Asp Gly Lys Val Ile Leu Ala  
225 230 235 240  
Glu Cys Ile Leu Pro Glu Thr Pro Asp Ser Ser Leu Ser Thr Lys Gln  
245 250 255  
Val Val His Val Asp Cys Ile Met Leu Ala His Asn Pro Gly Gly Lys  
260 265 270  
Glu Arg Thr Glu Lys Glu Phe Glu Ala Leu Ala Lys Ala Ser Gly Phe  
275 280 285  
Lys Gly Ile Lys Val Val Cys Asp Ala Phe Gly Val Asn Leu Ile Glu  
290 295 300  
Leu Leu Lys Lys Leu  
305

(2) INFORMATION FOR SEQ ID NO:2775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaaaccac cattcaaaca aaacacaaaa acaaaaaaaaa aaacatttcc ccaaaaaaaaa | 60  |
| aaaaacagag gatgaaacaa aaccagagca agtttttgag aataatctca acgcctctaa  | 120 |
| gagcttttag caaggcacgt gattttctac tgagaagcat caccggttgc gcaGctcgga  | 180 |
| ctcaatattc ctctctcgcc tccgtctccg ctctttttcc aagaagccgg agctctctct  | 240 |
| ccgcgcctt ctctctctcc gcatcatccc ggagaaccac cgatttcggg atagatgaag   | 300 |
| attacagcga gctagtgaga gctgcgtcgg tgaggagtgt agggcacaag aatgagatag  | 360 |
| acatgttgat acaagagaag ctgcaacagc agaagcaaca gaagcaagga gggttgccta  | 420 |
| agagctcgag tgctgggatg gcgaggatag aggaagagga agaaacagag gaaggatctg  | 480 |
| tgaatccgaa Ggtgaagaag actaagaaag tctctgatct tttgtatcct cgtagcaaat  | 540 |
| cttacgccgt tactactagt acccctatct tgtaacttct cttcttattt tttcttcttc  | 600 |
| ttaatttttag tattttgtgg attgattatc attttctagc tcgatttttc gtgcactgtg | 660 |
| aaatactatt ttcttagctt gatttt                                       |     |

(2) INFORMATION FOR SEQ ID NO:2776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1574142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2776:

Lys Pro Thr Ile Gln Thr Lys His Lys Asn Lys Lys Lys Asn Ile Ser  
1 5 10 15  
Pro Lys Lys Lys Lys Gln Arg Met Lys Gln Asn Gln Ser Lys Phe Leu  
20 25 30  
Arg Ile Ile Ser Thr Pro Leu Arg Ala Leu Gly Lys Ala Arg Asp Phe  
35 40 45  
Tyr Val Arg Ser Ile Thr Gly Cys Ala Ala Arg Thr Gln Tyr Ser Ser  
50 55 60  
Ser Ala Ser Val Ser Ala Pro Phe Pro Arg Ser Arg Ser Ser Ser Ser  
65 70 75 80  
Ala Ala Phe Ser Ser Ser Ala Ser Ser Arg Arg Thr Thr Asp Phe Gly  
85 90 95  
Ile Asp Glu Asp Tyr Ser Glu Leu Val Arg Ala Ala Ser Val Arg Ser  
100 105 110  
Leu Gly His Lys Asn Glu Ile Asp Met Leu Ile Gln Glu Lys Leu Gln  
115 120 125  
Gln Gln Lys Gln Gln Lys Gln Gly Gly Leu Pro Lys Ser Ser Ser Ala  
130 135 140  
Gly Met Ala Arg Ile Glu Glu Glu Glu Thr Glu Glu Gly Ser Val  
145 150 155 160  
Asn Pro Lys Val Lys Lys Thr Lys Lys Val Ser Asp Leu Leu Tyr Pro  
165 170 175  
Arg Ser Lys Ser Tyr Ala Val Thr Thr Ser Thr Pro Ile Leu  
180 185 190

(2) INFORMATION FOR SEQ ID NO:2777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1574143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2777:

Met Lys Gln Asn Gln Ser Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu  
1 5 10 15  
Arg Ala Leu Gly Lys Ala Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly  
20 25 30  
Cys Ala Ala Arg Thr Gln Tyr Ser Ser Ala Ser Val Ser Ala Pro  
35 40 45  
Phe Pro Arg Ser Arg Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala  
50 55 60  
Ser Ser Arg Arg Thr Thr Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu  
65 70 75 80  
Leu Val Arg Ala Ala Ser Val Arg Ser Leu Gly His Lys Asn Glu Ile  
85 90 95  
Asp Met Leu Ile Gln Glu Lys Leu Gln Gln Gln Lys Gln Gln Lys Gln  
100 105 110  
Gly Gly Leu Pro Lys Ser Ser Ser Ala Gly Met Ala Arg Ile Glu Glu  
115 120 125  
Glu Glu Glu Thr Glu Glu Gly Ser Val Asn Pro Lys Val Lys Lys Thr  
130 135 140  
Lys Lys Val Ser Asp Leu Leu Tyr Pro Arg Ser Lys Ser Tyr Ala Val  
145 150 155 160  
Thr Thr Ser Thr Pro Ile Leu  
165

(2) INFORMATION FOR SEQ ID NO:2778:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 892 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..892  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574148  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aatcaaaaaa | ctatccactc | tcagccgga  | aatttttcct | tgattcatta  | cgacagagag | 60  |
| aaccatgccg | gcgaaacaga | ggaccccgaa | gGtcaacaga | aaccctgata  | tgatcagggg | 120 |
| tgtttgtaaa | tactcgagat | cccagatgta | ccataagaga | ggtttggtgg  | ctatcaaggc | 180 |
| caaaaatgga | ggcgttttcc | cacgtcacga | cgctaaatct | aagggtgatg  | ctccggtgga | 240 |
| gaagccaccg | aagttctatc | cagctgaaga | tgtaagaaa  | cctctcccca  | acaggcgcac | 300 |
| ggcaaaacca | accaagctca | gagctagcat | tactccaggt | acagtgttga  | ttatccttgc | 360 |
| tggtagggtc | aagggaaaga | gagttgtctt | ccttaagcag | cttgccctctg | gtttgtctct | 420 |
| tgtgactgga | ccattcaaga | tcaatggtgt | tcctttgaga | cgtgttaacc  | aggcctatgt | 480 |
| gattggcact | tccacaaagg | ttgacatttc | tggagtcacc | ctcgataaat  | tcgatgataa | 540 |
| gtactttggc | aaggttgctg | agaagaaaaa | gaagaagaca | gaaggagagt  | tccttgaggc | 600 |
| tgagaaagag | gagaagaagg | agatcccaca | ggtgaagaaa | gatgaccaga  | aagctgtgga | 660 |
| tgcagctttg | atcaaagcca | ttgaagcagt | tccagagttg | aagacttacc  | ttggcgcaag | 720 |
| gttttcattg | aaacaaggaa | tgaagcccca | tgagcttggt | ttctagattt  | cattactttt | 780 |
| tttctgaggt | ctctagagta | tctgtctcct | gaagtgtttt | accttctaaa  | tggttggttt | 840 |
| gttcttggtc | actgaacaca | tacaattttt | ggcttatata | ttctctgttc  | tt         |     |

(2) INFORMATION FOR SEQ ID NO:2779:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 233 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..233  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574149  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2779:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ala | Lys | Gln | Arg | Thr | Pro | Lys | Val | Asn | Arg | Asn | Pro | Asp | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Arg | Gly | Val | Gly | Lys | Tyr | Ser | Arg | Ser | Gln | Met | Tyr | His | Lys | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Trp | Ala | Ile | Lys | Ala | Lys | Asn | Gly | Gly | Val | Phe | Pro | Arg | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Lys | Ser | Lys | Val | Asp | Ala | Pro | Val | Glu | Lys | Pro | Pro | Lys | Phe |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Pro | Ala | Glu | Asp | Val | Lys | Lys | Pro | Leu | Pro | Asn | Arg | Arg | Thr | Ala |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Pro | Thr | Lys | Leu | Arg | Ala | Ser | Ile | Thr | Pro | Gly | Thr | Val | Leu | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Leu | Ala | Gly | Arg | Phe | Lys | Gly | Lys | Arg | Val | Val | Phe | Leu | Lys | Gln |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Ala | Ser | Gly | Leu | Leu | Leu | Val | Thr | Gly | Pro | Phe | Lys | Ile | Asn | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Pro | Leu | Arg | Arg | Val | Asn | Gln | Ala | Tyr | Val | Ile | Gly | Thr | Ser | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | Asp | Ile | Ser | Gly | Val | Thr | Leu | Asp | Lys | Phe | Asp | Asp | Lys | Tyr |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Gly | Lys | Val | Ala | Glu | Lys | Lys | Lys | Lys | Lys | Thr | Glu | Gly | Glu | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Glu | Ala | Glu | Lys | Glu | Glu | Lys | Lys | Glu | Ile | Pro | Gln | Val | Lys | Lys |

180 185 190  
Asp Asp Gln Lys Ala Val Asp Ala Ala Leu Ile Lys Ala Ile Glu Ala  
195 200 205  
Val Pro Glu Leu Lys Thr Tyr Leu Gly Ala Arg Phe Ser Leu Lys Gln  
210 215 220  
Gly Met Lys Pro His Glu Leu Val Phe  
225 230

(2) INFORMATION FOR SEQ ID NO:2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1574150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2780:

Met Tyr His Lys Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn Gly Gly  
1 5 10 15  
Val Phe Pro Arg His Asp Ala Lys Ser Lys Val Asp Ala Pro Val Glu  
20 25 30  
Lys Pro Pro Lys Phe Tyr Pro Ala Glu Asp Val Lys Lys Pro Leu Pro  
35 40 45  
Asn Arg Arg Thr Ala Lys Pro Thr Lys Leu Arg Ala Ser Ile Thr Pro  
50 55 60  
Gly Thr Val Leu Ile Ile Leu Ala Gly Arg Phe Lys Gly Lys Arg Val  
65 70 75 80  
Val Phe Leu Lys Gln Leu Ala Ser Gly Leu Leu Val Thr Gly Pro  
85 90 95  
Phe Lys Ile Asn Gly Val Pro Leu Arg Arg Val Asn Gln Ala Tyr Val  
100 105 110  
Ile Gly Thr Ser Thr Lys Val Asp Ile Ser Gly Val Thr Leu Asp Lys  
115 120 125  
Phe Asp Asp Lys Tyr Phe Gly Lys Val Ala Glu Lys Lys Lys Lys Lys  
130 135 140  
Thr Glu Gly Glu Phe Phe Glu Ala Glu Lys Glu Lys Lys Glu Ile  
145 150 155 160  
Pro Gln Val Lys Lys Asp Asp Gln Lys Ala Val Asp Ala Ala Leu Ile  
165 170 175  
Lys Ala Ile Glu Ala Val Pro Glu Leu Lys Thr Tyr Leu Gly Ala Arg  
180 185 190  
Phe Ser Leu Lys Gln Gly Met Lys Pro His Glu Leu Val Phe  
195 200 205

(2) INFORMATION FOR SEQ ID NO:2781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1013

(D) OTHER INFORMATION: / Ceres Seq. ID 1574151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2781:

cacaacttac tcttgctgca tgcttacgcc gttgacgcat tcagaaaatg caaacagtgt 60  
gctggaggta aaataggaat tgcacacagt ccagcttggt tcgaaccaca agaccttgag 120  
catgttgagg gttccattga acgtgtgctt gatttcatcc taggatggca tttggctcca 180  
acaacttatg gagattatcc acaatcgatg aaggatcggt tcggtcatag attgccaata 240

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| ttcacagaag  | ctgagaagaa  | gttgctgaag  | ggttctacag  | attacgtag   | aatgaattac  | 300 |
| tatacttcag  | tgtttgcaaa  | agaaattagc  | cctgattccta | agaatccgag  | ttggacgact  | 360 |
| gattctcttg  | ttgattggga  | tagcaagagt  | gtggatggat  | acaaaattgg  | tagcaagccg  | 420 |
| tttaatggta  | aactggatgt  | gtattcaaaa  | ggtttgagat  | accttttgaa  | gtatattaag  | 480 |
| gataactatg  | gcgaccCaga  | agtttatcatt | gccgagaatg  | gatacgggaga | agacCttgga  | 540 |
| gagaAgcaca  | atgacgtaaa  | ctttgggaca  | caagatcaca  | acaggaaata  | ttatatccaa  | 600 |
| aggcatctct  | tgagtatgca  | cgacgccatt  | tgcaaggaca  | aagtgaacgt  | tacgggatac  | 660 |
| tttgtgtggt  | cgttgatgga  | caactttgag  | tggaagatg   | ggtacaaggc  | gaggttcggga | 720 |
| ctttactaca  | togattttcca | gaacaacttg  | acccgtcacc  | aaaaagtttc  | gggcaaattgg | 780 |
| tattccgaat  | tcttcaaacc  | acagttttcca | acctccaagc  | tgagggaaga  | actctagatg  | 840 |
| atcaagaatc  | ctatcgggac  | aaaataaattg | agtacaagag  | tcttgaagat  | gttgttgagg  | 900 |
| ataaatatcag | tttgtgtggt  | ctatgtagtcg | ttttcatcta  | ccggtccttc  | ctatgtttaga | 960 |
| aggactttgtg | agttgttcaa  | gttttaataaa | tatcaataaaa | tgtcttctttt | ttt         |     |

(2) INFORMATION FOR SEQ ID NO:2782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1574152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2782:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1574153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2783:

Met Lys Asp Arg Val Gly His Arg Leu Pro Lys Phe Thr Glu Ala Glu  
1 5 10 15  
Lys Lys Leu Leu Lys Gly Ser Thr Asp Tyr Val Gly Met Asn Tyr Tyr  
20 25 30  
Thr Ser Val Phe Ala Lys Glu Ile Ser Pro Asp Pro Lys Asn Pro Ser  
35 40 45  
Trp Thr Thr Asp Ser Leu Val Asp Trp Asp Ser Lys Ser Val Asp Gly  
50 55 60  
Tyr Lys Ile Gly Ser Lys Pro Phe Asn Gly Lys Leu Asp Val Tyr Ser  
65 70 75 80  
Lys Gly Leu Arg Tyr Leu Leu Lys Tyr Ile Lys Asp Asn Tyr Gly Asp  
85 90 95  
Pro Glu Val Ile Ile Ala Glu Asn Gly Tyr Gly Glu Asp Leu Gly Glu  
100 105 110  
Lys His Asn Asp Val Asn Phe Gly Thr Gln Asp His Asn Arg Lys Tyr  
115 120 125  
Tyr Ile Gln Arg His Leu Leu Ser Met His Asp Ala Ile Cys Lys Asp  
130 135 140  
Lys Val Asn Val Thr Gly Tyr Phe Val Trp Ser Leu Met Asp Asn Phe  
145 150 155 160  
Glu Trp Gln Asp Gly Tyr Lys Ala Arg Phe Gly Leu Tyr Tyr Ile Asp  
165 170 175  
Phe Gln Asn Asn Leu Thr Arg His Gln Lys Val Ser Gly Lys Trp Tyr  
180 185 190  
Ser Glu Phe Leu Lys Pro Gln Phe Pro Thr Ser Lys Leu Arg Glu Glu  
195 200 205  
Leu

(2) INFORMATION FOR SEQ ID NO:2784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1574154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784:

Met Asn Tyr Tyr Thr Ser Val Phe Ala Lys Glu Ile Ser Pro Asp Pro  
1 5 10 15  
Lys Asn Pro Ser Trp Thr Thr Asp Ser Leu Val Asp Trp Asp Ser Lys  
20 25 30  
Ser Val Asp Gly Tyr Lys Ile Gly Ser Lys Pro Phe Asn Gly Lys Leu  
35 40 45  
Asp Val Tyr Ser Lys Gly Leu Arg Tyr Leu Leu Lys Tyr Ile Lys Asp  
50 55 60  
Asn Tyr Gly Asp Pro Glu Val Ile Ile Ala Glu Asn Gly Tyr Gly Glu

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 65                                                              | 70  | 75  | 80  |
| Asp Leu Gly Glu Lys His Asn Asp Val Asn Phe Gly Thr Gln Asp His |     |     |     |
| 85                                                              | 90  | 95  |     |
| Asn Arg Lys Tyr Tyr Ile Gln Arg His Leu Leu Ser Met His Asp Ala |     |     |     |
| 100                                                             | 105 | 110 |     |
| Ile Cys Lys Asp Lys Val Asn Val Thr Gly Tyr Phe Val Trp Ser Leu |     |     |     |
| 115                                                             | 120 | 125 |     |
| Met Asp Asn Phe Glu Trp Gln Asp Gly Tyr Lys Ala Arg Phe Gly Leu |     |     |     |
| 130                                                             | 135 | 140 |     |
| Tyr Tyr Ile Asp Phe Gln Asn Asn Leu Thr Arg His Gln Lys Val Ser |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Gly Lys Trp Tyr Ser Glu Phe Leu Lys Pro Gln Phe Pro Thr Ser Lys |     |     |     |
| 165                                                             | 170 | 175 |     |
| Leu Arg Glu Glu Leu                                             |     |     |     |
| 180                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1097
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2785:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| gcattaactg atttcacatt cttcgataag gattttactc tccaaagaaa gaaaaaaaaa  | 60   |
| cctcctctgc ttttgtgacg ctttaaggaa aaagacgaaa tggcaacgga atcgtagcaa  | 120  |
| gccgccatta aaggactcaa tgatcttctc agtacgaaag cggatctcgg aaacgtcgcc  | 180  |
| gccgcgaaga tcaaagcggt gacggcggaG ctaaaggagc ttgactcaag caattcagac  | 240  |
| gcaattgaac gaatcaagac cggttttact caattcaaaa ccgagaaaata tttgaagaat | 300  |
| agtactttgt tcaatcatct tgccaagact cagaccccaa agtttctggt gtttgcttgc  | 360  |
| tctgattctc gagtttgtcc atctcacatc ttgaatttcc aacctggtga ggcttttgtt  | 420  |
| gtcagaaaca tagccaatat ggttccacct tttgaccaga agagacactc tggagttggc  | 480  |
| gccgccgttg aatacgcagt tgtacatctc aagggtggaga acatttttgt gataggccat | 540  |
| agctgctgtg gtggtattaa gggactcatg tccattgaag atgatgctgc cccaactcaa  | 600  |
| agtgacttca ttgaaaattg ggtgaagata ggcgcacag cgaggaacaa gatcaaggag   | 660  |
| gaacataaag acttgagcta cgatgatcaa tgcaacaagt gtgagaagga agctgtgaac  | 720  |
| gtatcgcttg gaaacttgct ttcgtagcca ttctgtgagag ctgaggtggt gaagaacaca | 780  |
| cttgcaataa gaggaggtca ctacaatttc gtcaaaggaa cgtttgatct ctgggagctc  | 840  |
| gatttcaaga ccaactcctg ttttgcttcc tcttaagaaa gaaagctacc ggaacatata  | 900  |
| aaactctttt gagataaaaa aagacacttt gactcatctt tcttcattct ctcattgtga  | 960  |
| tgattcctct ccaacttctt tgattttctt ttgttaattc aaaacttcaa ctttgctgct  | 1020 |
| tctatttcaa aagctcaaac aataaagctg taaccaacgt ttgaaacttc tatatttgtc  | 1080 |
| taattgatgt ttgaacc                                                 |      |

(2) INFORMATION FOR SEQ ID NO:2786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2786:

|                                                                 |         |
|-----------------------------------------------------------------|---------|
| Met Ala Thr Glu Ser Tyr Glu Ala Ala Ile Lys Gly Leu Asn Asp Leu |         |
| 1                                                               | 5 10 15 |
| Leu Ser Thr Lys Ala Asp Leu Gly Asn Val Ala Ala Ala Lys Ile Lys |         |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Ala | Leu | Thr | Ala | Glu | Leu | Lys | Glu | Leu | Asp | Ser | Ser | Asn | Ser | Asp | Ala |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Glu | Arg | Ile | Lys | Thr | Gly | Phe | Thr | Gln | Phe | Lys | Thr | Glu | Lys | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Asn | Ser | Thr | Leu | Phe | Asn | His | Leu | Ala | Lys | Thr | Gln | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Phe | Leu | Val | Phe | Ala | Cys | Ser | Asp | Ser | Arg | Val | Cys | Pro | Ser | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Leu | Asn | Phe | Gln | Pro | Gly | Glu | Ala | Phe | Val | Val | Arg | Asn | Ile | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Met | Val | Pro | Pro | Phe | Asp | Gln | Lys | Arg | His | Ser | Gly | Val | Gly | Ala |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Val | Glu | Tyr | Ala | Val | Val | His | Leu | Lys | Val | Glu | Asn | Ile | Leu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Gly | His | Ser | Cys | Cys | Gly | Gly | Ile | Lys | Gly | Leu | Met | Ser | Ile | Glu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Asp | Asp | Ala | Ala | Pro | Thr | Gln | Ser | Asp | Phe | Ile | Glu | Asn | Trp | Val | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Gly | Ala | Ser | Ala | Arg | Asn | Lys | Ile | Lys | Glu | Glu | His | Lys | Asp | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Tyr | Asp | Asp | Gln | Cys | Asn | Lys | Cys | Glu | Lys | Glu | Ala | Val | Asn | Val |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Leu | Gly | Asn | Leu | Leu | Ser | Tyr | Pro | Phe | Val | Arg | Ala | Glu | Val | Val |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Lys | Asn | Thr | Leu | Ala | Ile | Arg | Gly | Gly | His | Tyr | Asn | Phe | Val | Lys | Gly |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     | 240 |
| Thr | Phe | Asp | Leu | Trp | Glu | Leu | Asp | Phe | Lys | Thr | Thr | Pro | Ala | Phe | Ala |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Phe | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1574161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2787:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Pro | Phe | Asp | Gln | Lys | Arg | His | Ser | Gly | Val | Gly | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Glu | Tyr | Ala | Val | Val | His | Leu | Lys | Val | Glu | Asn | Ile | Leu | Val | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | His | Ser | Cys | Cys | Gly | Gly | Ile | Lys | Gly | Leu | Met | Ser | Ile | Glu | Asp |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Asp | Ala | Ala | Pro | Thr | Gln | Ser | Asp | Phe | Ile | Glu | Asn | Trp | Val | Lys | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Ala | Ser | Ala | Arg | Asn | Lys | Ile | Lys | Glu | Glu | His | Lys | Asp | Leu | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Asp | Asp | Gln | Cys | Asn | Lys | Cys | Glu | Lys | Glu | Ala | Val | Asn | Val | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Gly | Asn | Leu | Leu | Ser | Tyr | Pro | Phe | Val | Arg | Ala | Glu | Val | Val | Lys |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asn | Thr | Leu | Ala | Ile | Arg | Gly | Gly | His | Tyr | Asn | Phe | Val | Lys | Gly | Thr |
|     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |     |
| Phe | Asp | Leu | Trp | Glu | Leu | Asp | Phe | Lys | Thr | Thr | Pro | Ala | Phe | Ala | Phe |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |



Ser  
145

(2) INFORMATION FOR SEQ ID NO:2788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..683
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788:

|             |            |          |             |         |            |             |         |      |    |
|-------------|------------|----------|-------------|---------|------------|-------------|---------|------|----|
| aacaacttaa  | acagatat   | ttt cata | aggaaa      | atgaagg | gtg agt    | tttttcac    | attgat  | ggca | 60 |
| ataatgtctc  | tcctcttagc | cttctc   | gtta gtccat | ggag    | gaggag     | agtc tggaac | acct    | 120  |    |
| tctaattgcag | ccgctacccc | gactag   | ccca accgaa | Ggat    | ccagt      | ggttc aagt  | ggttca  | 180  |    |
| gctcatggac  | ctaattgggg | atata    | gttkg ggat  | gggg    | ttc cagccc | cggt        | ggttat  | 240  |    |
| ggctatgggt  | ctggttcggg | ttcgtc   | acca gat    | ggagg   | ag gaaa    | agggc       | tggtat  | 300  |    |
| ctggttcggg  | ttcgtc     | acca gat | ggagg       | ag gaaa | agggc      | tggtat      | ctggg   | 360  |    |
| tttggttcgg  | ggtcagg    | ttc agga | actgga      | tttggg  | ttctg      | gctc        | gggagg  | 420  |    |
| acagacggtg  | gttctggcca | tggaag   | tggtg       | gg accg | gacacg     | ctgg        | ttaagg  | 480  |    |
| ggaagtggaa  | atggtgaagg | atctc    | ctggt       | cgtag   | agaga      | ggag        | ccaaca  | 540  |    |
| aagttttctt  | gttattatta | ctacct   | taac acaat  | cacac   | atgc       | gtaaga      | tgata   | 600  |    |
| aaaagaagga  | aaaagaaaaa | tactat   | agta gc     | atct    | ttaat      | taatta      | aatgc   | 660  |    |
| accaaaggaa  | taagtagttg | ggctt    | taatt       | accg    | ctgtac     | ttt         | gtaatat |      |    |
| ataatatatt  | gtgttcttgc | gcc      |             |         |            |             |         |      |    |

(2) INFORMATION FOR SEQ ID NO:2789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asn | Leu | Asn | Arg | Tyr | Phe | Ile | Arg | Lys | Met | Lys | Gly | Glu | Phe | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Met | Ala | Ile | Met | Ser | Leu | Leu | Leu | Ala | Phe | Ser | Leu | Val | His |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Gly | Gly | Gly | Glu | Ser | Gly | Thr | Pro | Ser | Asn | Ala | Ala | Ala | Thr | Pro | Thr |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Ser | Pro | Thr | Glu | Gly | Ser | Ser | Gly | Ser | Ser | Gly | Ser | Ala | His | Gly | Pro |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Asn | Trp | Gly | Tyr | Ser | Xaa | Gly | Trp | Gly | Ser | Ala | Pro | Gly | Gly | Gly | Tyr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Tyr | Gly | Ser | Gly | Ser | Gly | Ser | Ser | Pro | Asp | Gly | Gly | Gly | Lys | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Gly | Phe | Gly | Phe | Gly | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Gly | Phe | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Gly | Ser | Gly | Gly | Gly | Gly | Ala | Thr | Asp | Gly | Gly | Ser | Gly | His | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Gly | Thr | Gly | His | Ala | Gly |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..157  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790:

Met Glu Glu Glu Ser Leu Glu His Leu Leu Met Gln Pro Leu Pro Arg  
1 5 10 15  
Leu Ala Gln Pro Lys Asp Pro Val Val Gln Val Val Gln Leu Met Asp  
20 25 30  
Leu Ile Gly Asp Ile Val Xaa Asp Gly Val Gln Pro Arg Glu Val Val  
35 40 45  
Met Ala Met Val Leu Val Arg Val Arg His Gln Met Glu Glu Glu Lys  
50 55 60  
Gly Leu Asp Ser Gly Leu Val Arg Gly Gln Val Gln Glu Leu Asp Leu  
65 70 75 80  
Gly Leu Ala Arg Glu Glu Glu Pro Gln Thr Val Val Leu Ala Met  
85 90 95  
Glu Val Gly Pro Asp Thr Leu Val Lys Ala Val Ala Gln Glu Val Glu  
100 105 110  
Met Val Lys Asp Leu Leu Val Val Glu Arg Gly Ala Asn Thr Ala Lys  
115 120 125  
Arg Ser Phe Leu Val Ile Ile Thr Thr Leu Thr Gln Ser His Met Arg  
130 135 140  
Lys Met Ile Arg Leu Lys Glu Gly Lys Arg Lys Ile Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2791:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1574165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2791:

Met Gln Pro Leu Pro Arg Leu Ala Gln Pro Lys Asp Pro Val Val Gln  
1 5 10 15  
Val Val Gln Leu Met Asp Leu Ile Gly Asp Ile Val Xaa Asp Gly Val  
20 25 30  
Gln Pro Arg Glu Val Val Met Ala Met Val Leu Val Arg Val Arg His  
35 40 45  
Gln Met Glu Glu Glu Lys Gly Leu Asp Ser Gly Leu Val Arg Gly Gln  
50 55 60  
Val Gln Glu Leu Asp Leu Gly Leu Ala Arg Glu Glu Glu Glu Pro Gln  
65 70 75 80  
Thr Val Val Leu Ala Met Glu Val Gly Pro Asp Thr Leu Val Lys Ala  
85 90 95  
Val Ala Gln Glu Val Glu Met Val Lys Asp Leu Leu Val Val Glu Arg  
100 105 110  
Gly Ala Asn Thr Ala Lys Arg Ser Phe Leu Val Ile Ile Thr Thr Leu  
115 120 125  
Thr Gln Ser His Met Arg Lys Met Ile Arg Leu Lys Glu Gly Lys Arg  
130 135 140  
Lys Ile Leu  
145

(2) INFORMATION FOR SEQ ID NO:2792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..2133  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574194  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2792:

atgcccttcg gactcaagaa cgccggggga acctatcaac gcttcgtcaa caaaatcttc 60  
gcattacaga tcgggaagac aatggaagtt tacatcgacg acatggttgg gaaatccatg 120  
acagagaaaag atcacatatc ccattttacgc gaatgtttca agcagcttaa cctctacaac 180  
gtcaagctca atcctgcaaa gtgcgcttc ggagtaagat ccggcatcga ggcaaatccg 240  
aagcaaatcg aggcattgtt cggaatggcg tcacctcaga acaagcgaga agtgcagtgc 300  
ctaaccggaa gagttgcggc ccttaaccgt ttcattcttc gctcaaccga aaaatgttta 360  
gccttttacg ttgtgcttcg gggaacaaa aagttcgaat ggacgacccg atgcgaagaa 420  
gcttttcagg aactcaagaa gtacctggca actccacca tcctcgcaaa acccgtaatc 480  
ggagaaccac aatacttgta tggtgctgta tcagatacta cggtcagcgg agaattagtc 540  
cgagaagaca gaggcgagca gaaactgatt ttttacgtct cgcaaaactt caccagcgca 600  
gaatctcgct atccgcaaat ggaaaaactt gcttttagcag tcgtaatgtc ggctcagaag 660  
ctgcgaccct acttccaatc ccattccatc atagtaattg gatccatgcc actctgcgtc 720  
atcttacaca gtccaagcca atcaggacgt ctggctaagt ggacaatcga gctcagcgaa 780  
tacgacatcg agtatcagaa caaaacatgt gcaaagtcac ggctcgtcat cgaagcaagg 840  
ctcggttgta ggcatccgtc tcacctcacc aacaggagag gtccctcgagt agtcattaag 900  
attaaacttc gaggtacca acaatgtggc cgactcatcg cgaatcaatt caacggagaa 960  
tacacaactc aggacaaaa gatggaagcc tacctgattc atgttcaaaa tctagcgaag 1020  
aatttcgacg aattcgagtt gacaaggatt ccacgaggag aaaatacatc ggctgatgcc 1080  
ctggctgctc tagcctcgac atctgacacg atcctgaaaa gagtcatccc ggtggaattc 1140  
attgagaagc caagtattga gctcggcaaa gaagaacatg tcctcccaat acaaactcagc 1200  
gcggatcaag acgaccaga tgactgcaac tcagaatgga tggaaacctat cataagctat 1260  
atatccgaag ggaaattgcc ctgagacaaa tggaaagctc ggaaacttaa agctcaggct 1320  
gcacgtttcg ttctagtaga tgcaaaactt tacaaatggc gattatccgg gcccttgatg 1380  
acatgctgag aagcagaagc gatttgcaag atcatgaagg aaattcacgg tggctcgtgc 1440  
ggaaatcatt ccgggggaag ggctttagcc attaaaataa aacgccaagg atttttctgg 1500  
ccgacaatga tcaaagacta mgaaaatttt tcaaaacaat gcgaaaaatg tcaaaggcat 1560  
gcgcaaacaa tccatcagcc ggccgagctc ttgtcttcaa tcgcctcgcc gtatccattc 1620  
atgcgatggc caatggatat aattggacca atgcatccct cgaaggagaa aaaaatagtt 1680  
ctcgtctga cagactattt ctctaagtgg atagaggccg aattttacgc cagcataaag 1740  
gacgctcaag tcgagaactt cgtgttgaaa catatcctat gtcgccacgg gataccttat 1800  
gagatcgtaa cggataacgg ctgcgagttt atatcgaccc gcttccaagg cttctgtgat 1860  
aaatggggaa ttgacttag caagtcaaca ccacaatatc cccaaggaaa cggccaagcc 1920  
gaggccgcca acgaactcga aggtgttcta tggttgcac ggacaactcc tcgcogagcc 1980  
acaagagaaa cccctttcgc ctccgtctac ggaacggaat gcgtaattcc agctgaaatg 2040  
attgtaccaa gcctacgcc aagtctatct cccgaggacg atcctgataa tactcagagg 2100  
cccctcgacg aactcgatct gatcgatgaa tga

(2) INFORMATION FOR SEQ ID NO:2793:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 710 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..710  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2793:

Met Pro Phe Gly Leu Lys Asn Ala Gly Ala Thr Tyr Gln Arg Phe Val  
1 5 10 15  
Asn Lys Ile Phe Ala Leu Gln Ile Gly Lys Thr Met Glu Val Tyr Ile

2025 RELEASE UNDER E.O. 14176

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Asp | Asp | Met | Leu | Val | Lys | Ser | Met | Thr | Glu | Lys | Asp | His | Ile | Ser | His |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Leu | Arg | Glu | Cys | Phe | Lys | Gln | Leu | Asn | Leu | Tyr | Asn | Val | Lys | Leu | Asn |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Pro | Ala | Lys | Cys | Arg | Phe | Gly | Val | Arg | Ser | Gly | Ile | Glu | Ala | Asn | Pro |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Lys | Gln | Ile | Glu | Ala | Leu | Phe | Gly | Met | Ala | Ser | Pro | Gln | Asn | Lys | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Gln | Cys | Leu | Thr | Gly | Arg | Val | Ala | Ala | Leu | Asn | Arg | Phe | Ile |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ser | Arg | Ser | Thr | Glu | Lys | Cys | Leu | Ala | Phe | Tyr | Val | Val | Leu | Arg | Gly |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Asn | Lys | Lys | Phe | Glu | Trp | Thr | Thr | Arg | Cys | Glu | Glu | Ala | Phe | Gln | Glu |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Leu | Lys | Lys | Tyr | Leu | Ala | Thr | Pro | Pro | Ile | Leu | Ala | Lys | Pro | Val | Ile |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |
| Gly | Glu | Pro | Gln | Tyr | Leu | Tyr | Val | Ala | Val | Ser | Asp | Thr | Thr | Val | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Glu | Leu | Val | Arg | Glu | Asp | Arg | Gly | Glu | Gln | Lys | Leu | Ile | Phe | Tyr |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Val | Ser | Gln | Thr | Phe | Thr | Ser | Ala | Glu | Ser | Arg | Tyr | Pro | Gln | Met | Glu |
|     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |
| Lys | Leu | Ala | Leu | Ala | Val | Val | Met | Ser | Ala | Gln | Lys | Leu | Arg | Pro | Tyr |
|     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |
| Phe | Gln | Ser | His | Ser | Ile | Ile | Val | Met | Gly | Ser | Met | Pro | Leu | Cys | Val |
|     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |
| Ile | Leu | His | Ser | Pro | Ser | Gln | Ser | Gly | Arg | Leu | Ala | Lys | Trp | Thr | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Leu | Ser | Glu | Tyr | Asp | Ile | Glu | Tyr | Gln | Asn | Lys | Thr | Cys | Ala | Lys |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Ser | Arg | Leu | Val | Ile | Glu | Ala | Arg | Leu | Gly | Cys | Arg | His | Pro | Ser | His |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |
| Leu | Thr | Asn | Arg | Arg | Gly | Pro | Arg | Val | Val | Ile | Lys | Ile | Lys | Leu | Arg |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |
| Gly | Tyr | Gln | Gln | Cys | Gly | Arg | Leu | Ile | Ala | Asn | Gln | Phe | Asn | Gly | Glu |
|     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |
| Tyr | Thr | Thr | Gln | Asp | Lys | Lys | Met | Glu | Ala | Tyr | Leu | Ile | His | Val | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asn | Leu | Ala | Lys | Asn | Phe | Asp | Glu | Phe | Glu | Leu | Thr | Arg | Ile | Pro | Arg |
|     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |
| Gly | Glu | Asn | Thr | Ser | Ala | Asp | Ala | Leu | Ala | Ala | Leu | Ala | Ser | Thr | Ser |
|     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |
| Asp | Thr | Ile | Leu | Lys | Arg | Val | Ile | Pro | Val | Glu | Phe | Ile | Glu | Lys | Pro |
|     |     |     |     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |
| Ser | Ile | Glu | Leu | Gly | Lys | Glu | Glu | His | Val | Leu | Pro | Ile | Gln | Ile | Ser |
|     |     |     |     | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |
| Ala | Asp | Gln | Asp | Asp | Pro | Asp | Asp | Cys | Asn | Ser | Glu | Trp | Met | Glu | Pro |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Ile | Ile | Ser | Tyr | Ile | Ser | Glu | Gly | Lys | Leu | Pro | Ser | Asp | Lys | Trp | Lys |
|     |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |
| Ala | Arg | Lys | Leu | Lys | Ala | Gln | Ala | Ala | Arg | Phe | Val | Leu | Val | Asp | Ala |
|     |     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |
| Lys | Leu | Tyr | Lys | Trp | Arg | Leu | Ser | Gly | Pro | Leu | Met | Thr | Cys | Val | Glu |
|     |     |     |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |
| Ala | Glu | Ala | Ile | Cys | Lys | Ile | Met | Lys | Glu | Ile | His | Gly | Gly | Ser | Cys |
|     |     |     |     | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |
| Gly | Asn | His | Ser | Gly | Gly | Arg | Ala | Leu | Ala | Ile | Lys | Ile | Lys | Arg | Gln |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Gly | Phe | Phe | Trp | Pro | Thr | Met | Ile | Lys | Asp | Xaa | Glu | Asn | Phe | Ser | Lys |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |

Case 4:03-cv-00000-000

Gln Cys Glu Lys Cys Gln Arg His Ala Gln Thr Ile His Gln Pro Ala  
515 520 525  
Glu Leu Leu Ser Ser Ile Ala Ser Pro Tyr Pro Phe Met Arg Trp Ser  
530 535 540  
Met Asp Ile Ile Gly Pro Met His Pro Ser Lys Glu Lys Lys Ile Val  
545 550 555 560  
Leu Val Leu Thr Asp Tyr Phe Ser Lys Trp Ile Glu Ala Glu Phe Tyr  
565 570 575  
Ala Ser Ile Lys Asp Ala Gln Val Glu Asn Phe Val Leu Lys His Ile  
580 585 590  
Leu Cys Arg His Gly Ile Pro Tyr Glu Ile Val Thr Asp Asn Gly Ser  
595 600 605  
Gln Phe Ile Ser Thr Arg Phe Gln Gly Phe Cys Asp Lys Trp Gly Ile  
610 615 620  
Arg Leu Ser Lys Ser Thr Pro Gln Tyr Pro Gln Gly Asn Gly Gln Ala  
625 630 635 640  
Glu Ala Ala Asn Glu Leu Glu Gly Val Leu Trp Leu His Arg Thr Thr  
645 650 655  
Pro Arg Arg Ala Thr Arg Glu Thr Pro Phe Ala Ser Val Tyr Gly Thr  
660 665 670  
Glu Cys Val Ile Pro Ala Glu Met Ile Val Pro Ser Leu Arg Arg Ser  
675 680 685  
Leu Ser Pro Glu Asp Asp Pro Asp Asn Thr Gln Arg Pro Leu Asp Glu  
690 695 700  
Leu Asp Leu Ile Asp Glu  
705 710

(2) INFORMATION FOR SEQ ID NO:2794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..683

(D) OTHER INFORMATION: / Ceres Seq. ID 1574197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794:

Met Glu Val Tyr Ile Asp Asp Met Leu Val Lys Ser Met Thr Glu Lys  
1 5 10 15  
Asp His Ile Ser His Leu Arg Glu Cys Phe Lys Gln Leu Asn Leu Tyr  
20 25 30  
Asn Val Lys Leu Asn Pro Ala Lys Cys Arg Phe Gly Val Arg Ser Gly  
35 40 45  
Ile Glu Ala Asn Pro Lys Gln Ile Glu Ala Leu Phe Gly Met Ala Ser  
50 55 60  
Pro Gln Asn Lys Arg Glu Val Gln Cys Leu Thr Gly Arg Val Ala Ala  
65 70 75 80  
Leu Asn Arg Phe Ile Ser Arg Ser Thr Glu Lys Cys Leu Ala Phe Tyr  
85 90 95  
Val Val Leu Arg Gly Asn Lys Lys Phe Glu Trp Thr Thr Arg Cys Glu  
100 105 110  
Glu Ala Phe Gln Glu Leu Lys Lys Tyr Leu Ala Thr Pro Pro Ile Leu  
115 120 125  
Ala Lys Pro Val Ile Gly Glu Pro Gln Tyr Leu Tyr Val Ala Val Ser  
130 135 140  
Asp Thr Thr Val Ser Gly Glu Leu Val Arg Glu Asp Arg Gly Glu Gln  
145 150 155 160  
Lys Leu Ile Phe Tyr Val Ser Gln Thr Phe Thr Ser Ala Glu Ser Arg  
165 170 175  
Tyr Pro Gln Met Glu Lys Leu Ala Leu Ala Val Val Met Ser Ala Gln

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|     |     |     |     |     |     |     |     |     |     |       |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|
|     |     |     |     |     |     |     |     |     |     |       |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |       |     |     | 190 |     |     |
| Lys | Leu | Arg | Pro | Tyr | Phe | Gln | Ser | His | Ser | Ile   | Ile | Val | Met | Gly | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |       |     | 205 |     |     |     |
| Met | Pro | Leu | Cys | Val | Ile | Leu | His | Ser | Pro | Ser   | Gln | Ser | Gly | Arg | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |       | 220 |     |     |     |     |
| Ala | Lys | Trp | Thr | Ile | Glu | Leu | Ser | Glu | Tyr | Asp   | Ile | Glu | Tyr | Gln | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235   |     |     |     |     | 240 |
| Lys | Thr | Cys | Ala | Lys | Ser | Arg | Leu | Val | Ile | Glu   | Ala | Arg | Leu | Gly | Cys |
|     |     |     |     | 245 |     |     |     |     | 250 |       |     |     |     | 255 |     |
| Arg | His | Pro | Ser | His | Leu | Thr | Asn | Arg | Arg | Gly   | Pro | Arg | Val | Val | Ile |
|     |     |     | 260 |     |     |     |     | 265 |     |       |     |     | 270 |     |     |
| Lys | Ile | Lys | Leu | Arg | Gly | Tyr | Gln | Gln | Cys | Gly   | Arg | Leu | Ile | Ala | Asn |
|     |     | 275 |     |     |     |     | 280 |     |     |       |     | 285 |     |     |     |
| Gln | Phe | Asn | Gly | Glu | Tyr | Thr | Thr | Gln | Asp | Lys   | Lys | Met | Glu | Ala | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |       | 300 |     |     |     |     |
| Leu | Ile | His | Val | Gln | Asn | Leu | Ala | Lys | Asn | Phe   | Asp | Glu | Phe | Glu | Leu |
| 305 |     |     |     | 310 |     |     |     |     |     | 315   |     |     |     |     | 320 |
| Thr | Arg | Ile | Pro | Arg | Gly | Glu | Asn | Thr | Ser | Ala   | Asp | Ala | Leu | Ala | Ala |
|     |     |     |     | 325 |     |     |     |     | 330 |       |     |     |     | 335 |     |
| Leu | Ala | Ser | Thr | Ser | Asp | Thr | Ile | Leu | Lys | Arg   | Val | Ile | Pro | Val | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |       |     |     | 350 |     |     |
| Phe | Ile | Glu | Lys | Pro | Ser | Ile | Glu | Leu | Gly | Lys   | Glu | Glu | His | Val | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |       |     | 365 |     |     |     |
| Pro | Ile | Gln | Ile | Ser | Ala | Asp | Gln | Asp | Asp | Pro   | Asp | Asp | Cys | Asn | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |       | 380 |     |     |     |     |
| Glu | Trp | Met | Glu | Pro | Ile | Ile | Ser | Tyr | Ile | Ser   | Glu | Gly | Lys | Leu | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395   |     |     |     |     | 400 |
| Ser | Asp | Lys | Trp | Lys | Ala | Arg | Lys | Leu | Lys | Ala   | Gln | Ala | Ala | Arg | Phe |
|     |     |     |     | 405 |     |     |     |     | 410 |       |     |     |     | 415 |     |
| Val | Leu | Val | Asp | Ala | Lys | Leu | Tyr | Lys | Trp | Arg   | Leu | Ser | Gly | Pro | Leu |
|     |     |     | 420 |     |     |     |     | 425 |     |       |     |     | 430 |     |     |
| Met | Thr | Cys | Val | Glu | Ala | Glu | Ala | Ile | Cys | Lys   | Ile | Met | Lys | Glu | Ile |
|     |     | 435 |     |     |     |     | 440 |     |     |       |     | 445 |     |     |     |
| His | Gly | Gly | Ser | Cys | Gly | Asn | His | Ser | Gly | Gly   | Arg | Ala | Leu | Ala | Ile |
|     | 450 |     |     |     |     | 455 |     |     |     |       | 460 |     |     |     |     |
| Lys | Ile | Lys | Arg | Gln | Gly | Phe | Phe | Trp | Pro | Thr   | Met | Ile | Lys | Asp | Xaa |
| 465 |     |     |     |     | 470 |     |     |     |     | 475   |     |     |     |     | 480 |
| Glu | Asn | Phe | Ser | Lys | Gln | Cys | Glu | Lys | Cys | Gln   | Arg | His | Ala | Gln | Thr |
|     |     |     |     | 485 |     |     |     |     | 490 |       |     |     |     | 495 |     |
| Ile | His | Gln | Pro | Ala | Glu | Leu | Leu | Ser | Ser | Ile   | Ala | Ser | Pro | Tyr | Pro |
|     |     |     | 500 |     |     |     |     | 505 |     |       |     |     | 510 |     |     |
| Phe | Met | Arg | Trp | Ser | Met | Asp | Ile | Ile | Gly | Pro   | Met | His | Pro | Ser | Lys |
|     |     | 515 |     |     |     |     | 520 |     |     |       |     | 525 |     |     |     |
| Glu | Lys | Lys | Ile | Val | Leu | Val | Leu | Thr | Asp | Tyr</ |     |     |     |     |     |

Arg Pro Leu Asp Glu Leu Asp Leu Ile Asp Glu  
675 680

(2) INFORMATION FOR SEQ ID NO:2795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795:

accgtcgctcg ttgaggcccc accgaagaca ccaccagttc caaatttcga tttcactccc 60  
ttcgactaca ttttgagaa atctgcttac aagaacgttt tagtcg

(2) INFORMATION FOR SEQ ID NO:2796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796:

Thr Val Val Val Ala Pro Pro Lys Thr Pro Pro Val Pro Asn Phe  
1 5 10 15  
Asp Phe Thr Pro Phe Asp Tyr Ile Leu Glu Lys Ser Ala Tyr Lys Asn  
20 25 30  
Val Leu Val  
35

(2) INFORMATION FOR SEQ ID NO:2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797:

Pro Ser Ser Leu Arg Pro His Arg Arg His His Gln Phe Gln Ile Ser  
1 5 10 15  
Ile Ser Leu Pro Ser Thr Thr Phe Trp Arg Asn Leu Leu Thr Arg Thr  
20 25 30  
Phe

(2) INFORMATION FOR SEQ ID NO:2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1574218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798:

acggatacat caaaggcgat agaacaaagc acatcctacc aaaattcttc tacacacacg 60  
atctacaaaa gagcgcgat gtacgagttc tacagatccg ttcgaaatgga atattctggc 120  
tgacttattc acaaaggcgc tacctactgc tactttcaag aa

(2) INFORMATION FOR SEQ ID NO:2799:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1574219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799:

Thr Asp Thr Ser Lys Ala Ile Glu Gln Ser Thr Ser Tyr Gln Asn Ser  
1 5 10 15  
Ser Thr His Thr Ile Tyr Lys Arg Ala Met Tyr Glu Phe Tyr Arg  
20 25 30  
Ser Val Arg Met Glu Tyr Ser Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:2800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1574220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800:

Gly Tyr Ile Lys Gly Asp Arg Thr Lys His Ile Leu Pro Lys Phe Phe  
1 5 10 15  
Tyr Thr His Asp Leu Gln Lys Ser Gly Asp Val Arg Val Leu Gln Ile  
20 25 30  
Arg Ser Asn Gly Ile Phe Trp Leu Thr Tyr Ser Gln Arg Arg Tyr Leu  
35 40 45  
Leu Leu Leu Ser Arg  
50

(2) INFORMATION FOR SEQ ID NO:2801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 581 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..581

(D) OTHER INFORMATION: / Ceres Seq. ID 1574260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801:

ataatggcat aattccatat ttctccagct gttccgccga gcgaacgacc cacaaccaga 60  
agccacccat tggcgtagcg gaggcgatcg gagcatcccg tccaagagg agaaactccg 120  
gccggcgacg cgggggaaaa tggggaagac gccgggtgagg atgaaggcgg tgggtgtacgc 180  
gctgtcgccc ttccagcaga aggtgatgcc ggggctgtgg aaggacatca ccaccaagat 240  
ccaccacaag gtcaccgaga actggatctc cgccacgctc ctctcacc ccgtcgtcgg 300



cacctaccaa tacgccatgt ggtacaaaga gcaggagaag ctttcccaca gatactaaat 360  
gggatgtcct ccaagttgct gcggcttgct gcagttgaat tttccatgat gggttgtata 420  
atctgtcaat gtcatttctt tgctcagttt tagttcaacc cattttcacc tttccatatg 480  
catatacggg atctgtgcct ggcaaacata ttttgaggct agctaaatat gaaccttttg 540  
tctcttaagt tgttaaataa agcaaaaAtba tctgacagtt t

(2) INFORMATION FOR SEQ ID NO:2802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802:

Asn Gly Ile Ile Pro Tyr Phe Ser Ser Cys Ser Ala Glu Arg Thr Thr  
1 5 10 15  
His Asn Gln Lys Pro Pro Ile Gly Val Arg Glu Ala Ile Gly Ala Ser  
20 25 30  
Arg Pro Lys Arg Arg Asn Ser Gly Arg Arg Arg Gly Gly Lys Trp Gly  
35 40 45  
Arg Arg Arg Cys Gly  
50

(2) INFORMATION FOR SEQ ID NO:2803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803:

Met Gly Lys Thr Pro Val Arg Met Lys Ala Val Val Tyr Ala Leu Ser  
1 5 10 15  
Pro Phe Gln Gln Lys Val Met Pro Gly Leu Trp Lys Asp Ile Thr Thr  
20 25 30  
Lys Ile His His Lys Val Thr Glu Asn Trp Ile Ser Ala Thr Leu Leu  
35 40 45  
Leu Thr Pro Val Val Gly Thr Tyr Gln Tyr Ala Met Trp Tyr Lys Glu  
50 55 60  
Gln Glu Lys Leu Ser His Arg Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:2804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2804:

Met Lys Ala Val Val Tyr Ala Leu Ser Pro Phe Gln Gln Lys Val Met  
1 5 10 15

Tyr  
65

(i) SEQUENCE CHARACTERISTICS:

- (A) NAME/KEY: -  
(B) LOCATION: 1..809  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574264

| (X1) SEQUENCE DESCRIPTION |            |            |            |             |             |     |
|---------------------------|------------|------------|------------|-------------|-------------|-----|
| caggataagtt               | tggctaccct | cgtcgtcgtc | tcactcacc  | cgccttcacg  | cctccctcac  | 60  |
| caaataaggt                | cccgcccttt | tccgacattc | acagggggga | caggaaatca  | goggccatgg  | 120 |
| cctcgattcc                | ggcgacgacc | ttcgccgtca | tcttatccgt | cctcttctgt  | gocgcggctg  | 180 |
| gcaccgccgt                | cgacaacgac | ctccccgact | acgtcatcca | gggcgcgcgtc | tattgcgaca  | 240 |
| cctgccgcgc                | cgggttcgtg | accaatgtca | ccgagtacat | cgcgggcgc   | aaggtgaggc  | 300 |
| tggagtgcaa                | gcacttcggc | acgggcaagc | tcgagcgcct | catcgacggg  | gtgaccgacg  | 360 |
| ggaacggcac                | gtacacgwtc | gagctcaagg | acagccacga | ggaggacatc  | tgcgaggtgg  | 420 |
| tcttggtgga                | gagcccgcg  | aaggactGgc | gaccaggtgc | aggcggacag  | ggaccgcgcc  | 480 |
| ggcgtcctgy                | tcaccaggaa | cgtcggcctc | agcgacaacc | tgcgccccgc  | caaccgcgtc  | 540 |
| ggctacctca                | aggacgtgcc | gctgcccatc | tgcgctcgc  | tgctcaaaca  | gttggaactcg | 600 |
| gacgacgacg                | acgdtcagta | atagcacatc | gacgacgacg | dtcgatatgt  | aatagcacgt  | 660 |
| cgtcgacgac                | cgaccgcagt | cgtcgcagac | tggctggcac | taaacccaa   | atcctcttca  | 720 |
| cctggaattac               | aaatatgtaa | ctgagaaaag | aaagaaaac  | aaaaatgtaa  | ctgcgtggct  | 780 |
| gtaccgaatt                | ctgagtgctg | gattcttgc  |            |             |             |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..207
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1574265

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ile | Pro | Ala | Thr | Thr | Phe | Ala | Val | Ile | Leu | Ser | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Cys | Ala | Ala | Ala | Gly | Thr | Ala | Val | Asp | Asn | Asp | Leu | Pro | Asp | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ile | Gln | Gly | Arg | Val | Tyr | Cys | Asp | Thr | Cys | Arg | Ala | Gly | Phe | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Asn | Val | Thr | Glu | Tyr | Ile | Ala | Gly | Ala | Lys | Val | Arg | Leu | Glu | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | His | Phe | Gly | Thr | Gly | Lys | Leu | Glu | Arg | Ser | Ile | Asp | Gly | Val | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Gly | Asn | Gly | Thr | Tyr | Thr | Xaa | Glu | Leu | Lys | Asp | Ser | His | Glu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ile | Cys | Glu | Val | Val | Leu | Val | Glu | Ser | Pro | Arg | Lys | Asp | Trp | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Gly | Ala | Gly | Gly | Gln | Gly | Pro | Arg | Arg | Arg | Pro | Xaa | His | Gln | Glu |

115 120 125  
Arg Arg His Gln Arg Gln Pro Ala Pro Arg Gln Pro Ala Arg Leu Pro  
130 135 140  
Gln Gly Arg Ala Ala Ala His Leu Arg Leu Ala Ala Gln Thr Val Gly  
145 150 155 160  
Leu Gly Arg Arg Arg Xaa Ser Val Ile Ala His Arg Arg Arg Xaa Ser  
165 170 175  
Ile Cys Asn Ser Thr Ser Ser Thr Thr Asp Arg Ser Arg Arg Arg Leu  
180 185 190  
Ala Gly Thr Lys Pro Gln Ile Leu Phe Thr Trp Ile Thr Asn Met  
195 200 205

(2) INFORMATION FOR SEQ ID NO:2807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..645
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2807:

atcggtgagg cgagccgcga gtggaactgt ggaagcgttg agcttttttc ttctttgtct 60  
tgctgcgcaa gaagaaggga aacgagaggc ggcggcgcat ggcgaagagg ctgctcccgt 120  
cgctgaaccg ggtgctggtg gagaagctgg tgcagcccaa gaagaccgcc ggcggcatcc 180  
tcgtcccgga aacatccaag cagattaggt tgatgtcttt cctgagactg ttgcctcaaa 240  
ggctacccca acttatcagg caggtggagc aagatgttga gactgtaac cacgttctcc 300  
agccgggtcc aataggaatt Ggtggagcac aaattcacag acgcggagat cttagaggcc 360  
agggctacag tgaaaagaGg cagtggataa ttggcgaaga aattggaccc ttgagagaaa 420  
tgttagcaga taaatggaaa aaatataccc ctggtgtctt ctatcaacag twattgnbvk 480  
raatagggtg ccatggctgg atgcagttgt tgccattagt tagatttgag cacgatctgc 540  
ttatcgggag ttatgttaac tgttctaaat gatcagtcgt tttctctttg tttcatggtt 600  
tgaaacgttc atatttagag aatgcagtaa ttcgactccg attcg

(2) INFORMATION FOR SEQ ID NO:2808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2808:

Met Ala Lys Arg Leu Leu Pro Ser Leu Asn Arg Val Leu Val Glu Lys  
1 5 10 15  
Leu Val Gln Pro Lys Lys Thr Ala Gly Gly Ile Leu Val Pro Glu Thr  
20 25 30  
Ser Lys Gln Ile Arg Leu Met Ser Phe Leu Arg Leu Leu Pro Gln Arg  
35 40 45  
Leu Pro Gln Leu Ile Arg Gln Val Glu Gln Asp Val Glu Thr Val Ile  
50 55 60  
His Val Leu Gln Pro Gly Pro Ile Gly Ile Gly Gly Ala Gln Ile His  
65 70 75 80  
Arg Arg Gly Asp Leu Arg Gly Gln Gly Tyr Ser Glu Lys Arg Gln Trp  
85 90 95  
Ile Ile Gly Glu Glu Ile Gly Pro Leu Arg Glu Met Leu Ala Asp Lys  
100 105 110  
Trp Lys Lys Tyr Thr Pro Gly Val Phe Tyr Gln Gln Xaa Leu Xaa Xaa

115 120 125  
Ile Gly Cys His Gly Trp Met Gln Leu Leu Pro Leu Val Arg Phe Glu  
130 135 140  
His Asp Leu Leu Ile Gly Ser Tyr Val Asn Cys Ser Lys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809:

Met Ser Phe Leu Arg Leu Leu Pro Gln Arg Leu Pro Gln Leu Ile Arg  
1 5 10 15  
Gln Val Glu Gln Asp Val Glu Thr Val Ile His Val Leu Gln Pro Gly  
20 25 30  
Pro Ile Gly Ile Gly Gly Ala Gln Ile His Arg Arg Gly Asp Leu Arg  
35 40 45  
Gly Gln Gly Tyr Ser Glu Lys Arg Gln Trp Ile Ile Gly Glu Glu Ile  
50 55 60  
Gly Pro Leu Arg Glu Met Leu Ala Asp Lys Trp Lys Lys Tyr Thr Pro  
65 70 75 80  
Gly Val Phe Tyr Gln Xaa Leu Xaa Xaa Ile Gly Cys His Gly Trp  
85 90 95  
Met Gln Leu Leu Pro Leu Val Arg Phe Glu His Asp Leu Leu Ile Gly  
100 105 110  
Ser Tyr Val Asn Cys Ser Lys  
115

(2) INFORMATION FOR SEQ ID NO:2810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..766
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810:

agatcagcat tcaaactagg gtttactcct gccgctccga gaaaacaaac aagcgctcast 60  
ccgccggcgtt cctccgcgct ttctccccgc cgycgccgcc gccgctcctt ccctacgcca 120  
ggcacgccaa gatgaagctc gtcagggttcc ttatgaagct gaacaatgag acggtcacca 180  
tcgagctcaa gaacggcacg gttgtacacg gcaccatcac cgggtgttgac ataagcatga 240  
acactcatct gaagacagtg aagcttacac tgaaagggaa gaacctgta acacttgacc 300  
acctcagcgt gcgaggaaac aacatccgct actacatcct tcccgcacagc ttaaacctgg 360  
aaaccttgct ggtagaggaa acccctaggg tgaagcctaa gaagccaact acaggaaagc 420  
ctttggggcg tggtcgcggc cgaggtcgtg gacgtggtcg gggccggggg Ccagctgag 480  
ctttatcggt cccctgctgt cggtccctt gcaagacaag ttctctctac aatgtaaaac 540  
dtctttcttc tgcacgctgt gtgaaagaat gttgcatcgt tacccttctg atgaaggtgg 600  
acgdaatatc tcaatgtcag tagttcttgc tgtgaaatca cgctgtctac ctggccccc 660  
tactcatgcc trtcttaggt ttacactcta gttratttgt aatgtttttt ttctcccccg 720  
tggaatacat gtaagctgcc gcagagcttt ggatgtctag ggttgt

(2) INFORMATION FOR SEQ ID NO:2811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Ile | Gln | Thr | Arg | Val | Tyr | Ser | Cys | Arg | Ser | Glu | Lys | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Arg | Xaa | Ser | Ala | Gly | Phe | Leu | Arg | Ala | Phe | Ser | Pro | Pro | Xaa | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Leu | Leu | Pro | Tyr | Ala | Arg | His | Ala | Lys | Met | Lys | Leu | Val | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Met | Lys | Leu | Asn | Asn | Glu | Thr | Val | Thr | Ile | Glu | Leu | Lys | Asn |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Thr | Val | Val | His | Gly | Thr | Ile | Thr | Gly | Val | Asp | Ile | Ser | Met | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | His | Leu | Lys | Thr | Val | Lys | Leu | Thr | Leu | Lys | Gly | Lys | Asn | Pro | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Leu | Asp | His | Leu | Ser | Val | Arg | Gly | Asn | Asn | Ile | Arg | Tyr | Tyr | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Asp | Ser | Leu | Asn | Leu | Glu | Thr | Leu | Leu | Val | Glu | Glu | Thr | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Val | Lys | Pro | Lys | Lys | Pro | Thr | Thr | Gly | Lys | Pro | Leu | Gly | Arg | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Pro | Arg |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1574314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..108  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574315  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813:  
Met Lys Leu Asn Asn Glu Thr Val Thr Ile Glu Leu Lys Asn Gly Thr  
1 5 10 15  
Val Val His Gly Thr Ile Thr Gly Val Asp Ile Ser Met Asn Thr His  
20 25 30  
Leu Lys Thr Val Lys Leu Thr Leu Lys Gly Lys Asn Pro Val Thr Leu  
35 40 45  
Asp His Leu Ser Val Arg Gly Asn Asn Ile Arg Tyr Tyr Ile Leu Pro  
50 55 60  
Asp Ser Leu Asn Leu Glu Thr Leu Leu Val Glu Glu Thr Pro Arg Val  
65 70 75 80  
Lys Pro Lys Lys Pro Thr Thr Gly Lys Pro Leu Gly Arg Gly Arg Gly  
85 90 95  
Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Pro Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:2814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..533  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814:

aacgaagctt gcttctacga gaggatatag agaggaagaa cagctcgtcc gagaccatga 60  
agagcagccc acacctggtg ctgatacctgt gcctccaggc cgctctggtc atgggCgtct 120  
tcgcccgttt ggctaaagaa aatgccctgg ttgagagcaa ggccatcgac atcaaccggg 180  
ggcagctcaa gtgctgcacc aactgcaact tctccttctc ggggctctac acctgcgacg 240  
acgtcaaaaa ggactgcgac cccgtctgca agaagtgcgt cgtcgccgtg cagcctcct 300  
actcgggcaa caacaagttc aggtgcaccg acaccttcct cggcattgtc ggcccaagt 360  
gctagctaga gaggaagaac gcgcgctgct gctagctgct atagcttctg tctccgccg 420  
ccggccgGcc gccggcCggt gNcatggttc acgtactgtg tgttgtgcta Ctacgtactg 480  
gcttcttgtg tgttcggttc ttgttggtct ctcgacagtg caccttgccg gcc

(2) INFORMATION FOR SEQ ID NO:2815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2815:

Arg Ser Leu Leu Leu Arg Glu Asp Ile Glu Arg Lys Asn Ser Ser Ser  
1 5 10 15  
Glu Thr Met Lys Ser Ser Pro His Leu Val Leu Ile Leu Cys Leu Gln  
20 25 30  
Ala Ala Leu Val Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala  
35 40 45

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Leu Val Glu Ser Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys  
50 55 60  
Cys Thr Asn Cys Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp  
65 70 75 80  
Val Lys Lys Asp Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val  
85 90 95  
His Ala Ser Tyr Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe  
100 105 110  
Leu Gly Met Cys Gly Pro Lys Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:2816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1574378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816:

Met Lys Ser Ser Pro His Leu Val Leu Ile Leu Cys Leu Gln Ala Ala  
1 5 10 15  
Leu Val Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala Leu Val  
20 25 30  
Glu Ser Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys Cys Thr  
35 40 45  
Asn Cys Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp Val Lys  
50 55 60  
Lys Asp Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val His Ala  
65 70 75 80  
Ser Tyr Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe Leu Gly  
85 90 95  
Met Cys Gly Pro Lys Cys  
100

(2) INFORMATION FOR SEQ ID NO:2817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1574379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817:

Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala Leu Val Glu Ser  
1 5 10 15  
Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys Cys Thr Asn Cys  
20 25 30  
Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp Val Lys Lys Asp  
35 40 45  
Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val His Ala Ser Tyr  
50 55 60  
Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe Leu Gly Met Cys  
65 70 75 80  
Gly Pro Lys Cys

(2) INFORMATION FOR SEQ ID NO:2818:

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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 818 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..818  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818:

```
gggccaaca cgaggctccc ggactcctca gttccttcgc tcctctgtaa cccrrrgcgg 60
ccgacgaggc cggngaccac cgacggcgac gatgggcggc ggcgagggca agtccaagaa 120
acgccgctct tctacctcct cagcggagga agaagggggg gaacggaaga ggcGggacaa 180
gaaggagagc aagaggagga gccgagacga cagggaggat gacgatgaca gacacaagaa 240
gaaggggaaa cacatcgaca ggaacaaagg aaaagagaga gattcgaaag ataggcattc 300
caaggagaag acgagcaaga gaaaagacaa ggacgcggcc ttcaaagaaa tatccaagga 360
tgactacttt gcaaagaaca acgagttcgc tacctggttg aaggaggaaa agggcaaata 420
tttctcagat ttgtcttcag agtctgctcg tgatcttttc ttgaagtttg tgaaacaatg 480
gaacaaaggc aagctgccat cacaatacta tgaggggatt acgagtggcc cacgatcagc 540
gcacaattgg aacatcaaag catgatacgt tttctggttc atcgggtctt cggcttgaga 600
tgtttttttg tttcctggcg agatttttct tatagttgca tctagcaact gcttttaata 660
ttctgggttg ttgtatttaa gctgatgttc agaatgtctg tctaaagcag gagggtagat 720
cgtgggtctc tctagtatcc agtgtttaac atcaacgcta cttttccatt gatcactact 780
gtctgatcct acaatgagca aacatactgt ttctgggg
```

(2) INFORMATION FOR SEQ ID NO:2819:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 187 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..187  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819:

```
Gly Pro Thr Arg Gly Ser Arg Thr Pro Gln Phe Leu Arg Ser Ser Val
1 5 10 15
Thr Xaa Xaa Gly Arg Arg Gly Arg Xaa Pro Pro Thr Ala Thr Met Gly
20 25 30
Gly Gly Glu Gly Lys Ser Lys Lys Arg Arg Ser Ser Thr Ser Ser Ala
35 40 45
Glu Glu Glu Gly Gly Glu Arg Lys Arg Arg Asp Lys Lys Glu Ser Lys
50 55 60
Arg Arg Ser Arg Asp Asp Arg Glu Asp Asp Asp Arg Arg His Lys Lys
65 70 75 80
Lys Gly Lys His Ile Asp Arg Asn Lys Gly Lys Glu Arg Asp Ser Lys
85 90 95
Asp Arg His Ser Lys Glu Lys Thr Ser Lys Arg Lys Asp Lys Asp Ala
100 105 110
Ala Phe Lys Glu Ile Ser Lys Asp Tyr Phe Ala Lys Asn Asn Glu
115 120 125
Phe Ala Thr Trp Leu Lys Glu Lys Gly Lys Tyr Phe Ser Asp Leu
130 135 140
Ser Ser Glu Ser Ala Arg Asp Leu Phe Leu Lys Phe Val Lys Gln Trp
145 150 155 160
Asn Lys Gly Lys Leu Pro Ser Gln Tyr Tyr Glu Gly Ile Thr Ser Gly
165 170 175
Pro Arg Ser Ala His Asn Trp Asn Ile Lys Ala
180 185
```



(2) INFORMATION FOR SEQ ID NO:2820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2820:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Gly | Gly | Glu | Gly | Lys | Ser | Lys | Lys | Arg | Arg | Ser | Ser | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ala | Glu | Glu | Glu | Gly | Gly | Glu | Arg | Lys | Arg | Arg | Asp | Lys | Lys | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Lys | Arg | Arg | Ser | Arg | Asp | Asp | Arg | Glu | Asp | Asp | Asp | Asp | Arg | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Lys | Lys | Gly | Lys | His | Ile | Asp | Arg | Asn | Lys | Gly | Lys | Glu | Arg | Asp |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Ser | Lys | Asp | Arg | His | Ser | Lys | Glu | Lys | Thr | Ser | Lys | Arg | Lys | Asp | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ala | Ala | Phe | Lys | Glu | Ile | Ser | Lys | Asp | Asp | Tyr | Phe | Ala | Lys | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Glu | Phe | Ala | Thr | Trp | Leu | Lys | Glu | Glu | Lys | Gly | Lys | Tyr | Phe | Ser |
|     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |
| Asp | Leu | Ser | Ser | Glu | Ser | Ala | Arg | Asp | Leu | Phe | Leu | Lys | Phe | Val | Lys |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Gln | Trp | Asn | Lys | Gly | Lys | Leu | Pro | Ser | Gln | Tyr | Tyr | Glu | Gly | Ile | Thr |
|     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| Ser | Gly | Pro | Arg | Ser | Ala | His | Asn | Trp | Asn | Ile | Lys | Ala |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..696
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2821:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| gcatccacgc  | tcgattcggc | cgttttccgc  | atccacggag | ccaggcgacc | gccgccgctt | 60  |
| ccctactcac  | ccttgccgg  | cgacgacgag  | cgccaccacg | gcaggatgac | gacgctgagg | 120 |
| aacctcaaga  | tcaagacgtc | gacgtgcaag  | aggatcgtga | aggAdctgcg | ctcgtacgag | 180 |
| aaggaggtgg  | agaaggaggc | ggccaagacc  | gccgacatga | aggagaaggg | cgctgatccc | 240 |
| tacgacctca  | aacagcagga | gaatgttttg  | gctgagtcaa | ggatgatggg | cccagactgc | 300 |
| cacaaacgac  | ttgaaactgc | actggctgac  | ttgaaagcaa | cactggctga | actgaaggag | 360 |
| tcaaattgagc | aaggtgccga | gattggagaa  | gctgagagta | caatcgcaga | agttgaagca | 420 |
| gttgtcaagc  | cagcagaaga | ttaaaactaaa | aaaactcttg | gtttgctgaa | ctgttagcgc | 480 |
| acatcctatt  | ttcgcatatt | gagcccttgt  | gagcttatta | cgagatgttt | gaggcgtgaa | 540 |
| atcctgtacc  | attatcatca | cttctatctt  | gaaatttgag | ttctgttcc  | caagttctaa | 600 |
| gcgttactgt  | ttgttgtctg | ggagagcgca  | catccctggc | ttctccggga | agttgttagt | 660 |
| gtaaattgaa  | attaagaaaa | atggacgaat  | ttgaat     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..147
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2822:

Ala Ser Thr Leu Asp Ser Ala Val Phe Arg Ile His Gly Ala Arg Arg  
1 5 10 15  
Pro Pro Pro Leu Pro Tyr Ser Pro Leu Ala Gly Asp Asp Glu Arg His  
20 25 30  
His Gly Arg Met Thr Thr Leu Arg Asn Leu Lys Ile Lys Thr Ser Thr  
35 40 45  
Cys Lys Arg Ile Val Lys Xaa Leu Arg Ser Tyr Glu Lys Glu Val Glu  
50 55 60  
Lys Glu Ala Ala Lys Thr Ala Asp Met Lys Glu Lys Gly Ala Asp Pro  
65 70 75 80  
Tyr Asp Leu Lys Gln Gln Glu Asn Val Leu Ala Glu Ser Arg Met Met  
85 90 95  
Val Pro Asp Cys His Lys Arg Leu Glu Thr Ala Leu Ala Asp Leu Lys  
100 105 110  
Ala Thr Leu Ala Glu Leu Lys Glu Ser Asn Glu Gln Gly Ala Glu Ile  
115 120 125  
Gly Glu Ala Glu Ser Thr Ile Ala Glu Val Glu Ala Val Val Lys Pro  
130 135 140  
Ala Glu Asp  
145

(2) INFORMATION FOR SEQ ID NO:2823:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..77
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2823:

Ile His Ala Arg Phe Gly Arg Phe Pro His Pro Arg Ser Gln Ala Thr  
1 5 10 15  
Ala Ala Ala Ser Leu Leu Thr Leu Gly Arg Arg Arg Arg Ala Pro Pro  
20 25 30  
Arg Gln Asp Asp Asp Ala Glu Glu Pro Gln Asp Gln Asp Val Asp Val  
35 40 45  
Gln Glu Asp Arg Glu Gly Xaa Ala Leu Val Arg Glu Gly Gly Gly Glu  
50 55 60  
Gly Gly Gly Gln Asp Arg Arg His Glu Gly Glu Gly Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2824:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..112
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1574389
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2824:

(2) INFORMATION FOR SEQ ID NO:2825:

(A) LENGTH: 560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..560

(D) OTHER INFORMATION: / Ceres Seq. ID 1574403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2825:

| (A1) SEQUENCE DESCRIPTION: SEQ. INFORMATION |            |            |            |            |            |     |
|---------------------------------------------|------------|------------|------------|------------|------------|-----|
| tctcttcaga                                  | aaacgaaatc | cactcaggag | cgaggaaaga | gggacagagg | agggatagat | 60  |
| ccccgggtc                                   | cacgcctcca | caaccatccg | tcccgatccc | gaccagcttt | gagatcgcg  | 120 |
| tggcggacgg                                  | ccgctgctgc | accttctctg | agatcctctt | cgccatcatc | ctcccgcccc | 180 |
| tcggcgtctt                                  | cctccgattc | ggctgctgca | gaatagagtt | ctgcatctgc | ctgctgctca | 240 |
| caatccttgg                                  | ctacgtcccc | ggaatcatct | acgcgatcta | tgtccttggt | gctctcgact | 300 |
| ctgaccagca                                  | cgagagggaa | tactacaccc | ttgcttagag | catctggttg | tgccaggcgg | 360 |
| gcctgcacag                                  | ttgagtcgaa | atcagtattt | tttttctcat | gtggattgtc | tgacatggca | 420 |
| taagcggcaa                                  | tgggtaacca | agtgttgtgg | tctatatctc | tgttacccaa | cttgtgagct | 480 |
| ctctttattg                                  | tgtccagatt | attcaaAtct | gtaattgtga | tactacaAga | gaataagatg | 540 |
| cgcattatc                                   | tctgaagact |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1574404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2826:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2827:

60  
120

```
cggccatgga gcacaagggc gccagcacc tcgcaagaaa cccgttcggc caaatcccag 180
cgtttcagga cggggacacg atgctctttg aatcccagc aatcgccaag tacgtgctcc 240
gcaaatactc caagtcagct caagtcgacc tgctccgtga gggcaaccg gaggaagccg 300
ccatggtaga cgtgtggacg gaggtcgagg cgcacaccta cctacccGgc catcgcgccc 360
wtyttctacg agtacgRtgg tgtaccccg cagacatggc acbacgccc accaggaggt 420
ggtggacgag agtgtggaga ggytcaggaa ggtcctcgac gtctacgagg cgcacctgta 480
caagaccaag cagctctatc tcgccgggga ctacttcagc ctgcgcgrts tcaaccacgt 540
cccgtacacc ttccacctca tgaggacacc gcnacgcgtc gctcttcgag gcgtatcctc 600
acgttaaggc ctggtgggag agagttatag cagcccgctc gctgcagaag ctgcgcccg 660
atatggtgat caaagcctga ttgcacgtac ctttgatca tcagattctt ccttggggtg 720
tatatatgca aggggtacct ttcttgcaar ataaataaag arataaataa atccgac
```

(2) INFORMATION FOR SEQ ID NO:2830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1574422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2830:

```
Gln Ala Lys Ile Ala Pro Val Arg Val Phe Gly Thr Ala Asp Phe Val
1 5 10 15
Asn Ala Ala Arg Val Met Ala Cys Leu Glu Glu Val Gly Val Glu Tyr
20 25 30
Glu Val Val Glu Val Asp Tyr Ala Ala Met Glu His Lys Gly Ala Gln
35 40 45
His Leu Ala Arg Asn Pro Phe Gly Gln Ile Pro Ala Phe Gln Asp Gly
50 55 60
Asp Thr Met Leu Phe Glu Ser Arg Ala Ile Ala Lys Tyr Val Leu Arg
65 70 75 80
Lys Tyr Ser Lys Ser Ala Gln Val Asp Leu Leu Arg Glu Gly Asn Pro
85 90 95
Glu Glu Ala Ala Met Val Asp Val Trp Thr Glu Val Glu Ala His Thr
100 105 110
Tyr Leu Pro Gly His Arg Ala Xaa Xaa Leu Arg Val Xaa Trp Cys Thr
115 120 125
Pro Pro Ser Met Ala Xaa Arg Pro Thr Arg Arg Trp Trp Thr Arg Val
130 135 140
Trp Arg Xaa Ser Gly Arg Ser Ser Thr Ser Thr Arg Arg Thr Cys Thr
145 150 155 160
Arg Pro Ser Ser Ser Ile Ser Pro Gly Thr Thr Ser Ala Ser Pro Xaa
165 170 175
Ser Thr Thr Ser Arg Thr Pro Ser Thr Ser
180 185
```

(2) INFORMATION FOR SEQ ID NO:2831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1574423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2831:

```
Met Ala Cys Leu Glu Val Gly Val Glu Tyr Glu Val Val Glu Val
1 5 10 15
```

(A) NAME/KEY: -

| Parameter                                 | Estimate | Standard Error | z-Statistic | p-Value |
|-------------------------------------------|----------|----------------|-------------|---------|
| Intercept                                 | 1.0000   | 0.0000         |             |         |
| Age                                       | 0.0000   | 0.0000         |             |         |
| Age squared                               | 0.0000   | 0.0000         |             |         |
| Age cubed                                 | 0.0000   | 0.0000         |             |         |
| Age quartic                               | 0.0000   | 0.0000         |             |         |
| Age quintic                               | 0.0000   | 0.0000         |             |         |
| Age sextic                                | 0.0000   | 0.0000         |             |         |
| Age septic                                | 0.0000   | 0.0000         |             |         |
| Age octic                                 | 0.0000   | 0.0000         |             |         |
| Age nonic                                 | 0.0000   | 0.0000         |             |         |
| Age decic                                 | 0.0000   | 0.0000         |             |         |
| Age undecic                               | 0.0000   | 0.0000         |             |         |
| Age duodecic                              | 0.0000   | 0.0000         |             |         |
| Age tredecic                              | 0.0000   | 0.0000         |             |         |
| Age quattuordecic                         | 0.0000   | 0.0000         |             |         |
| Age quindecic                             | 0.0000   | 0.0000         |             |         |
| Age sexdecic                              | 0.0000   | 0.0000         |             |         |
| Age septendecic                           | 0.0000   | 0.0000         |             |         |
| Age octodecic                             | 0.0000   | 0.0000         |             |         |
| Age novemdecic                            | 0.0000   | 0.0000         |             |         |
| Age vigintic                              | 0.0000   | 0.0000         |             |         |
| Age unguic                                | 0.0000   | 0.0000         |             |         |
| Age sexagesim                             | 0.0000   | 0.0000         |             |         |
| Age sexagesim squared                     | 0.0000   | 0.0000         |             |         |
| Age sexagesim cubed                       | 0.0000   | 0.0000         |             |         |
| Age sexagesim quartic                     | 0.0000   | 0.0000         |             |         |
| Age sexagesim quintic                     | 0.0000   | 0.0000         |             |         |
| Age sexagesim sextic                      | 0.0000   | 0.0000         |             |         |
| Age sexagesim septic                      | 0.0000   | 0.0000         |             |         |
| Age sexagesim octic                       | 0.0000   | 0.0000         |             |         |
| Age sexagesim nonic                       | 0.0000   | 0.0000         |             |         |
| Age sexagesim decic                       | 0.0000   | 0.0000         |             |         |
| Age sexagesim undecic                     | 0.0000   | 0.0000         |             |         |
| Age sexagesim duodecic                    | 0.0000   | 0.0000         |             |         |
| Age sexagesim tredecic                    | 0.0000   | 0.0000         |             |         |
| Age sexagesim quattuordecic               | 0.0000   | 0.0000         |             |         |
| Age sexagesim quindecic                   | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexdecic                    | 0.0000   | 0.0000         |             |         |
| Age sexagesim septendecic                 | 0.0000   | 0.0000         |             |         |
| Age sexagesim octodecic                   | 0.0000   | 0.0000         |             |         |
| Age sexagesim novemdecic                  | 0.0000   | 0.0000         |             |         |
| Age sexagesim vigintic                    | 0.0000   | 0.0000         |             |         |
| Age sexagesim unguic                      | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim                   | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim squared           | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim cubed             | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim quartic           | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim quintic           | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sextic            | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim septic            | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim octic             | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim nonic             | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim decic             | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim undecic           | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim duodecic          | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim tredecic          | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim quattuordecic     | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim quindecic         | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexdecic          | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim septendecic       | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim octodecic         | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim novemdecic        | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim vigintic          | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim unguic            | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim         | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim squared | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim cubed   | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim quartic | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim quintic | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim sextic  | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim septic  | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim octic   | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim nonic   | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim decic   | 0.0000   | 0.0000         |             |         |
| Age sexagesim sexagesim sexagesim und     |          |                |             |         |

(B) LOCATION: 1..756

(D) OTHER INFORMATION: / Ceres Seq. ID 1574438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2833:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aaaaaactta | gccgcgtgga | cgcacaccag | cacctgccct | cctcgcggtc  | gctgcctccc | 60  |
| tccgcgcgac | cgatctaccc | tccgcgcgca | ccatgtcgct | gatcgcgagg  | gaggacttcc | 120 |
| agcatatcct | gcgttttctg | aacaccaacg | tggatgggaa | gcagaagatc  | atgttcgcca | 180 |
| tgacctcaat | caaggggtgc | gggcgcgcgt | tctccaacat | cgtctgcaag  | aaggccgaca | 240 |
| tgcacatgaa | caagagggcc | ggcgaGctga | cgcctgatga | gctggagcgc  | ctRgatgNac | 300 |
| ggtcgtggcc | aaccctaggc | agttcaaggt | gccggactgg | ttcctcaaca  | ggaagaagga | 360 |
| ttacaaggac | ggcaggttct | cgcaggtcgt | ctccaacgcc | cttgatatga  | agctcagggg | 420 |
| cgaccttgag | aggctcaaga | agatcaggaa | ccaccgtggt | ctgcgtcact  | actggggcct | 480 |
| ccgtgtccgt | ggccagcaca | ccaagactac | tggcaggcgt | gbaaagaccg  | ttggtgtctc | 540 |
| caagaagcga | tgagctytat | atcaccccg  | caaattcttg | ccgcactacc  | atgtcggttt | 600 |
| gtgtccaaac | agtcctgatg | aagggtttct | gttkaggcwg | tkkcostgaaa | tgggtgtktg | 660 |
| ctctaggaca | atatcgcggt | tattgaacck | taatatatcg | tgtccctggg  | atgtgttttt | 720 |
| tttttgccac | tttataagta | atttcatttg | gatgag     |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1574439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2834:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Leu | Ala | Ala | Trp | Thr | His | Thr | Ser | Thr | Cys | Pro | Pro | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Arg | Cys | Leu | Pro | Pro | Arg | Asp | Arg | Ser | Thr | Leu | Arg | Arg | His | His | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asp | Arg | Arg | Gly | Gly | Leu | Pro | Ala | Tyr | Pro | Ala | Phe | Ala | Glu | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Arg | Gly | Trp | Glu | Ala | Glu | Asp | His | Val | Arg | His | Asp | Leu | Asn | Gln |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Cys | Arg | Ala | Pro | Leu | Gln | His | Arg | Leu | Gln | Glu | Gly | Arg | His |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | His | Glu | Gln | Glu | Gly | Arg | Arg | Ala | Asp | Ala |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1574440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2835:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Ile | Ala | Gly | Glu | Asp | Phe | Gln | His | Ile | Leu | Arg | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Thr | Asn | Val | Asp | Gly | Lys | Gln | Lys | Ile | Met | Phe | Ala | Met | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Lys | Gly | Val | Gly | Arg | Arg | Phe | Ser | Asn | Ile | Val | Cys | Lys | Lys | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ile | Asp | Met | Asn | Lys | Arg | Ala | Gly | Glu | Leu | Thr | Pro | Asp | Glu | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Arg | Xaa | Asp | Xaa | Arg | Ser | Trp | Pro | Thr | Leu | Gly | Ser | Ser | Arg | Cys |

Trp Gly Trp Leu Arg Ala Ile Gln Lys His Ser Ser Glu Asn Tyr Ser



20 25 30  
Val Gly Pro Lys Met Val Ser Leu Lys Val Pro Lys Arg Leu Ala Ala  
35 40 45  
Ser Val Leu Lys Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu  
50 55 60  
Val Ser Glu Ile Ser Met Ala Asn Ser Arg Lys Thr Tyr Pro Leu Ala  
65 70 75 80  
Pro Pro Leu Arg Leu Ile Ala His Trp Val Gly Val Val Trp Ile Ser  
85 90 95  
Gly

(2) INFORMATION FOR SEQ ID NO:2839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2839:

Met Val Ser Leu Lys Val Pro Lys Arg Leu Ala Ala Ser Val Leu Lys  
1 5 10 15  
Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Val Ser Glu Ile  
20 25 30  
Ser Met Ala Asn Ser Arg Lys Thr Tyr Pro Leu Ala Pro Pro Leu Arg  
35 40 45  
Leu Ile Ala His Trp Val Gly Val Val Trp Ile Ser Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..751
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2840:

aacacccgcca aaccctaaac accaaagccc cgcataataa taccttcccc tcccatcttt 60  
tccccctctcc tgccgcgcgcc gccgctcccc ctcccagctc gtgttccgct tcttgagcc 120  
gtcgccgcga agCGctccag agaacttccg tcaacatggg gaagacacgt ggtatgggag 180  
ccgggocgcaa Gctcaagacc caccgcaGga accagcgggt ggctgacaag gcatacaaga 240  
agagccatttt gggcaatgag tggaagaaac ctttcgctgg gtcattcccat gccaaagggca 300  
ttgtcctgga gaagattggt attgaggcca agcagcccaa ctccgctatc cgtaagtgtg 360  
ctcgtgttca gcttggttaag aatggcaaga agattgctgc cttcgtgcca aatgacgggt 420  
gtttgaacta cattgaggaa aatgatgagg tcttgattgc tggatttggt cgtaaggggc 480  
acgctgtggg agatatctct ggtgtccggt tcaaggctgt caaggtttcc ggtgtgtctc 540  
tgcttgccct tttcaaggag aagaaagaga agccaaggtc ttagattgct cttgctacca 600  
aaatcagcaa gcgtggagtt gaaacgggag ggcgttagat gattaagaag aatggttgct 660  
tgctatgttt gcagtgcatt cgtgcaattg ttaacctaaag attttgttgg tgaaaaacgat 720  
ttcttttctcag acctgttctt gttgagtgcc g

(2) INFORMATION FOR SEQ ID NO:2841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..193  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574510  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2841:

His Arg Gln Thr Leu Asn Thr Lys Ala Pro His Ile Asn Thr Phe Pro  
1                  5                  10                  15  
Ser His Leu Phe Pro Ser Pro Ala Ala Ala Ala Pro Ala Pro Ser  
          20                  25                  30  
Ser Cys Ser Ala Ser Cys Ser Arg Arg Glu Ala Leu Gln Arg Thr  
          35                  40                  45  
Ser Val Asn Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu  
          50                  55                  60  
Lys Thr His Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys  
65                  70                  75                  80  
Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His  
          85                  90                  95  
Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro  
          100                 105                 110  
Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly  
          115                 120                 125  
Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile  
          130                 135                 140  
Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His  
145                 150                 155                 160  
Ala Val Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser  
          165                 170                 175  
Gly Val Ser Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg  
          180                 185                 190  
Ser

- (2) INFORMATION FOR SEQ ID NO:2842:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 142 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..142  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1574511  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2842:

Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His  
1                  5                  10                  15  
Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu  
          20                  25                  30  
Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly  
          35                  40                  45  
Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala  
          50                  55                  60  
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile  
65                  70                  75                  80  
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn  
          85                  90                  95  
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly  
          100                 105                 110  
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser  
          115                 120                 125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2843:

Met Gly Ala Gly Arg Lys Leu Lys Thr His Arg Arg Asn Gln Arg Trp  
1 5 10 15  
Ala Asp Lys Ala Tyr Lys Lys Ser His Leu Gly Asn Glu Trp Lys Lys  
20 25 30  
Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Val Leu Glu Lys Ile  
35 40 45  
Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg  
50 55 60  
Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn  
65 70 75 80  
Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala  
85 90 95  
Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg  
100 105 110  
Phe Lys Val Lys Val Ser Gly Val Ser Leu Leu Ala Leu Phe Lys  
115 120 125  
Glu Lys Lys Glu Lys Pro Arg Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:2844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2844:

aaaggaaact cactccact ttactcctat ccactgcggc ctggacgcgt gcgagaggct 60  
tgaccaagca gcagcagcag cagcagcgat ggcgctctg aagctgtacg ggatgccgct 120  
gtccccaac gtggtgcgcg tggccaccgt gctcaacgag aagggcctcg acttcgagat 180  
cgtccccgtc gacctacca ccggcgccca caagcagccc gacttcctca ccctcaaccc 240  
tttcggccag atcccggctc tcgtcgacgg agacgaakyc tcttcgagtc ccgcgcgatc 300  
aaccggtaca tcgccagcaa gtacgcgtca gggcacggac ctgctccccg cgacggcgctc 360  
ggcggcgaac tggaggtgtg gctggagggtg gagtcgcacc acttctaccc gaacgcacgc 420  
ccgctggtgt tccagctgct cgtgaggccg ctccctggcg gcgccccgam gcggcggtgg 480  
tggaagaagca cgcggagcag ctcgccaagg tgctcgacgt gtacgaggcg cacctggccc 540  
gcaacaagta ccCtcgccgg ggacaagttc acgctcgccg acgccaacca cgcgtcctac 600  
ctgctctacc tcagcaagac cccaaggcc gggctcgctg ccgcccgcgc ccacgtcaag 660  
gcctggtggg aggccatcgc cgcgcgcgcc gcgttcacaga agaccgtcgc cgccatcccc 720  
ttgccccgc cgccctctc ctcggttga cctgccttg cgtgcctgg gtcgcggatg 780  
cgtcggagcc ccgagtcgaa taaaagaggc cgcacactgt cttgcatttg ctstgcgcca 840  
tgtgctataa cagcctgtgt aataaacact gttgctttcg tgtgtgttca ttgcctttt 900  
gttggttgtt ccttgcatat cctactagtg ctgatctttt tgtgaagctt ggattggatg 960  
gacgcgtttt cttgcgcc

(2) INFORMATION FOR SEQ ID NO:2845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1574524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2845:

Lys Glu Thr His Ser His Phe Thr Pro Ile His Cys Gly Leu Asp Ala  
1 5 10 15  
Cys Glu Arg Leu Asp Gln Ala Ala Ala Ala Ala Ala Met Ala Pro  
20 25 30  
Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val Arg Val Ala  
35 40 45  
Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp  
50 55 60  
Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Thr Leu Asn Pro  
65 70 75 80  
Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa Ser Ser Ser  
85 90 95  
Pro Ala Arg Ser Thr Gly Thr Ser Pro Ala Ser Thr Arg Gln Gly Thr  
100 105 110  
Asp Leu Leu Pro Ala Thr Ala Ser Ala Ala Asn Trp Arg Cys Gly Trp  
115 120 125  
Arg Trp Ser Arg Thr Thr Ser Thr Arg Thr His Arg Arg Trp Cys Ser  
130 135 140  
Ser Cys Ser  
145

(2) INFORMATION FOR SEQ ID NO:2846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1574525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2846:

Met Ala Pro Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val  
1 5 10 15  
Arg Val Ala Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val  
20 25 30  
Pro Val Asp Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Thr  
35 40 45  
Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa  
50 55 60  
Ser Ser Ser Pro Ala Arg Ser Thr Gly Thr Ser Pro Ala Ser Thr Arg  
65 70 75 80  
Gln Gly Thr Asp Leu Leu Pro Ala Thr Ala Ser Ala Ala Asn Trp Arg  
85 90 95  
Cys Gly Trp Arg Trp Ser Arg Thr Thr Ser Thr Arg Thr His Arg Arg  
100 105 110  
Trp Cys Ser Ser Cys Ser  
115

(2) INFORMATION FOR SEQ ID NO:2847:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2849:

(2) INFORMATION FOR SEQ ID NO:2850:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1574549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2850:

(2) INFORMATION FOR SEQ ID NO:2851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1574550

Ile Arg Ile Pro Val Thr Pro Pro Thr Arg Pro Gln Pro Glu Ala Ala  
1 5 10 15  
Lys Ala Pro Leu Thr Leu Ser Ala His Pro Ile Ala Arg Lys Lys Arg

20 25 30  
Glu Met Ser Tyr Tyr Gly Gln Gln Pro Pro Val Xaa Val Pro Pro Gln  
35 40 45  
Gln Gly Tyr Pro Gly Lys Asp Gly Tyr Pro Pro Ala Gly Tyr Pro Pro  
50 55 60  
Ala Gly Tyr Pro Pro Pro Ala Gln Gly Tyr Pro Pro Gln Gly Tyr Pro  
65 70 75 80  
Pro Gln Tyr Ala Gln Pro Pro Pro Pro Gln Gln Gln Gln Ser Ser Gly  
85 90 95  
Pro Ser Phe Met Glu Gly Cys Leu Ala Leu Cys Cys Cys Cys Leu  
100 105 110  
Leu Asp Ala Cys Phe  
115

(2) INFORMATION FOR SEQ ID NO:2854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2854:

Pro Tyr Ser Arg His Ala Pro Asn Thr Pro Thr Thr Arg Ser Ser Glu  
1 5 10 15  
Ser Ser Pro Asn Pro Leu Arg Ala Ser Asp Arg Lys Glu Glu Glu Gly  
20 25 30  
Asp Glu Leu Leu Arg Ala Ala Ala Pro Arg Xaa Arg Pro Ala Ala Ala  
35 40 45  
Arg Leu Pro Gly Gln Gly Arg Leu Pro Ala Ser Gly Val Pro Ala Gly  
50 55 60  
Arg Leu Pro Pro Ala Gly Ala Gly Leu Pro Ser Ala Gly Leu Pro Ser  
65 70 75 80  
Ala Val Arg Ala Ala Ala Ala Ser Thr Ala Ala Ala Glu Gln Arg Ala  
85 90 95  
Phe Leu His Gly Gly Met Leu Gly Cys Pro Leu Leu Leu Leu Pro Pro  
100 105 110  
Gly Arg Leu Leu Leu Arg Val Arg Gly Ala Asp Arg Arg Ile Arg His  
115 120 125  
Gly Asp Lys  
130

(2) INFORMATION FOR SEQ ID NO:2855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2855:

Met Ser Tyr Tyr Gly Gln Gln Pro Pro Val Xaa Val Pro Pro Gln Gln  
1 5 10 15  
Gly Tyr Pro Gly Lys Asp Gly Tyr Pro Pro Ala Gly Tyr Pro Pro Ala  
20 25 30  
Gly Tyr Pro Pro Pro Ala Gln Gly Tyr Pro Pro Gln Gly Tyr Pro Pro  
35 40 45

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Gln Tyr Ala Gln Pro Pro Pro Gln Gln Gln Gln Ser Ser Gly Pro  
50 55 60  
Ser Phe Met Glu Gly Cys Leu Ala Ala Leu Cys Cys Cys Leu Leu  
65 70 75 80  
Asp Ala Cys Phe

(2) INFORMATION FOR SEQ ID NO:2856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2856:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| agctagctag | cagcgcaaca | ccaccgatca  | gctatacaag | caaggtagct | acctagtaga | 60  |
| gtacgtagag | gccgggtctc | cagaagacga  | acatgtcgtg | gagctccgac | gagaaccaca | 120 |
| ggttcgagca | ggcgctggca | gattacgacg  | aggatactcc | aggacgctgg | cagctcgtrg | 180 |
| cccaggcggt | cggcgggcgg | aggacggcgg  | acgacgtctg | gcgccactac | ctgcacctgg | 240 |
| agggggacat | cgacgacatg | ggcgccaggg  | agcgggcgaa | ccgccgccgc | caacagtacc | 300 |
| gccgcaacgc | ccagcagcac | caacaccagc  | acggcgccaa | cgccaacgcc | aacgcccacg | 360 |
| ccagccgcaa | ccatattagt | cggcgggagCa | acggcggcgg | cgccagcagc | agtaacacta | 420 |
| acaacattag | tagtcatcgc | gctactaaca  | gcaacgacag | agccaaacgc | ccgcagGaat | 480 |
| gagacgccgg | ccggcaggag | agacgatgaa  | ccacacaacg | tacgtactat | cctactacca | 540 |
| taatatggtg | gatatcgcca | cctttccgcg  | tacgaacgtg | tatgctctaa | ttaaggaata | 600 |
| atcctagcta | tagcctatag | ccccagcta   | agggccttgt | cggttagctc | ttaatccata | 660 |
| tggattgaat | gggattggat | gggtttgaac  | ccaaacaagt | caaacttctt | ctcaattttt | 720 |
| tccaatctca | tccaatccat | gtgtattggg  | aataaccaaa | caagctctaa | tgtgtattgc | 780 |
| tctaattgtg | attgcatgca | tgccgcgtac  | gacggacgta | cgcaagtgta | aaaccttggg | 840 |
| cactatttat | atgtataaag | ttatatcgc   |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2857:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Trp | Ser | Ser | Asp | Glu | Asn | His | Arg | Phe | Glu | Gln | Ala | Leu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Tyr | Asp | Glu | Asp | Thr | Pro | Gly | Arg | Trp | Gln | Leu | Xaa | Ala | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gly | Gly | Gly | Arg | Thr | Ala | Asp | Asp | Val | Trp | Arg | His | Tyr | Leu | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | Gly | Asp | Ile | Asp | Asp | Met | Gly | Ala | Arg | Glu | Arg | Ala | Asn | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Arg | Gln | Gln | Tyr | Arg | Arg | Asn | Ala | Gln | Gln | His | Gln | His | Gln | His |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ala | Asn | Ala | Asn | Ala | Asn | Ala | His | Ala | Ser | Arg | Asn | His | Ile | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Arg | Ser | Asn | Gly | Gly | Gly | Ala | Ser | Ser | Ser | Asn | Thr | Asn | Asn | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ser | Ser | His | Arg | Ala | Thr | Asn | Ser | Asn | Asp | Arg | Ala | Lys | Arg | Pro | Gln |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |

Glu

(2) INFORMATION FOR SEQ ID NO:2858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2858:

Met Gly Ala Arg Glu Arg Ala Asn Arg Arg Arg Gln Gln Tyr Arg Arg  
1 5 10 15  
Asn Ala Gln Gln His Gln His Gln His Gly Ala Asn Ala Asn Ala Asn  
20 25 30  
Ala His Ala Ser Arg Asn His Ile Ser Arg Arg Ser Asn Gly Gly Gly  
35 40 45  
Ala Ser Ser Ser Asn Thr Asn Asn Ile Ser Ser His Arg Ala Thr Asn  
50 55 60  
Ser Asn Asp Arg Ala Lys Arg Pro Gln Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:2859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2859:

ttggttcgcg gccacatcac caagctccgg gcgctgctgt acgtcgccgc ccagctgctg 60  
gcgtcctccc tgcctgcat cctcctccgc tacctcagcg gcggcatggt gaccccagtg 120  
cacgccctgg gcgctggcat caaccgatg cagggcttgg tgatggagggt gatcctcacc 180  
ttctcgctgc tcttcgtcac ctacgccatg atcctggacc cgcgascag gtccgcacca 240  
tcggcccgtg gctgacgggg ctcatagtcg gcgccaacag cctcgccggc ggcaacttca 300  
ccggcgcgtc catgaaccgg gcgcgggtCt tcgggtcccgc catggccacc ggggtctgga 360  
ccaaccactg ggtctactgg atcgcccgcg tgctcggcgg gtccctggcc ggcttcgtgt 420  
acgagtcgct gttcatggtg aacaagacgc acgagccgct gctcaatgga gacatctgac 480  
gaccgtcggc ccccagggca gtgagcacgg ttcattgctt ttttctgtaa aatagttcgt 540  
tacctacaag catgatgcat atattgacca aggtaattaa ttagagaggg ttgctgttaa 600  
atagttaccc tgggtgggatt gtgggatgta gaaattgttg ctgggctttg cttttctttt 660  
ttcttttttt cttttcctcc caaggaattt tttaagaggg ctgggttctg taaaggattt 720  
gtttaggcta ttagttagct atatagtaga aaactagaga atgctatacg ttggacgtga 780  
ttttttttca cgtatattgt tgtacgatat ggtatttttt atcttccgga tgg

(2) INFORMATION FOR SEQ ID NO:2860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574617

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2860:

Leu Val Arg Gly His Ile Thr Lys Leu Arg Ala Leu Leu Tyr Val Ala  
1 5 10 15  
Ala Gln Leu Leu Ala Ser Ser Leu Ala Cys Ile Leu Leu Arg Tyr Leu  
20 25 30  
Ser Gly Gly Met Val Thr Pro Val His Ala Leu Gly Ala Gly Ile Asn  
35 40 45  
Pro Met Gln Gly Leu Val Met Glu Val Ile Leu Thr Phe Ser Leu Leu  
50 55 60  
Phe Val Thr Tyr Ala Met Ile Leu Asp Pro Arg Xaa Arg Ser Ala Pro  
65 70 75 80  
Ser Ala Arg Cys

(2) INFORMATION FOR SEQ ID NO:2861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2861:

Gly Ser Arg Pro His His Gln Ala Pro Gly Ala Ala Val Arg Arg Arg  
1 5 10 15  
Pro Ala Ala Gly Val Leu Pro Arg Leu His Pro Pro Pro Leu Pro Gln  
20 25 30  
Arg Arg His Gly Asp Pro Ser Ala Arg Pro Gly Arg Trp His Gln Pro  
35 40 45  
Asp Ala Gly Leu Gly Asp Gly Gly Asp Pro His Leu Leu Ala Ala Leu  
50 55 60  
Arg His Leu Arg His Asp Pro Gly Pro Ala Xaa Gln Val Arg Thr Ile  
65 70 75 80  
Gly Pro Leu Leu Thr Gly Leu Ile Val Gly Ala Asn Ser Leu Ala Gly  
85 90 95  
Gly Asn Phe Thr Gly Ala Ser Met Asn Pro Ala Arg Ser Phe Gly Pro  
100 105 110  
Ala Met Ala Thr Gly Val Trp Thr Asn His Trp Val Tyr Trp Ile Gly  
115 120 125  
Pro Leu Leu Gly Gly Ser Leu Ala Gly Phe Val Tyr Glu Ser Leu Phe  
130 135 140  
Met Val Asn Lys Thr His Glu Pro Leu Leu Asn Gly Asp Ile  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2862:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atcctcatca caggcaacaa ggcaccacac ctcttcttct tcttctctct cctcctagca | 60  |
| cagCtagcgc ctgctcccct tcgcctgtga tcatgtcttg cagcagcggc aagtgcgact | 120 |
| gtggctccag ctgctcctgc ggcagctcat gcaactgcat gtcccctaac gtggagaccg | 180 |
| ccgccgccag cagcatcaag accacggtcc tcgccgcgcc gaccaccaag gccagcgccg | 240 |

gcgggttcga ggcggccacc gagggcgccg gctgcgactg caacacctgc aactgcggca 300  
ccagctgcgg ctgctcctgc tgcagctgca actgagccgg tcaggcgatg gcgcacgaga 360  
gtcgagagga cgacgacgag tcgtataaat ataatagcgg cgtctaaata agatcctgtc 420  
aactgcaccc gccattatcg atccatggtc gctcctgggg ttcatgttca tctgtaacgt 480  
gctcgcggtc atgtccgtct cgtgccggat ttaatatatta tatgcatgta tttgtgtt

(2) INFORMATION FOR SEQ ID NO:2863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1574620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2863:

Pro His His Arg Gln Gln Gly Thr Thr Pro Leu Leu Leu Leu Pro Pro  
1 5 10 15  
Pro Pro Ser Thr Ala Ser Ala Cys Ser Pro Ser Pro Val Ile Met Ser  
20 25 30  
Cys Ser Ser Gly Lys Cys Asp Cys Gly Ser Ser Cys Ser Cys Gly Ser  
35 40 45  
Ser Cys Asn Cys Met Ser Pro Asn Val Glu Thr Ala Ala Ala Ser Ser  
50 55 60  
Ile Lys Thr Thr Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly  
65 70 75 80  
Gly Phe Glu Ala Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys  
85 90 95  
Asn Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1574621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2864:

Met Ser Cys Ser Ser Gly Lys Cys Asp Cys Gly Ser Ser Cys Ser Cys  
1 5 10 15  
Gly Ser Ser Cys Asn Cys Met Ser Pro Asn Val Glu Thr Ala Ala Ala  
20 25 30  
Ser Ser Ile Lys Thr Thr Val Leu Ala Ala Pro Thr Thr Lys Ala Ser  
35 40 45  
Ala Gly Gly Phe Glu Ala Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn  
50 55 60  
Thr Cys Asn Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..58  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574622  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2865:

```
Met Ser Pro Asn Val Glu Thr Ala Ala Ala Ser Ser Ile Lys Thr Thr
1 5 10 15
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala
 20 25 30
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Asn Cys Gly Thr
 35 40 45
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn
50 55
```

(2) INFORMATION FOR SEQ ID NO:2866:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 657 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..657  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2866:

```
arngccgtct ttcttctggtta cctgcccccg ctccccgaag ctccaaccct ttacagccgg 60
cgaagaagat gcacctgtgg ccatcgctcc ggatccgcga ctcgttcaag cacggctacc 120
tccagaagct ggagctcaac ctcggaaca tgaagcgcg gcagCGgcag cgccagggcc 180
ggcagggaga gagccaggag gaccaggacg gccagcccg cggcaacggg aaggcgccgc 240
tgctcgagga ccgctcgcca tcggggtoog tgcttgccgg cgcgctcgag ctgcgctggg 300
acgccgtctt gctcctcacc tgctgctgct gttgcttctg ctgcggagCt tgtagcgacg 360
aagaggatca cccaactgcc cgctaagaag caacttcagg tgcctgataa ttcacagat 420
cacgaaaacc agataatttg tgggcataat gaattggagt caaatagttc aaatagtttt 480
gatcagcttt gtacatatgg tttctatctc atccttatgc cgcccataga tgtcattgat 540
aaacgggaaa aaggatcctt aatttttttg ttggaaaccc gttgtgtagg tattttgggg 600
gtgtaatcag gtcgtatctg tathtaggat aatctgtggg gttgctgttt ctcacct
```

(2) INFORMATION FOR SEQ ID NO:2867:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 117 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..117  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2867:

```
Xaa Pro Ser Phe Phe Val Thr Cys Pro Arg Ser Pro Lys Leu Glu Pro
1 5 10 15
Phe Thr Ala Gly Glu Glu Asp Ala Pro Val Ala Ile Ala Pro Asp Pro
 20 25 30
Arg Leu Val Gln Ala Arg Leu Pro Pro Glu Ala Gly Ala Gln Pro Arg
 35 40 45
Gln His Glu Ala Arg Ala Ala Ala Ala Pro Gly Pro Ala Gly Arg Glu
 50 55 60
Pro Gly Gly Pro Gly Arg Pro Ala Arg Arg Gln Arg Glu Gly Ala Ala
 65 70 75 80
Ala Arg Gly Pro Leu Ala Ile Gly Val Arg Ala Cys Arg Arg Ala Arg
 85 90 95
```

Ala Arg Leu Gly Arg Arg Leu Ala Pro His Leu Leu Leu Leu Leu Leu  
100 105 110  
Leu Leu Arg Ser Leu  
115

(2) INFORMATION FOR SEQ ID NO:2868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2868:

Xaa Arg Leu Ser Ser Leu Pro Ala Pro Ala Pro Arg Ser Ser Asn Pro  
1 5 10 15  
Leu Gln Pro Ala Lys Lys Met His Leu Trp Pro Ser Leu Arg Ile Arg  
20 25 30  
Asp Ser Phe Lys His Gly Tyr Leu Gln Lys Leu Glu Leu Asn Leu Gly  
35 40 45  
Asn Met Lys Arg Ala Gln Arg Gln Arg Gln Gly Arg Gln Gly Glu Ser  
50 55 60  
Gln Glu Asp Gln Asp Gly Gln Pro Gly Gly Asn Gly Lys Ala Pro Leu  
65 70 75 80  
Leu Glu Asp Arg Ser Pro Ser Gly Ser Val Leu Ala Gly Ala Leu Glu  
85 90 95  
Leu Ala Trp Asp Ala Val Leu Leu Leu Thr Cys Cys Cys Cys Cys Phe  
100 105 110  
Cys Cys Gly Ala Cys Ser Asp Glu Asp His Pro Thr Ala Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2869:

Met His Leu Trp Pro Ser Leu Arg Ile Arg Asp Ser Phe Lys His Gly  
1 5 10 15  
Tyr Leu Gln Lys Leu Glu Leu Asn Leu Gly Asn Met Lys Arg Ala Gln  
20 25 30  
Arg Gln Arg Gln Gly Arg Gln Gly Glu Ser Gln Glu Asp Gln Asp Gly  
35 40 45  
Gln Pro Gly Gly Asn Gly Lys Ala Pro Leu Leu Glu Asp Arg Ser Pro  
50 55 60  
Ser Gly Ser Val Leu Ala Gly Ala Leu Glu Leu Ala Trp Asp Ala Val  
65 70 75 80  
Leu Leu Leu Thr Cys Cys Cys Cys Phe Cys Cys Gly Ala Cys Ser  
85 90 95  
Asp Glu Glu Asp His Pro Thr Ala Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:2870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..853
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574636
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2870:

```
anactcatcc caaaccagag cgaagaagaa tcgccatcac agcaagctac gcgcactgaa 60
atcctccaat ccacaggaca cagctctact tccacagttc gcagactcgc acgcaccgag 120
cggctagcga ntcaacgaga aatgtcgctg gtgaggcgca cagcgtgttc gacctattct 180
ctgtggacct cttagacccc ttcgacagca tggtccgctc catcgtgccg ccgtcgttgt 240
cgtcgtcggc ggccctccgag accgccgcct tcgccagcgc ccgcacgcac tggaaggaga 300
cgcccgaggc gcacgtgttc aaggccgacc tccccggcgt gaagaaggag gaggtcaagg 360
tgagggtgga ggacggcaac gtgctgtctc tcagcgggca gcgcaGcagg gagaaggagg 420
acaagggcga caagtggcac cgcgtggagc gcagCagcgg ccagttcgtg cggcgcttcc 480
gcctgccgga gaacgccaag acggaggagg tgagggccgc gctggagaac ggcgtgtctc 540
cggtcaccgt gcccaggcc gaggtcaaga agcccgaggt taagagcatc cagatctccg 600
totgaagaag acatggacgc gaggtgaatg gtcgcgtcgc gttcgcgtcg cggcgtcggg 660
tcttggtttt cagcgacgcg actcgtgtgt gtggtactgt ggttgctctg ctttggtatg 720
tctggtgtgt acgtgtgctg ttcagtggtt cgtgggtcatc gtctgtacat tgtgtgttcc 780
ggtgagctcc ccgactcagt gtgttgtgtt ctgcgagtga ataaataaaa acaaaccagc 840
tgtcgtctcg tgt
```

(2) INFORMATION FOR SEQ ID NO:2871:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..113
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574637
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2871:

```
Xaa Leu Ile Pro Asn Gln Ser Glu Glu Ser Pro Ser Gln Gln Ala
1 5 10 15
Thr Arg Thr Glu Ile Leu Gln Ser Thr Gly His Ser Ser Thr Ser Thr
20 25 30
Val Arg Arg Leu Ala Arg Thr Glu Arg Leu Ala Xaa Gln Arg Glu Met
35 40 45
Ser Leu Val Arg Arg Thr Ala Cys Ser Thr His Ser Leu Trp Thr Ser
50 55 60
Ser Thr Pro Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg Cys
65 70 75 80
Arg Arg Arg Arg Pro Pro Arg Pro Pro Pro Ser Pro Ala Pro Ala Ser
85 90 95
Thr Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser Pro
100 105 110
Ala
```

(2) INFORMATION FOR SEQ ID NO:2872:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1574638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2872:

Met Ser Leu Val Arg Arg Thr Ala Cys Ser Thr His Ser Leu Trp Thr  
1 5 10 15  
Ser Ser Thr Pro Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg  
20 25 30  
Cys Arg Arg Arg Arg Pro Pro Arg Pro Pro Pro Ser Pro Ala Pro Ala  
35 40 45  
Ser Thr Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser  
50 55 60  
Pro Ala  
65

(2) INFORMATION FOR SEQ ID NO:2873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1574639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2873:

Met Phe Arg Ser Ile Val Pro Pro Ser Leu Ser Ser Ser Ala Ala Ser  
1 5 10 15  
Glu Thr Ala Ala Phe Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro  
20 25 30  
Glu Ala His Val Phe Lys Ala Asp Leu Pro Gly Val Lys Lys Glu Glu  
35 40 45  
Val Lys Val Glu Val Glu Asp Gly Asn Val Leu Leu Ile Ser Gly Gln  
50 55 60  
Arg Ser Arg Glu Lys Glu Asp Lys Gly Asp Lys Trp His Arg Val Glu  
65 70 75 80  
Arg Ser Ser Gly Gln Phe Val Arg Arg Phe Arg Leu Pro Glu Asn Ala  
85 90 95  
Lys Thr Glu Glu Val Arg Ala Ala Leu Glu Asn Gly Val Leu Thr Val  
100 105 110  
Thr Val Pro Lys Ala Glu Val Lys Lys Pro Glu Val Lys Ser Ile Gln  
115 120 125  
Ile Ser Val  
130

(2) INFORMATION FOR SEQ ID NO:2874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..962

(D) OTHER INFORMATION: / Ceres Seq. ID 1574673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2874:

aacaagcatc agagctcggg gtcacaaaac ctgaccgatg gcggccccggg gctccacagc 60  
tgccctccgtg gtcagaacag gatcgcgaga cctctcccc tccttttcct tcacagccgc 120  
ggcgctcccc tcggcgcgctc tgaggccggg aggagcgtgg gtccgcgggtg gaggggtacac 180  
ctgcaggctc cgcgcgcgtct gcgccatggg ctccgcgccg tcgtcggtccc aatccccgtc 240  
gccgcacacg ccttcaggac aaaccaagg gaaagcagat tataaatcac tgagtgaaga 300  
ggagtgggaag aagcgccctga ctgaagagca gtattatgtt actcggcaga agggcactga 360



|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| aagagcattc  | actggggaat  | actggaatac  | taaaacccca | ggcattttatc | agtgtgtctg | 420 |
| ctgcgacacc  | cctctgtttc  | agtcatacaac | caaatttgat | agtgggtactg | ggtggccatc | 480 |
| ctattataaa  | ccaattgggtg | aaaatgtcaa  | gagcaagctt | gatattgtcaa | tcatttttat | 540 |
| gccccggacc  | gaggtgctct  | gtgcaacCtg  | tgatgtcat  | ctggggcatg  | tcCTTTttcg | 600 |
| atgacgggcc  | accaccaaca  | gggaagagat  | actgtatcaa | tagtgcactc  | ctgaaattga | 660 |
| agccccaaata | gttgctggat  | actttagcaa  | gaagtcaact | ataacgctgg  | tccgccctat | 720 |
| gtaaaacttcg | gggttatgta  | tataaactac  | tcgagttgta | gcatatttat  | tattctcttt | 780 |
| gttatgtaat  | atatgtgttc  | acaaaccgat  | gaaagtatga | aacaaacagc  | cgctacttca | 840 |
| ctctgggtatt | ctggtctaga  | attaaggtgt  | tgtttgggtg | acgaattgta  | acgtaaatgg | 900 |
| caacggtaat  | ggtttgcaact | cgagtgcacg  | ttgacaacgg | taataaattt  | aaatagatct | 960 |
| tt          |             |             |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2875:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Arg | Cys | Ser | Thr | Ala | Ala | Ser | Val | Val | Arg | Thr | Gly | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Leu | Ser | Pro | Ser | Phe | Ser | Phe | Thr | Ala | Ala | Ala | Leu | Pro | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Arg | Leu | Arg | Pro | Val | Gly | Ala | Trp | Val | Arg | Gly | Gly | Gly | Tyr | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Cys | Arg | Leu | Arg | Ala | Val | Cys | Ala | Met | Gly | Ser | Ala | Pro | Ser | Ser | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ser | Pro | Ser | Pro | His | Thr | Pro | Ser | Gly | Gln | Thr | Gln | Gly | Lys | Ala |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Tyr | Lys | Ser | Leu | Ser | Glu | Glu | Glu | Trp | Lys | Lys | Arg | Leu | Thr | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Gln | Tyr | Tyr | Val | Thr | Arg | Gln | Lys | Gly | Thr | Glu | Arg | Ala | Phe | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Glu | Tyr | Trp | Asn | Thr | Lys | Thr | Pro | Gly | Ile | Tyr | Gln | Cys | Val | Cys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Cys | Asp | Thr | Pro | Leu | Phe | Gln | Ser | Ser | Thr | Lys | Phe | Asp | Ser | Gly | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Trp | Pro | Ser | Tyr | Tyr | Lys | Pro | Ile | Gly | Glu | Asn | Val | Lys | Ser | Lys |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Asp | Met | Ser | Ile | Ile | Phe | Met | Pro | Arg | Thr | Glu | Val | Leu | Cys | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Cys | Asp | Ala | His | Leu | Gly | His | Val | Leu | Phe | Arg |     |     |     |     |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2876:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ala | Pro | Ser | Ser | Ser | Gln | Ser | Pro | Ser | Pro | His | Thr | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Ser Gly Gln Thr Gln Gly Lys Ala Asp Tyr Lys Ser Leu Ser Glu Glu  
20 25 30  
Glu Trp Lys Lys Arg Leu Thr Glu Gln Tyr Tyr Val Thr Arg Gln  
35 40 45  
Lys Gly Thr Glu Arg Ala Phe Thr Gly Glu Tyr Trp Asn Thr Lys Thr  
50 55 60  
Pro Gly Ile Tyr Gln Cys Val Cys Cys Asp Thr Pro Leu Phe Gln Ser  
65 70 75 80  
Ser Thr Lys Phe Asp Ser Gly Thr Gly Trp Pro Ser Tyr Tyr Lys Pro  
85 90 95  
Ile Gly Glu Asn Val Lys Ser Lys Leu Asp Met Ser Ile Ile Phe Met  
100 105 110  
Pro Arg Thr Glu Val Leu Cys Ala Thr Cys Asp Ala His Leu Gly His  
115 120 125  
Val Leu Phe Arg  
130

(2) INFORMATION FOR SEQ ID NO:2877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1574676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2877:

Met Leu Leu Gly Arg Arg Ala Leu Lys Glu His Ser Leu Gly Asn Thr  
1 5 10 15  
Gly Ile Leu Lys Pro Gln Ala Phe Ile Ser Val Ser Ala Ala Thr Pro  
20 25 30  
Leu Cys Phe Ser His Gln Pro Asn Leu Ile Val Val Leu Gly Gly His  
35 40 45  
Pro Ile Ile Asn Gln Leu Val Lys Met Ser Arg Ala Ser Leu Ile Cys  
50 55 60  
Gln Ser Phe Leu Cys Pro Gly Pro Arg Cys Ser Val Gln Pro Val Met  
65 70 75 80  
Leu Ile Trp Gly Met Ser Phe Phe Asp Asp Gly Pro Pro Pro Thr Gly  
85 90 95  
Lys Arg Tyr Cys Ile Asn Ser Ala Ser Leu Lys Leu Lys Pro Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..755

(D) OTHER INFORMATION: / Ceres Seq. ID 1574677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2878:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| agatctcaac | gcaactaaaa | cattttatct | tctctatcgc | tactccaaga | gtacccaatc | 60  |
| accgagccat | ggccatctca | gtcactgccg | tggccgcott | gcccgtttct | cggctcaaag | 120 |
| aagcctcccg | cagccgtccc | gccagagggg | cgtagcgttc | atcgtcgtcc | ggccggtgcg | 180 |
| cgcgcaccgc | cgttttgtgg | gcgtggcggc | cagctcgcgc | cccacgccgc | cggatctcgc | 240 |
| aaagaaggtg | tccgagagca | tcaagcaggc | ccaggagacg | tgcgagatg  | acccggtgag | 300 |
| cggcgagtgc | gtggcggcgt | gggacgagct | ggaggagctc | agcgcgggcg | ccagccactt | 360 |
| gcgcgaccgc | cagaagggcg | ccgacccgct | cgaggagtac | tgcaaggaca | accccgagGa | 420 |

ccgacgagtg ccCgcacgta cgaggactga accacgcgcg cgcgaggttg gatcgctgtc 480  
acttgatcta gctagGcagc ttagctcggc atgatggcga catgtgtaga cgtgcaatgg 540  
atcgggtatg atccttcggt gattcagctt ggcttggtgt ggaataaaac gaggtttgct 600  
gtttattata agtaacattt aggagctcct actgtagtct caaggcaggt gtaatcctta 660  
gaaacatttg atggtgtgct tctagccttg tagtactcga tatgtgcaat tctgtaaagt 720  
atcgcagatt ttccacctga gcatgatatt gctgc

(2) INFORMATION FOR SEQ ID NO:2879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1574678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2879:

Asp Leu Asn Ala Thr Lys Thr Phe Tyr Leu Leu Tyr Arg Tyr Ser Lys  
1 5 10 15  
Ser Thr Gln Ser Pro Ser His Gly His Leu Ser His Cys Arg Gly Arg  
20 25 30  
Leu Ala Arg Phe Ser Ala Gln Arg Ser Leu Pro Gln Pro Ser Arg Gln  
35 40 45  
Arg Val Val Ala Phe Ile Val Val Arg Pro Val Arg Ala His Arg Arg  
50 55 60  
Phe Val Gly Val Ala Ala Ser Ser Pro Pro Thr Pro Pro Asp Leu Ala  
65 70 75 80  
Lys Lys Val Ser Glu Ser Ile Lys Gln Ala Gln Glu Thr Cys Ala Asp  
85 90 95  
Asp Pro Val Ser Gly Glu Cys Val Ala Ala Trp Asp Glu Leu Glu Glu  
100 105 110  
Leu Ser Ala Ala Ala Ser His Leu Arg Asp Arg Gln Lys Gly Ala Asp  
115 120 125  
Pro Leu Glu Glu Tyr Cys Lys Asp Asn Pro Glu Asp Arg Arg Val Pro  
130 135 140  
Ala Arg Thr Arg Thr Glu Pro Arg Ala Arg Glu Val Gly Ser Leu Ser  
145 150 155 160  
Leu Asp Leu Ala Arg Gln Leu Ser Ser Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:2880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1114

(D) OTHER INFORMATION: / Ceres Seq. ID 1574693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2880:

aacgcccctt tcttgcgagt gaggccaaag ccgagcaaac aaaacgatat gccgctgccc 60  
tgaaccgaga ccaccaccgc tctgcctcgc ctgcctcacc ctcacctcat ctcacctcgc 120  
cgactagggt tttgtaccgc cgtggatctc gccgtccccg ccattggacgt ctgcacgcgc 180  
ggactctccg tcgcccgcga ggctccgacc accggggagc accggatggg gactaccatc 240  
gtcgggtctc gctacgaggc cggcgctcgtc ctggggcgccg attccaggac cagcactgga 300  
atgtatgtag ccaaccgtgc ttcagacaag attactcaac tgacagacaa tgtgtatgtc 360  
tgtcgtcttg gatctgctgc tgatacaca gtcatttcgg attatgtacg ctatttcctc 420  
caccaacaca caatccagct tgGacaacca gctaccgtta aagttgcagc camctTgatt 480  
aggtTgctag cttatcagaA caagaacatg ttgcaagctg gcatgattgt tggaggatgg 540

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| ggacaagtac | gagggaggcc  | aaattttctc | agtccctctc | ggtggaacga | tcttgaagca  | 600  |
| accatttgca | attggagggt  | caggtccagt | tacctatatg | ctcttcttga | tcattgaatgg | 660  |
| aaagagggaa | tgagtcagga  | agaggcagag | aaatttgtgg | tgaaggtagt | ttcccttgcg  | 720  |
| atggcccgtg | atgggtgctag | tggaggggtt | gtccgcacag | ttacaataaa | tgcggatggc  | 780  |
| gtgaagagga | actttttacc  | tggcgacaag | ctaccctctg | ggcacgacga | gctggaaccc  | 840  |
| cagaactcgt | tgcttgatat  | tcttgctgct | gggaaccctg | atcccatggg | gcagtgaact  | 900  |
| cgccctccac | ttactttgtg  | aacttttcac | tgtatctgac | ttgttcttga | ttatttctcc  | 960  |
| ttgaactatg | tcagaccaga  | gtaatttacg | aattgttggt | atcgcacctt | aataaattca  | 1020 |
| tgtttagctg | ggtgattggc  | gttttgagtt | aatgggtact | ggtaagcgtg | ctactgctgt  | 1080 |
| agttaagcct | gtggcaagta  | ttcaaatttt | cagt       |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1574694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2881:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Val | Ser | His | Ala | Gly | Ser | Ser | Val | Ala | Gly | Glu | Ala | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gly | Glu | His | Arg | Met | Gly | Thr | Thr | Ile | Val | Gly | Val | Cys | Tyr | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Val | Val | Leu | Gly | Ala | Asp | Ser | Arg | Thr | Ser | Thr | Gly | Met | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ala | Asn | Arg | Ala | Ser | Asp | Lys | Ile | Thr | Gln | Leu | Thr | Asp | Asn | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Val | Cys | Arg | Ser | Gly | Ser | Ala | Ala | Asp | Thr | Gln | Val | Ile | Ser | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Val | Arg | Tyr | Phe | Leu | His | Gln | His | Thr | Ile | Gln | Leu | Gly | Gln | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Thr | Val | Lys | Val | Ala | Ala | Xaa | Leu | Ile | Arg | Leu | Leu | Ala | Tyr | Gln |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asn | Lys | Asn | Met | Leu | Gln | Ala | Gly | Met | Ile | Val | Gly | Gly | Trp | Gly | Gln |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Arg | Gly | Arg | Pro | Asn | Phe | Leu | Ser | Pro | Ser | Arg | Trp | Asn | Asp | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Thr | Ile | Cys | Asn | Trp | Arg | Phe | Arg | Ser | Ser | Tyr | Leu | Tyr | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Leu | Asp | His | Glu | Trp | Lys | Glu | Gly | Met | Ser | Gln | Glu | Glu | Ala | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Phe | Val | Val | Lys | Val | Val | Ser | Leu | Ala | Met | Ala | Arg | Asp | Gly | Ala |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Gly | Gly | Val | Val | Arg | Thr | Val | Thr | Ile | Asn | Ala | Asp | Gly | Val | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Asn | Phe | Tyr | Pro | Gly | Asp | Lys | Leu | Pro | Leu | Trp | His | Asp | Glu | Leu |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Glu | Pro | Gln | Asn | Ser | Leu | Leu | Asp | Ile | Leu | Ala | Ala | Gly | Asn | Pro | Asp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Pro | Met | Val | Gln |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1574695

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Thr | Thr | Ile | Val | Gly | Val | Cys | Tyr | Glu | Gly | Gly | Val | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Asp | Ser | Arg | Thr | Ser | Thr | Gly | Met | Tyr | Val | Ala | Asn | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Lys | Ile | Thr | Gln | Leu | Thr | Asp | Asn | Val | Tyr | Val | Cys | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Ala | Ala | Asp | Thr | Gln | Val | Ile | Ser | Asp | Tyr | Val | Arg | Tyr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | His | Gln | His | Thr | Ile | Gln | Leu | Gly | Gln | Pro | Ala | Thr | Val | Lys | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ala | Xaa | Leu | Ile | Arg | Leu | Leu | Ala | Tyr | Gln | Asn | Lys | Asn | Met | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ala | Gly | Met | Ile | Val | Gly | Gly | Trp | Gly | Gln | Val | Arg | Gly | Arg | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Phe | Leu | Ser | Pro | Ser | Arg | Trp | Asn | Asp | Leu | Glu | Ala | Thr | Ile | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Trp | Arg | Phe | Arg | Ser | Ser | Tyr | Leu | Tyr | Ala | Leu | Leu | Asp | His | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Lys | Glu | Gly | Met | Ser | Gln | Glu | Glu | Ala | Glu | Lys | Phe | Val | Val | Lys |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Val | Ser | Leu | Ala | Met | Ala | Arg | Asp | Gly | Ala | Ser | Gly | Gly | Val | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Thr | Val | Thr | Ile | Asn | Ala | Asp | Gly | Val | Lys | Arg | Asn | Phe | Tyr | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asp | Lys | Leu | Pro | Leu | Trp | His | Asp | Glu | Leu | Glu | Pro | Gln | Asn | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Asp | Ile | Leu | Ala | Ala | Gly | Asn | Pro | Asp | Pro | Met | Val | Gln |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(D) OTHER INFORMATION: / Ceres Seq. ID 1574696

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Val | Ala | Asn | Arg | Ala | Ser | Asp | Lys | Ile | Thr | Gln | Leu | Thr | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Val | Tyr | Val | Cys | Arg | Ser | Gly | Ser | Ala | Ala | Asp | Thr | Gln | Val | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Asp | Tyr | Val | Arg | Tyr | Phe | Leu | His | Gln | His | Thr | Ile | Gln | Leu | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Pro | Ala | Thr | Val | Lys | Val | Ala | Ala | Xaa | Leu | Ile | Arg | Leu | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Gln | Asn | Lys | Asn | Met | Leu | Gln | Ala | Gly | Met | Ile | Val | Gly | Gly | Trp |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Gln | Val | Arg | Gly | Arg | Pro | Asn | Phe | Leu | Ser | Pro | Ser | Arg | Trp | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Leu | Glu | Ala | Thr | Ile | Cys | Asn | Trp | Arg | Phe | Arg | Ser | Ser | Tyr | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Ala | Leu | Leu | Asp | His | Glu | Trp | Lys | Glu | Gly | Met | Ser | Gln | Glu | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ala Glu Lys Phe Val Val Lys Val Val Ser Leu Ala Met Ala Arg Asp  
130 135 140  
Gly Ala Ser Gly Gly Val Val Arg Thr Val Thr Ile Asn Ala Asp Gly  
145 150 155 160  
Val Lys Arg Asn Phe Tyr Pro Gly Asp Lys Leu Pro Leu Trp His Asp  
165 170 175  
Glu Leu Glu Pro Gln Asn Ser Leu Leu Asp Ile Leu Ala Ala Gly Asn  
180 185 190  
Pro Asp Pro Met Val Gln  
195

(2) INFORMATION FOR SEQ ID NO:2884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..762
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2884:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agctttgttt ttggtgtgtg cagchvgrcg gtccgagcta cggcgtggag ctggggcgggc | 60  |
| tggacggcaa gacgttcaac agggccatcg tgaagcacgt cctcccgggc cccggcttca  | 120 |
| acctggacca gctcaacgcc ctcttcgcgc agaacggcct cacgcagacg gacatgatcg  | 180 |
| cgctctcagg cgcgcacacg atcgggggtga cgcactgcga caagttcgtg cggcggatct | 240 |
| acacgttcaa gcagcggtg gcgtggaacc cgccgatgaa cctggacttc ctgcgctcgc   | 300 |
| tgcggcgggt gtgccccctc agctacagcc ccacgGcggt cgccatgctg gacgtcacca  | 360 |
| cgcccagggt cttcgacaac gctacttca acaacctccg ctacaacaag ggctgctcg    | 420 |
| cctccgacca ggtgctcttc accgaccgcc gctcccgacc caccgtcaac ctcttcgccg  | 480 |
| ccaacgccac cgctttctac gaggcattcg tcgcgcgcat ggccaagctc ggcaggatcg  | 540 |
| gcctcaagac cggcgcgcgac ggcgagatac gccgcgtctg caccgccgtc aactaagcct | 600 |
| gcattggctg cttgctgctt gcgtgcgtgg gtttcaacta ttctacttct tctttctctt  | 660 |
| gtttatatac gtacgtttgt cggatggatt ttggtagcca tgagatgaca tccttgctct  | 720 |
| gagctagcgg acctgccccg attggatgat atagattgat cc                     |     |

(2) INFORMATION FOR SEQ ID NO:2885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2885:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ala Leu Phe Leu Val Cys Ala Xaa Xaa Arg Ser Glu Leu Arg Arg Gly |  |
| 1 5 10 15                                                       |  |
| Ala Gly Ala Ala Gly Arg Gln Asp Val Gln Gln Gly His Arg Glu Ala |  |
| 20 25 30                                                        |  |
| Arg Pro Pro Gly Pro Arg Leu Gln Pro Gly Pro Ala Gln Arg Pro Leu |  |
| 35 40 45                                                        |  |
| Arg Ala Glu Arg Pro His Ala Asp Gly His Asp Arg Ala Leu Arg Arg |  |
| 50 55 60                                                        |  |
| Ala His Asp Arg Gly Asp Ala Leu Arg Gln Val Arg Ala Ala Asp Leu |  |
| 65 70 75 80                                                     |  |
| His Val Gln Ala Ala Ala Gly Val Glu Pro Ala Asp Glu Pro Gly Leu |  |
| 85 90 95                                                        |  |
| Pro Ala Leu Ala Ala Gly Val Pro Gln Leu Gln Pro His Gly         |  |
| 100 105 110                                                     |  |

(ii) MOLECULE TYPE: peptide

[illegible]

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2887:

Met Ile Ala Leu Ser Gly Ala His Thr Ile Gly Val Thr His Cys Asp  
1 5 10 15  
Lys Phe Val Arg Arg Ile Tyr Thr Phe Lys Gln Arg Leu Ala Trp Asn  
20 25 30  
Pro Pro Met Asn Leu Asp Phe Leu Arg Ser Leu Arg Arg Val Cys Pro  
35 40 45  
Leu Ser Tyr Ser Pro Thr Ala Phe Ala Met Leu Asp Val Thr Thr Pro  
50 55 60  
Arg Val Phe Asp Asn Ala Tyr Phe Asn Asn Leu Arg Tyr Asn Lys Gly  
65 70 75 80  
Leu Leu Ala Ser Asp Gln Val Leu Phe Thr Asp Arg Arg Ser Arg Pro  
85 90 95  
Thr Val Asn Leu Phe Ala Ala Asn Ala Thr Ala Phe Tyr Glu Ala Phe  
100 105 110  
Val Ala Ala Met Ala Lys Leu Gly Arg Ile Gly Leu Lys Thr Gly Ala  
115 120 125  
Asp Gly Glu Ile Arg Arg Val Cys Thr Ala Val Asn  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..736
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2888:

cccaaaatac tccaccaccg caccactag ggtttccgca ccgcattgca gaacctcgcc 60  
gcttcacccc tcaccacacc accggcgatg tccacagcgg cggcgcaggg cggcagcgac 120  
aagccggcgc tccggaggcc cgtcttcacc aaggtcgacc agctcaggcc gggcaccaac 180  
gggcacaccc tcaccgtcaa ggtcgtcagc gccaccccg tgcCtggGcg cgcgcgccCa 240  
ggcgcacccg ccgcgcggccc atcNccgCgc gccgcgcacg gccgagtgc tctcggggga 300  
cgagaccggc gccatcgtct tcaccgcccg caacgaccaa gttgacttgc tgaagcccaa 360  
tgcgacagtg atcttgcgca atgccaaaat agacatgttc aaaggatcaa tgaggcttgc 420  
agtggacaag tgggggcgga ttgaggctgt agagccagcc agtttcacgg tgaagggaaga 480  
caacaacctg tctctaatag agtatgaatt ggtaaatgtg gctgagtaac tgtccaatcc 540  
aagcgtttct gcccccttta tttcgtgcc taagaaggaa gtaccatgaa tgaacattat 600  
aaagcctctt gaagcgaagc gagtttattt gctacgggtg gtagataaaa ggtcaaggct 660  
gtatggcctg tgttagaact ttggataaat taagatgaat tgcccttgca tctatgagat 720  
tgttatccat ctttgt

(2) INFORMATION FOR SEQ ID NO:2889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2889:

Pro Lys Tyr Ser Thr Thr Ala Pro Thr Arg Val Ser Ala Pro His Cys

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|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Arg Thr Ser Pro Pro Pro Ser Pro His His Arg Arg Cys Pro Gln     |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Arg Arg Arg Arg Ala Ala Ala Thr Ser Arg Arg Ser Gly Gly Pro Ser |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Ser Pro Arg Ser Thr Ser Ser Gly Arg Ala Pro Thr Gly Thr Pro Ser |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Pro Ser Arg Ser Ser Ala Pro Pro Pro Cys Leu Gly Ala Arg Ala Gln |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Ala His Pro Pro Pro His Xaa Arg Ala Pro Arg Ile Ala Glu Cys     |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Leu Val Gly Asp Glu Thr Gly Ala Ile Val Phe Thr Ala Arg Asn Asp |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Gln Val Asp Leu Leu Lys Pro Asn Ala Thr Val Ile Leu Arg Asn Ala |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Lys Ile Asp Met Phe Lys Gly Ser Met Arg Leu Ala Val Asp Lys Trp |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Gly Arg Ile Glu Ala Val Glu Pro Ala Ser Phe Thr Val Lys Glu Asp |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Asn Asn Leu Ser Leu Ile Glu Tyr Glu Leu Val Asn Val Ala Glu     |     |     |     |
|                                                                 | 165 | 170 | 175 |

(2) INFORMATION FOR SEQ ID NO:2890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2890:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Gln Asn Thr Pro Pro Pro His Pro Leu Gly Phe Pro His Arg Ile Ala |     |
| 1                                                               | 15  |
| Glu Pro Arg Arg Leu His Pro His His Thr Thr Gly Asp Val His Ser |     |
|                                                                 | 30  |
| Gly Gly Ala Gly Arg Gln Arg Gln Ala Gly Ala Pro Glu Ala Arg Leu |     |
|                                                                 | 45  |
| His Gln Gly Arg Pro Ala Gln Ala Gly His Gln Arg Ala His Pro His |     |
|                                                                 | 60  |
| Arg Gln Gly Arg Gln Arg His Pro Arg Ala Trp Ala Arg Ala Pro Arg |     |
| 65                                                              | 80  |
| Arg Thr Arg Arg Arg Pro Ile Xaa Ala Arg Arg Ala Ser Pro Ser Ala |     |
|                                                                 | 95  |
| Ser Ser Gly Thr Arg Pro Ala Pro Ser Ser Ser Pro Pro Ala Thr Thr |     |
|                                                                 | 110 |
| Lys Leu Thr Cys                                                 |     |
|                                                                 | 115 |

(2) INFORMATION FOR SEQ ID NO:2891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2891:

aaaaccattc cccgttcctg attccaattc caaccagccc atcccccttc gagcacacgc 60  
gcagagcggg ggcgaaggca agagcaaaca gagtagccgc cgcgcgcgtc gccgtcgtcg 120  
tcgtgtgtgt gtgtggagag gaaagaccgg gttttgtttt ttacggctta gcgttgagca 180  
gctgagatgt tgcgagcgct gccggcgagg tgctgcgGcc actggcgcgC gggcgccgcg 240  
gcggcgtcct gctcaccagg aacgtcggca tcagctacaa cctgcgcccc gccaacccgc 300  
tcggctactt caaggacgtg ccgctgccca tctgcgcctc gctgctcaag cagttggact 360  
cggacgacga cgacgatcag taatagcaca tcgtcgacga ccgcagactg gctggcacta 420  
aaccacaaat cctcttcacc tggattacaa atatgtaact gagaaaggaa aggaaaacaa 480  
aaatgtaact gcgtggctgt accaaattct gagtgctgga ttcttgotat tgtc

(2) INFORMATION FOR SEQ ID NO:2892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2892:

Lys Pro Phe Pro Val Pro Asp Ser Asn Ser Asn Gln Pro Ile Pro Leu  
1 5 10 15  
Arg Ala His Ala Gln Ser Gly Gly Glu Gly Lys Ser Lys Gln Ser Ser  
20 25 30  
Arg Arg Arg Arg Arg Arg Arg Arg Arg Val Cys Val Trp Arg Gly Lys  
35 40 45  
Thr Gly Phe Cys Phe Leu Arg Leu Ser Val Glu Gln Leu Arg Cys Cys  
50 55 60  
Glu Arg Trp Arg Arg Gly Ala Ala Ala Thr Gly Arg Arg Ala Pro Arg  
65 70 75 80  
Arg Arg Pro Ala His Gln Glu Arg Arg His Gln Leu Gln Pro Ala Pro  
85 90 95  
Arg Gln Pro Ala Arg Leu Leu Gln Gly Arg Ala Ala Ala His Leu Arg  
100 105 110  
Leu Ala Ala Gln Ala Val Gly Leu Gly Arg Arg Arg Arg Ser Val Ile  
115 120 125  
Ala His Arg Arg Arg Pro Gln Thr Gly Trp His  
130 135

(2) INFORMATION FOR SEQ ID NO:2893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2893:

Met Leu Arg Ala Leu Ala Ala Arg Cys Cys Gly His Trp Pro Pro Gly  
1 5 10 15  
Ala Ala Ala Ala Ser Cys Ser Pro Gly Thr Ser Ala Ser Ala Thr Thr  
20 25 30  
Cys Ala Pro Pro Thr Arg Ser Ala Thr Ser Arg Thr Cys Arg Cys Pro  
35 40 45  
Ser Ala Pro Arg Cys Ser Ser Ser Trp Thr Arg Thr Thr Thr Thr Ile  
50 55 60  
Ser Asn Ser Thr Ser Ser Thr Thr Ala Asp Trp Leu Ala Leu Asn His  
65 70 75 80

Lys Ser Ser Ser Pro Gly Leu Gln Ile Cys Asn  
85 90

(2) INFORMATION FOR SEQ ID NO:2894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2894:

```
agttctggtac cgccggc aaa gcagtcgttt tcgtcctctt ccttgattaa accttccgta 60
cccatatcca cctgctgctc cgaccttcca gtcttctccg taggggcttc gctccataga 120
tttcgccgca aggggcaacg gcacaccac caactgacct gacccacgag ggatccgcag 180
atgaagatca ttccggtccc ttgcctggat gacaactatg cctacttaat cgtggacgag 240
agcaccaaga aggcagcggc cgttgacct gtggaaccgg agaaggttct caaggcggcc 300
ggcgaggtcg ggcgctacgt cgactgcgtt ctcaccaccc atcaccactg ggatcatgct 360
ggtggcaatg agaagatgag gctgcagggt ccagggataa aggtatttgg aggatccctg 420
gacaatgtga aaggctgcac tgatcagggt gagaatggaa tgaagttgtc acttggaag 480
gacattgaga tactatgcct acacacgcct tgccacacta aAggtcatat cagctactat 540
gttactagta aggaggtgaa gatccagcgg tcttcaccgg agataccttg ttcattgctg 600
ggtgtgggaa gttttttgag ggttctgcag agcaaagtga tcagtccctt attgttacac 660
tgggttgcgt gccaaagtca acccgagttt actgtgggca tgagtacact gtgaagaacc 720
taaaattcat gctgacactg gagccagaga atgagaagac gaaacagaaa ctggaatggg 780
ctgaaaagca ggcggaagcg aatcagccaa cagtgccttc gactatagga gatgagtttg 840
agataaatac tttcatgcgt gttgatctac cagaaatata ggcgaaattc agtgtcaact 900
ctccagttga agcaatgata gaggtcagga agaccaagga taattggaga ggttgaggac 960
acccatggcc gccactagtc tgttgaacca gcattccaaa gtgaactaat gcagaaacct 1020
tgccctgtag gtgggaatga ggtttactgc cgtgcaatgc tttgagaaat gtgttggtgt 1080
gaaggagaag actcctacaa taastccgcg ttaatgagta gtaacaatac gctccttgta 1140
acttggtgtc tgtttgcaa taataatgta cgaactgtag tgcct
```

(2) INFORMATION FOR SEQ ID NO:2895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2895:

```
Met Lys Ile Ile Pro Val Pro Cys Leu Asp Asp Asn Tyr Ala Tyr Leu
1 5 10 15
Ile Val Asp Glu Ser Thr Lys Lys Ala Ala Ala Val Asp Pro Val Glu
20 25 30
Pro Glu Lys Val Leu Lys Ala Ala Gly Glu Val Gly Ala Tyr Val Asp
35 40 45
Cys Val Leu Thr Thr His His Trp Asp His Ala Gly Gly Asn Glu
50 55 60
Lys Met Arg Leu Gln Val Pro Gly Ile Lys Val Phe Gly Gly Ser Leu
65 70 75 80
Asp Asn Val Lys Gly Cys Thr Asp Gln Val Glu Asn Gly Met Lys Leu
85 90 95
Ser Leu Gly Lys Asp Ile Glu Ile Leu Cys Leu His Thr Pro Cys His
100 105 110
Thr Lys Gly His Ile Ser Tyr Tyr Val Thr Ser Lys Glu Val Lys Ile
```

115 120 125  
Gln Arg Ser Ser Pro Glu Ile Pro Cys Ser Leu Leu Gly Val Gly Ser  
130 135 140  
Phe Leu Arg Val Leu Gln Ser Lys Cys Ile Ser Pro Leu Leu Leu His  
145 150 155 160  
Trp Val Arg Cys Gln Ser Gln Pro Glu Phe Thr Val Gly Met Ser Thr  
165 170 175  
Leu

(2) INFORMATION FOR SEQ ID NO:2896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2896:

Met Arg Leu Gln Val Pro Gly Ile Lys Val Phe Gly Gly Ser Leu Asp  
1 5 10 15  
Asn Val Lys Gly Cys Thr Asp Gln Val Glu Asn Gly Met Lys Leu Ser  
20 25 30  
Leu Gly Lys Asp Ile Glu Ile Leu Cys Leu His Thr Pro Cys His Thr  
35 40 45  
Lys Gly His Ile Ser Tyr Tyr Val Thr Ser Lys Glu Val Lys Ile Gln  
50 55 60  
Arg Ser Ser Pro Glu Ile Pro Cys Ser Leu Leu Gly Val Gly Ser Phe  
65 70 75 80  
Leu Arg Val Leu Gln Ser Lys Cys Ile Ser Pro Leu Leu Leu His Trp  
85 90 95  
Val Arg Cys Gln Ser Gln Pro Glu Phe Thr Val Gly Met Ser Thr Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2897:

Met Tyr Gln Ser Leu Ile Val Thr Leu Gly Ser Leu Pro Lys Ser Thr  
1 5 10 15  
Arg Val Tyr Cys Gly His Glu Tyr Thr Val Lys Asn Leu Lys Phe Met  
20 25 30  
Leu Thr Leu Glu Pro Glu Asn Glu Lys Thr Lys Gln Lys Leu Glu Trp  
35 40 45  
Ala Glu Lys Gln Arg Glu Ala Asn Gln Pro Thr Val Pro Ser Thr Ile  
50 55 60  
Gly Asp Glu Phe Glu Ile Asn Thr Phe Met Arg Val Asp Leu Pro Glu  
65 70 75 80  
Ile Gln Ala Lys Phe Ser Val Asn Ser Pro Val Glu Ala Met Ile Glu  
85 90 95

Val Arg Lys Thr Lys Asp Asn Trp Arg Gly  
100 105

(2) INFORMATION FOR SEQ ID NO:2898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..691
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2898:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atcactaggc | caccaccag  | cggcgggctc | cagtcgcaac | tcgcaacaca | gtcacagacg | 60  |
| ccgccgcca  | aagaaagacg | tcaactccag | gagacaagac | agtgagaact | gaagagaagg | 120 |
| atgggcttcg | agaagcagat | cctgagatcc | ggcaccggcc | ccaagccgat | aaagggccag | 180 |
| aaggtcaccg | ttcactgcac | cggctacggg | aaggatcgtg | atcttccaag | aaattttgga | 240 |
| gcaccaagga | ccctgggcag | cagccattca | gtttcagcat | tggtcagggg | tcagtgatca | 300 |
| aaggatggga | cgagggagtt | atgaccatgc | aagtgggtga | agttgctcgt | atccagtgca | 360 |
| cgcttgatta | tgttatgga  | gccggcgggt | tcccagcctg | gggaattcaa | ccaaactcag | 420 |
| tgcttggtTt | tcgagattga | agtcctcagt | gcccagtaat | tcgcatctgt | cagctatgga | 480 |
| aacggtggcc | atgcttctca | agtAaatgaa | ataattccgt | tgtcacctca | tgctacatac | 540 |
| agcagattgg | tgttacgagb | baaatcctgt | gamactttag | cattctgtaa | ccgtggatgt | 600 |
| cgagtttatg | gagttccttg | tgtggcgcc  | caagtcaagt | tctcgtaaaa | gattgtaatc | 660 |
| tgatggcttc | cattgtgact | tgtaggcsgc | t          |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2899:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Phe Glu Lys Gln Ile Leu Arg Ser Gly Thr Gly Pro Lys Pro |  |
| 1 5 10 15                                                       |  |
| Ile Lys Gly Gln Lys Val Thr Val His Cys Thr Gly Tyr Gly Lys Asp |  |
| 20 25 30                                                        |  |
| Arg Asp Leu Pro Arg Asn Phe Gly Ala Pro Arg Thr Leu Gly Ser Ser |  |
| 35 40 45                                                        |  |
| His Ser Val Ser Ala Leu Val Arg Val Gln                         |  |
| 50 55                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2900:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Thr Met Gln Val Gly Glu Val Ala Arg Ile Gln Cys Thr Pro Asp |  |
| 1 5 10 15                                                       |  |
| Tyr Ala Tyr Gly Ala Gly Gly Phe Pro Ala Trp Gly Ile Gln Pro Asn |  |

20 25 30  
Ser Val Leu Val Phe Arg Asp  
35

(2) INFORMATION FOR SEQ ID NO:2901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..37
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2901:

Met Gln Val Gly Glu Val Ala Arg Ile Gln Cys Thr Pro Asp Tyr Ala  
1 5 10 15  
Tyr Gly Ala Gly Gly Phe Pro Ala Trp Gly Ile Gln Pro Asn Ser Val  
20 25 30  
Leu Val Phe Arg Asp  
35

(2) INFORMATION FOR SEQ ID NO:2902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2902:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcatacacaag caaaagcaac aaggcagcag cacaagcaag aaccacacct cctcccttcg | 60  |
| cctgtgatca tgcgtctctg ctgcggcggc aagtgcgggt gcggctccag ctgctcctgc  | 120 |
| ggcagcggat gcaacggctg cggatatgtac cctgacgtgg agaccgccgc caccagcagc | 180 |
| gtcaagacca cggctcctgc cgcgcgcgacc accaaggcca gcgcgcggcg cttcgaggcg | 240 |
| gccaccgagg gcgcgcggctg cgactgcaac aactgcaagt gcggcaccag ctgcggctgc | 300 |
| tcctgctgca gctgcaactg agccggcccg gcccgcgcat ggcgcacgag agtcgagagg  | 360 |
| aggaggacga cgacgaggcB dtdtaaatat aatagcggcg tccagtaaat aagatcctgt  | 420 |
| caactgcacc cgccattatc catggtcgtc cgctccNtcg cctgcgtctc ctggtcctgg  | 480 |
| ggttcgtctg aacgtcctcg cggcttcacg acgcgatgcc gcctccgtcg atcctgtccg  | 540 |
| tctcgtgcgc grbkaatat tagatctata tgcgtgtttt tctgcgttat tactacatct   | 600 |

(2) INFORMATION FOR SEQ ID NO:2903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2903:

Ser Ser Gln Ala Lys Ala Thr Arg Gln Gln His Lys Gln Glu Pro His  
1 5 10 15  
Leu Leu Pro Ser Pro Val Ile Met Ser Ser Cys Cys Gly Gly Lys Cys  
20 25 30  
Gly Cys Gly Ser Ser Cys Ser Cys Gly Ser Gly Cys Asn Gly Cys Gly

35 40 45  
Met Tyr Pro Asp Val Glu Thr Ala Ala Thr Ser Ser Val Lys Thr Thr  
50 55 60  
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala  
65 70 75 80  
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Lys Cys Gly Thr  
85 90 95  
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
100 105

(2) INFORMATION FOR SEQ ID NO:2904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2904:

Met Ser Ser Cys Gly Gly Lys Cys Gly Cys Gly Ser Ser Cys Ser  
1 5 10 15  
Cys Gly Ser Gly Cys Asn Gly Cys Gly Met Tyr Pro Asp Val Glu Thr  
20 25 30  
Ala Ala Thr Ser Ser Val Lys Thr Thr Val Leu Ala Ala Pro Thr Thr  
35 40 45  
Lys Ala Ser Ala Gly Gly Phe Glu Ala Ala Thr Glu Gly Gly Gly Cys  
50 55 60  
Asp Cys Asn Thr Cys Lys Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys  
65 70 75 80  
Ser Cys Asn

(2) INFORMATION FOR SEQ ID NO:2905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2905:

Met Tyr Pro Asp Val Glu Thr Ala Ala Thr Ser Ser Val Lys Thr Thr  
1 5 10 15  
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala  
20 25 30  
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Lys Cys Gly Thr  
35 40 45  
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
50 55

(2) INFORMATION FOR SEQ ID NO:2906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..842

(D) OTHER INFORMATION: / Ceres Seq. ID 1574762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2906:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ctcgaaatct | cgccctcgt  | tgcagttgtc | catatccctt  | cctctcttcc | tcgccaggcc | 60  |
| aaccgctgat | tgttgttcag | acagaggaag | gaaggaagga  | aggaggagat | cagaagcatc | 120 |
| agccatgtcg | aactcggcgt | cggaatggc  | cgtttgtgac  | gaatgcaaac | tcaagttcct | 180 |
| ggaactcaag | gcgaagagga | gcttccgttt | catcgtgttc  | aagatcaacg | agaacgtgca | 240 |
| gcaggtggtg | gtggacaggc | ttgggggacc | aggtgaaagc  | tacgatgcgt | tcagggcctg | 300 |
| ctttcccgcg | aacgagTgyc | gtacgcgggt | gtttgatttt  | gactttgtca | ctgatgagaa | 360 |
| ctgccagaag | agcaagatct | tcttcatctc | ttgggcccc   | gatgcatcga | gggtgagaag | 420 |
| caagatgttg | tacgcaagct | ccaaggaccg | gttcaagagg  | gagctcgacg | gcattcaggt | 480 |
| ggagctacaa | gcaactgagc | cgagcgaaat | gagcatggac  | atcatcaagt | cgcgagccct | 540 |
| ctgaaacagc | cgcgcatcag | ctcctgcatg | cccgctcgatt | cttcggtgtt | ggtaacggtc | 600 |
| atccgttttc | gtgtccttgt | ttttcctgga | agcaaaagcc  | ttgcgttctg | tatgagactt | 660 |
| ctgtatacca | tttcccctct | ctnknntttc | ccaatctctg  | ccgtagtcct | gcactcctgc | 720 |
| tactgtctga | aactagwact | tatttgctgt | tttgtctcgt  | ggcattgtcg | agtcgcttat | 780 |
| gtgtctatgc | aatgctagtt | gtgagaagcc | taatgtacct  | tagcttaatc | accgaattgc | 840 |
| tc         |            |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1574763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2907:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Arg | Pro | Ser | Leu | Gln | Leu | Ser | Ile | Ser | Leu | Pro | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Arg | Pro | Thr | Ala | Asp | Cys | Cys | Ser | Asp | Arg | Gly | Arg | Lys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Arg | Arg | Arg | Ser | Glu | Ala | Ser | Ala | Met | Ser | Asn | Ser | Ala | Ser | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Ala | Val | Cys | Asp | Glu | Cys | Lys | Leu | Lys | Phe | Leu | Glu | Leu | Lys | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Ser | Phe | Arg | Phe | Ile | Val | Phe | Lys | Ile | Asn | Glu | Asn | Val | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Val | Val | Val | Asp | Arg | Leu | Gly | Gly | Pro | Gly | Glu | Ser | Tyr | Asp | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Arg | Ala | Cys | Phe | Pro | Ala | Asn | Glu | Xaa | Arg | Tyr | Ala | Val | Phe | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Asp | Phe | Val | Thr | Asp | Glu | Asn | Cys | Gln | Lys | Ser | Lys | Ile | Phe | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Trp | Ala | Pro | Asp | Ala | Ser | Arg | Val | Arg | Ser | Lys | Met | Leu | Tyr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ser | Ser | Lys | Asp | Arg | Phe | Lys | Arg | Glu | Leu | Asp | Gly | Ile | Gln | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Leu | Gln | Ala | Thr | Glu | Pro | Ser | Glu | Met | Ser | Met | Asp | Ile | Ile | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Arg | Ala | Leu |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..672

(D) OTHER INFORMATION: / Ceres Seq. ID 1574769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2910:

|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| acagccgtca  | cgcacttcaa | tccagcagcc  | tctgctctgc | ctgcgctcgca | gccagtggct | 60  |
| cagcggtgc   | gcccgtgcct | gtcacgtctt  | gtcctcaatc | tctctctctc  | tcaatcctca | 120 |
| cctctccggc  | tctctttctc | ctccccagtc  | cccaacggtg | aggcccccgc  | cgtgcagccc | 180 |
| atcgacgat   | tgccgctgca | aGgcgsggac  | accgagggct | agaagcggcg  | gcggtgccag | 240 |
| ggctcggcgc  | tcggttggca | atggcgaggc  | ggcttatgCt | ggcgctccct  | gtgctcctct | 300 |
| tcttattgct  | cgtcgggcgc | cggggattct  | tccgtgctaa | tggggaatgg  | gtcacatgct | 360 |
| tctgttcattg | gcactggcac | ggtggatctg  | aagtttactt | cgggaaagat  | cgtgcagctg | 420 |
| aagaacgtgc  | atcatgtccc | kkctatacac  | aagaatctcg | ttagcggaac  | ccttctatgt | 480 |
| agagatgggt  | tcaaggtagt | tttagagtcc  | aataaattag | ttgtgtccaa  | gtctggacaa | 540 |
| tttattggta  | aaggctatga | ttgcggaggc  | ttgttccgct | tttctttgtt  | agatttcaat | 600 |
| aataagtctg  | tgaaccatat | ttgtgctaata | gttgatgatc | ttgcgagtat  | ttggcattct | 660 |
| cgtttgtgct  | at         |             |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1574770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2911:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Val | Thr | His | Phe | Asn | Pro | Ala | Ala | Ser | Ala | Leu | Pro | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |
| Gln | Pro | Val | Ala | Gln | Arg | Leu | Arg | Pro | Cys | Leu | Ser | Arg | Leu | Val | Leu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |
| Asn | Leu | Ser | Leu | Ser | Gln | Ser | Ser | Pro | Leu | Arg | Leu | Ser | Phe | Ser | Ser |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Pro | Val | Pro | Asn | Gly | Glu | Ala | Pro | Ala | Val | Gln | Pro | Ile | Asp | Ala | Leu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Pro | Leu | Gln | Gly | Xaa | Asp | Thr | Glu | Gly |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1574771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2912:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Ser | Arg | Thr | Ser | Ile | Gln | Gln | Pro | Leu | Leu | Cys | Leu | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |
| Ser | Gln | Trp | Leu | Ser | Gly | Cys | Ala | Arg | Ala | Cys | His | Val | Leu | Ser | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |
| Ile | Ser | Leu | Ser | Leu | Asn | Pro | His | Leu | Ser | Gly | Ser | Leu | Ser | Pro | Pro |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Gln | Ser | Pro | Thr | Val | Arg | Pro | Pro | Pro | Cys | Ser | Pro | Ser | Thr | His | Cys |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Arg | Cys | Lys | Ala | Xaa | Thr | Pro | Arg | Ala | Arg | Ser | Gly | Gly | Gly | Ala | Arg |
| 65  |     |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 75  |

Ala Arg Arg Ser Val Gly Asn Gly Glu Ala Ala Tyr Ala Gly Ala Pro  
85 90 95  
Cys Ala Pro Leu Leu Ile Ala Arg Arg Ala Pro Gly Ile Leu Pro Cys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1574772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2913:

Met Gly Asn Gly Ser His Ala Ser Val His Gly Thr Gly Thr Val Asp  
1 5 10 15  
Leu Lys Phe Thr Ser Gly Lys Ile Val Gln Leu Lys Asn Val His His  
20 25 30  
Val Xaa Xaa Ile His Lys Asn Leu Val Ser Gly Thr Leu Leu Cys Arg  
35 40 45  
Asp Gly Phe Lys Val Val Leu Glu Ser Asn Lys Leu Val Val Ser Lys  
50 55 60  
Ser Gly Gln Phe Ile Gly Lys Gly Tyr Asp Cys Gly Gly Leu Phe Arg  
65 70 75 80  
Phe Ser Leu Leu Asp Phe Asn Asn Lys Ser Val Asn His Ile Cys Ala  
85 90 95  
Asn Val Asp Asp Leu Ala Ser Ile Trp His Ser Arg Leu Cys His  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1574773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2914:

aacctactga cgagctcgcc atggcctccc tctcctctgc cgccgtcacc gcccttctct 60  
tcgccgcacc agcgccaccc gcgccgtggt cagaaggagg tccttcaccg tgcgcgcctc 120  
tctccgcaag gccaccggca ccgcccgcgt ggcaatggct gccagcgccc tgcttgccgg 180  
cggtgccatg gcccaggagg tgctgctggg cgcaggcgac ggccgggctcg tcttcgagcc 240  
cagccagttc accgtcaagg ccggcgacac catcTacatt caagaacaac gccggcttcc 300  
cgcacaacgT cktcttcgac gaagacgagg tgccgagcgg cgtcgacacc accaagatct 360  
cgcaggagga gtacctcaac gcgccaggcg agacctactc cgtcaccctc accgtgcgcg 420  
gaacctacgg cttctactgc gagccgcata aaggagccgg aatggtcggc aagatcacccg 480  
tcaactaatt aagctagcta tcgatcgata tccattcatg tatttagctgt tgcttctctgc 540  
tttgtactcc gccgatctgt ccattctctwc atgttttcgk cttcacac

(2) INFORMATION FOR SEQ ID NO:2915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1574774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2915:

Asn Leu Leu Thr Ser Ser Pro Trp Pro Pro Ser Pro Leu Pro Pro Ser  
1 5 10 15  
Pro Pro Leu Pro Ser Pro His Gln Arg His Pro Arg Arg Gly Gln Lys  
20 25 30  
Glu Val Leu His Arg Ala Arg Leu Ser Pro Gln Gly His Arg His Arg  
35 40 45  
Arg Arg Gly Asn Gly Cys Gln Arg Pro Ala Cys Arg Arg Cys His Gly  
50 55 60  
Pro Gly Gly Ala Ala Gly Arg Arg Arg Arg Arg Ala Arg Leu Arg Ala  
65 70 75 80  
Gln Pro Val His Arg Gln Gly Arg Arg His His Leu His Ser Arg Thr  
85 90 95  
Thr Pro Ala Ser Arg Thr Thr Xaa Ser Ser Thr Lys Thr Arg Cys Arg  
100 105 110  
Ala Ala Ser Thr Pro Pro Arg Ser Arg Arg Arg Ser Thr Ser Thr Arg  
115 120 125  
Gln Ala Arg Pro Thr Pro Ser Pro Ser Pro Cys Arg Glu Pro Thr Ala  
130 135 140  
Ser Thr Ala Ser Arg Ile Lys Glu Pro Glu Trp Ser Ala Arg Ser Pro  
145 150 155 160  
Ser Thr Asn

(2) INFORMATION FOR SEQ ID NO:2916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1574775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2916:

Pro Thr Asp Glu Leu Ala Met Ala Ser Leu Ser Ser Ala Ala Val Thr  
1 5 10 15  
Ala Pro Ser Phe Ala Ala Pro Ala Pro Pro Ala Pro Trp Ser Glu Gly  
20 25 30  
Gly Pro Ser Pro Cys Ala Pro Leu Ser Ala Arg Pro Pro Ala Pro Pro  
35 40 45  
Pro Trp Gln Trp Leu Pro Ala Pro Cys Leu Pro Ala Val Pro Trp Pro  
50 55 60  
Arg Arg Cys Cys Trp Ala Gln Ala Thr Ala Gly Ser Ser Ser Ser Pro  
65 70 75 80  
Ala Ser Ser Pro Ser Arg Pro Ala Thr Pro Ser Thr Phe Lys Asn Asn  
85 90 95  
Ala Gly Phe Pro His Asn Val Xaa Phe Asp Glu Asp Glu Val Pro Ser  
100 105 110  
Gly Val Asp Thr Thr Lys Ile Ser Gln Glu Glu Tyr Leu Asn Ala Pro  
115 120 125  
Gly Glu Thr Tyr Ser Val Thr Leu Thr Val Pro Gly Thr Tyr Gly Phe  
130 135 140  
Tyr Cys Glu Pro His Gln Gly Ala Gly Met Val Gly Lys Ile Thr Val  
145 150 155 160  
Asn

(2) INFORMATION FOR SEQ ID NO:2917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2917:

Met Ala Ser Leu Ser Ser Ala Ala Val Thr Ala Pro Ser Phe Ala Ala  
1 5 10 15  
Pro Ala Pro Pro Ala Pro Trp Ser Glu Gly Gly Pro Ser Pro Cys Ala  
20 25 30  
Pro Leu Ser Ala Arg Pro Pro Ala Pro Pro Pro Trp Gln Trp Leu Pro  
35 40 45  
Ala Pro Cys Leu Pro Ala Val Pro Trp Pro Arg Arg Cys Cys Trp Ala  
50 55 60  
Gln Ala Thr Ala Gly Ser Ser Ser Pro Ala Ser Ser Pro Ser Arg  
65 70 75 80  
Pro Ala Thr Pro Ser Thr Phe Lys Asn Asn Ala Gly Phe Pro His Asn  
85 90 95  
Val Xaa Phe Asp Glu Asp Glu Val Pro Ser Gly Val Asp Thr Thr Lys  
100 105 110  
Ile Ser Gln Glu Glu Tyr Leu Asn Ala Pro Gly Glu Thr Tyr Ser Val  
115 120 125  
Thr Leu Thr Val Pro Gly Thr Tyr Gly Phe Tyr Cys Glu Pro His Gln  
130 135 140  
Gly Ala Gly Met Val Gly Lys Ile Thr Val Asn  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2918:

gataaatctc tccatcaggc agcacctagc tagcagcagc caatgacgaa gccttcgcag 60  
gtgctgttg cgcgctcgc gcgctggcg gtggtcctgc tgctgctgtg cgccgcccgc 120  
ccgcggggcg cCgacgcgc gacggcgtgc gacgccacgc agctgacgcc gtgcgccggc 180  
gccatcatca tcgggaggtc gccagcgcg gcgtgctgca gtaggctcaa ggagcagcag 240  
ccgtgcctgt gcacgtacgc gcgcgacccc aatcttcagc gctacgtcaa ctgcgccaac 300  
ggcaagaagg ccatggccgc gtgcaagggtg cccgtrccgt cgtgctagtt aacttctgtt 360  
tgcrcgcgcg ccgcgtacgt gtcgtgtcgt gcctgtgtca gtagcagcaa ggcccactgg 420  
acagggacag agtatggcgt cactttctgt ttccgtacat acgtac

(2) INFORMATION FOR SEQ ID NO:2919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1574798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2919:

Met Thr Lys Pro Ser Gln Val Leu Leu Ala Ala Leu Ala Xaa Trp Ala  
1 5 10 15  
Val Val Leu Leu Leu Leu Cys Ala Ala Ala Pro Arg Gly Ala Asp Ala  
20 25 30  
Ala Thr Ala Cys Asp Ala Thr Gln Leu Thr Pro Cys Ala Gly Ala Ile  
35 40 45  
Ile Ile Gly Arg Ser Pro Ser Ala Ala Cys Cys Ser Arg Leu Lys Glu  
50 55 60  
Gln Gln Pro Cys Leu Cys Thr Tyr Ala Arg Asp Pro Asn Leu Gln Arg  
65 70 75 80  
Tyr Val Asn Ser Pro Asn Gly Lys Lys Ala Met Ala Ala Cys Lys Val  
85 90 95  
Pro Xaa Pro Ser Cys  
100

(2) INFORMATION FOR SEQ ID NO:2920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..743

(D) OTHER INFORMATION: / Ceres Seq. ID 1574803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2920:

aggatcctct cggcgcgagg ctccgagttg ccgtctccgc ctctctgagt tagcgttctc 60  
caccaagagc agcatggagt ccgacgtgta cagctacggc gtggtgctgc tggagctgct 120  
cacgaggagg gcggcgggtg atccctcggt tcccgcaggc acggacatag tcagctgggc 180  
gtcgtccgcc ctgaacSggc accgacaaaa tcgaggccgt ctgcgaccgc gctctcatgg 240  
aggaagtctt cggcacggtg gagatggagg aggtgagtaa ggtcctgtca gtggcgctgc 300  
ggtgcgcggc cagggaggcg agccaaaggc cctccatgac cgccgtcgtg aaggagctga 360  
cggatgcacg gcctgccact ggcggcggcc ggtcgttgtc caagtcgaag caggggaaac 420  
caggatcgca atccaacagc agcgccctacc ggcagtagga tctctgactc tgccgagctg 480  
tttggggaca ccaactttac tcaacttgta gtctctactc tatagGtacc ctgcgttggt 540  
gtacatcctg attggttagt tggcaaagat tagttgtagt tcaaataaaa cggagagatg 600  
ctggactTcg tgtcagtgcg agtgaagcaa gctgcttggt ctgaaatctg tggactgtgg 660  
cttgtccgtg gcttccaggg acgggaccag gagagaatgg gtattcgaaa ttgtactaaa 720  
ggaaaaaaaa attagatggt ctg

(2) INFORMATION FOR SEQ ID NO:2921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1574804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2921:

Gly Ser Ser Arg Pro Arg Ala Pro Ser Cys Arg Leu Arg Leu Ser Glu  
1 5 10 15  
Leu Ala Phe Ser Thr Lys Ser Ser Met Glu Ser Asp Val Tyr Ser Tyr  
20 25 30  
Gly Val Val Leu Leu Glu Leu Leu Thr Arg Arg Ala Ala Val Asp Pro  
35 40 45  
Ser Phe Pro Asp Gly Thr Asp Ile Val Ser Trp Ala Ser Ser Ala Leu

00000000-00000000

50                      55                      60  
Asn Xaa His Arg Gln Asn Arg Gly Arg Leu Arg Pro Gly Ser His Gly  
65                      70                      75                      80  
Gly Ser Leu Arg His Gly Gly Asp Gly Gly Gly Glu  
                    85                      90

(2) INFORMATION FOR SEQ ID NO:2922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2922:

Met Glu Ser Asp Val Tyr Ser Tyr Gly Val Val Leu Leu Glu Leu Leu  
1                      5                      10                      15  
Thr Arg Arg Ala Ala Val Asp Pro Ser Phe Pro Asp Gly Thr Asp Ile  
                    20                      25                      30  
Val Ser Trp Ala Ser Ser Ala Leu Asn Xaa His Arg Gln Asn Arg Gly  
                    35                      40                      45  
Arg Leu Arg Pro Gly Ser His Gly Gly Ser Leu Arg His Gly Gly Asp  
50                      55                      60  
Gly Gly Gly Glu  
65

(2) INFORMATION FOR SEQ ID NO:2923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2923:

Met Glu Glu Val Phe Gly Thr Val Glu Met Glu Glu Val Ser Lys Val  
1                      5                      10                      15  
Leu Ser Val Ala Leu Arg Cys Ala Ala Arg Glu Ala Ser Gln Arg Pro  
                    20                      25                      30  
Ser Met Thr Ala Val Val Lys Glu Leu Thr Asp Ala Arg Pro Ala Thr  
                    35                      40                      45  
Gly Gly Gly Arg Ser Leu Ser Lys Ser Lys Gln Gly Lys Pro Gly Ser  
50                      55                      60  
Gln Ser Asn Ser Ser Ala Tyr Arg Gln  
65                      70

(2) INFORMATION FOR SEQ ID NO:2924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..582
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2924:

```
aaaacttcgt tgcgaagaag ctcagaacag aagccatcaa aagcgaggct gcgagagcgg 60
agagagagag tgaRgggagg cgccgacgcc gagtcctttc ttcacacctgc atctgccgct 120
gtttccgaca ggatgtttct caccgaggac gagtacgacc gtggggtgaa caccttctct 180
ccggaggggc ggctgttcca ggtcgagtac gccatcgagg ccatcaagtt gggatccact 240
gcgatcggtt tgaagacaaa ggatggtggt gtcctcgccg ttgagaaaacg tgtgacctca 300
ccactgctgg aaccaagcag tgtggaaaaa ataatggaaa ttgatgagca cataggctgt 360
gccatgagtg gacttattgc tgatgctaga acactagtgg aacatgctcg tgttgaaact 420
cagaatcata ggttctcata cggagagcca atgactgtag aatcttcgac acaagctatc 480
tgtgacttag ctctgcgttt tggcgaaggt gacgaagagt caatgtcacg gccatttgga 540
gtctctctcc taattgctgg acatgatgag aatggaccta gc
```

(2) INFORMATION FOR SEQ ID NO:2925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1574815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2925:

```
Lys Thr Ser Phe Ala Arg Ser Ser Glu Gln Lys Pro Ser Lys Ala Arg
1 5 10 15
Leu Arg Glu Arg Arg Glu Arg Val Xaa Gly Gly Ala Asp Ala Glu Ser
 20 25 30
Phe Leu His Pro Ala Ser Ala Ala Val Ser Asp Arg Met Phe Leu Thr
 35 40 45
Arg Thr Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser Pro Glu Gly Arg
 50 55 60
Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys Leu Gly Ser Thr
 65 70 75 80
Ala Ile Gly Leu Lys Thr Lys Asp Gly Val Val Leu Ala Val Glu Lys
 85 90 95
Arg Val Thr Ser Pro Leu Leu Glu Pro Ser Ser Val Glu Lys Ile Met
 100 105 110
Glu Ile Asp Glu His Ile Gly Cys Ala Met Ser Gly Leu Ile Ala Asp
 115 120 125
Ala Arg Thr Leu Val Glu His Ala Arg Val Glu Thr Gln Asn His Arg
 130 135 140
Phe Ser Tyr Gly Glu Pro Met Thr Val Glu Ser Ser Thr Gln Ala Ile
 145 150 155 160
Cys Asp Leu Ala Leu Arg Phe Gly Glu Gly Asp Glu Glu Ser Met Ser
 165 170 175
Arg Pro Phe Gly Val Ser Leu Leu Ile Ala Gly His Asp Glu Asn Gly
 180 185 190
Pro Ser
```

(2) INFORMATION FOR SEQ ID NO:2926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1574816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2926:

```
Met Phe Leu Thr Arg Thr Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser
```



1 5 10 15  
Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys  
20 25 30  
Leu Gly Ser Thr Ala Ile Gly Leu Lys Thr Lys Asp Gly Val Val Leu  
35 40 45  
Ala Val Glu Lys Arg Val Thr Ser Pro Leu Leu Glu Pro Ser Ser Val  
50 55 60  
Glu Lys Ile Met Glu Ile Asp Glu His Ile Gly Cys Ala Met Ser Gly  
65 70 75 80  
Leu Ile Ala Asp Ala Arg Thr Leu Val Glu His Ala Arg Val Glu Thr  
85 90 95  
Gln Asn His Arg Phe Ser Tyr Gly Glu Pro Met Thr Val Glu Ser Ser  
100 105 110  
Thr Gln Ala Ile Cys Asp Leu Ala Leu Arg Phe Gly Glu Gly Asp Glu  
115 120 125  
Glu Ser Met Ser Arg Pro Phe Gly Val Ser Leu Leu Ile Ala Gly His  
130 135 140  
Asp Glu Asn Gly Pro Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:2927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..905
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2927:

aaaccctttc gatctgctca actaccaaac tctgctcctc cctgcttccg tcacgcgaga 60  
gcactccact ccCacgcgaa Accctagcag tggttctccc tcggggcccc gctaagcagc 120  
ttggttccaa gctgtagaag catctccgat cccatccgcg gcgggttgag gccatcagct 180  
ccggtttctg cagccggatt tgggatccgc gagatgtctt ggtccgcgcc cgacgacatc 240  
ctcctctcca cctccctcgc cggtctcttg gacaagaaac ttattgtcct gctaagagat 300  
ggacggaaac tgcttggcac cctctgctca tttgatcagt ttgcaaagt tggtcttcag 360  
ggtgcttggt aacgagtgt tgtgggggaa caatattgtg atgttcctct tgggctgtac 420  
gtaatccggg gagagaacgt tgttttaatc ggagaattgg atcgcgaaaa ggatgaactc 480  
cctgctcaca tgacctgtgt ttcagaagca gaaataagaa aggctgaaaa ggcagaacgg 540  
gaagccagag atctgaaagg gacgatgagg aaacggatgg agttcctgga cttcgattaa 600  
caccgtcacc Ygcggccgtt gccgtcccc attgtggcgg aatctttagt gccggcctgt 660  
gtgccataca tgcttggtga ccgcgcgggc gcaocttgga ttgctggagg gtttagcgaa 720  
cagtttcttt ttaactagca gtgctgtttt ataactotcgt ggccacagac cctttTgagc 780  
gctcctgat acagctttgt caccactctg atcattgcct cgatgaattt tatatacctg 840  
acgttttgga ttggatctgc gccaaaacgc catttctatg gagagagtct ctactcttat 900  
agctc

(2) INFORMATION FOR SEQ ID NO:2928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2928:

Met Ser Trp Ser Ala Pro Asp Asp Ile Leu Leu Ser Thr Ser Leu Ala  
1 5 10 15

Gly Phe Leu Asp Lys Lys Leu Ile Val Leu Leu Arg Asp Gly Arg Lys  
20 25 30  
Leu Leu Gly Thr Leu Cys Ser Phe Asp Gln Phe Ala Asn Val Val Leu  
35 40 45  
Gln Gly Ala Cys Glu Arg Val Ile Val Gly Glu Gln Tyr Cys Asp Val  
50 55 60  
Pro Leu Gly Leu Tyr Val Ile Arg Gly Glu Asn Val Val Leu Ile Gly  
65 70 75 80  
Glu Leu Asp Arg Glu Lys Asp Glu Leu Pro Ala His Met Thr Cys Val  
85 90 95  
Ser Glu Ala Glu Ile Arg Lys Ala Glu Lys Ala Glu Arg Glu Ala Arg  
100 105 110  
Asp Leu Lys Gly Thr Met Arg Lys Arg Met Glu Phe Leu Asp Phe Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..666
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2929:

gtaacgaggc atcgacactg acagagtcca cggcacggct tgtttaccac caaccatccg 60  
gcccttcccc gaccCatggc ggcggcacc cctcgctggt ggccgctcct cctgcagctc 120  
gcaatcgccc ttggcatcct gctcgcdgcg gccgaggctt ggacggggga gatccgcggc 180  
cgcgctgctt ggcagctctg cggcgacgca gccatcggcc cggaggacca cgccctcgaa 240  
ggtgcgaggg ttgctgtcct ctgcatcaca aaatctggtg aggttatcaa ctatcaagcc 300  
ttcacaaact ccaagggcgt gtatactgtc gccgagacta tgccggagag cgacaggtgg 360  
gactcgtgct tggcgaggcc tatgagcagc ttccatctac attgcacacg gcgggggtgat 420  
gctcactctg ggggtgaagtt cacttacaac aaatcgtctg ggaaccacac caccgtcaag 480  
cctttcctct acaagccggc caccatccct ctgtattgta gttaaacac acatcttgct 540  
ggaacgcaga agatagaaca tacaggaaga aaatatgtat tcgtgccccg actccatata 600  
taagtaaaaca cttttgatgt aaatcaaaga ttcagctgtc tatgggagct gttctagtgt 660  
ctggtc

(2) INFORMATION FOR SEQ ID NO:2930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2930:

Asn Glu Ala Ser Thr Leu Thr Glu Ser Thr Ala Arg Leu Val Tyr His  
1 5 10 15  
Gln Pro Ser Gly Pro Ser Pro Thr His Gly Gly Gly Thr Pro Ser Leu  
20 25 30  
Val Ala Ala Pro Pro Ala Ala Arg Asn Arg Pro Trp His Pro Ala Arg  
35 40 45  
Xaa Gly Arg Gly Leu Asp Gly Gly Asp Pro Arg Pro Arg Arg Leu Arg  
50 55 60  
Arg Leu Arg Arg Arg Ser His Arg Pro Gly Gly Pro Arg Pro Arg Arg

80

(i) SEQUENCE CHARACTERISTICS:

- [illegible]

(i) SEQUENCE CHARACTERISTICS:

- |            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| aaattccatt | ccaaatccgc  | agtcgcgaga | cgagagtgga | agcggggcac | agacaggaag  | 60  |
| agaagccaat | ggcgctgtcc  | Ctctccctcg | cgcgccccgc | gccCctcgcc | gtttccgcgc  | 120 |
| gcgcaggagc | caggaagcta  | cccgagcca  | gcctcgcat  | cccggcgaaa | tccttcttcg  | 180 |
| gcgcgcgcgt | ggccgccacc  | gcggcctccg | tcgcgtcgcc | gctcccgcgc | aaGccggcca  | 240 |
| ctccaccac  | ctcgctcgag  | gtcgtcgcg  | cggggaagaa | gggctacaag | atgaagacgc  | 300 |
| acaaggcgct | ggcgaacggt  | tcggggtgac | ggggaggggc | aagatcgtgc | ggcggtcgc   | 360 |
| cgggaagca  | cacttgctcg  | ccaagaagaa | caccaagcgc | aagaagaggc | tctcgaagat  | 420 |
| ggtgcaagtc | aacaagagtg  | actacgacaa | tgttacgggt | gcactgccct | acctcaaagt  | 480 |
| gaatagggaa | gcaaaactgag | agctacgtgg | tcttcaaaaa | atcattaagt | ttcgttccac  | 540 |
| caaattgtaa | ttttgtgtat  | cttccactgt | atttccttct | caaaaatact | gagggcatcat | 600 |
| ttcaaagcaa | gcaaaaaaca  | actcctggta | tcaacagtat | agcgatattt | cagaatgagg  | 660 |
| tgcactgctt | gctatagttg  | ttatttagtc | gcaaatatgt | gcaagtaaga | gtggcacttg  | 720 |
| agccattgct | tctcttagg   | atatggccag | cagatcgtgt | atatggctgt | gcaagacact  | 780 |
| qttttgcacc | attttatata  | tagactgcac | tgtttg     |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1574839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2933:

Lys Phe His Ser Lys Ser Ala Val Arg Arg Glu Trp Lys Arg Gly  
1 5 10 15  
Thr Asp Arg Lys Arg Ser Gln Trp Arg Cys Pro Ser Pro Ser Arg Ala  
20 25 30  
Pro Arg Pro Ser Pro Phe Pro Pro Ala Gln Glu Pro Gly Ser Tyr Pro  
35 40 45  
Gln Pro Ala Ser His Ser Arg Arg Asn Pro Ser Ser Ala Arg Arg Trp  
50 55 60  
Pro Pro Pro Arg Pro Pro Ser Arg Arg Arg Ser Arg Ala Ser Arg Pro  
65 70 75 80  
Pro Pro Pro Pro Arg Ser Arg Ser Ser Arg Arg Gly Arg Arg Ala Thr  
85 90 95  
Arg

(2) INFORMATION FOR SEQ ID NO:2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1574840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2934:

Asn Ser Ile Pro Asn Pro Gln Ser Ala Asp Glu Ser Gly Ser Gly Ala  
1 5 10 15  
Gln Thr Gly Arg Glu Ala Asn Gly Ala Val Pro Leu Pro Arg Ala Pro  
20 25 30  
Arg Ala Pro Arg Arg Phe Arg Arg Arg Arg Ser Gln Glu Ala Thr Arg  
35 40 45  
Ser Gln Pro Arg Ile Pro Gly Glu Ile Leu Leu Arg Arg Ala Ala Gly  
50 55 60  
Arg His Arg Gly Leu Arg Arg Val Ala Ala Pro Ala Gln Ala Gly His  
65 70 75 80  
Leu His His Leu Ala Arg Gly Arg Arg Gly Gly Glu Glu Gly Leu Gln  
85 90 95  
Asp Glu Asp Ala Gln Gly Val Gly Glu Arg Phe Arg Val Thr Gly Arg  
100 105 110  
Gly Lys Ile Val Arg Arg Cys Ala Gly Lys Gln His Leu Leu Ala Lys  
115 120 125  
Lys Asn Thr Lys Arg Lys Lys Arg Leu Ser Lys Met Val Gln Val Asn  
130 135 140  
Lys Ser Asp Tyr Asp Asn Val Thr Gly Ala Leu Pro Tyr Leu Lys Val  
145 150 155 160  
Asn Arg Lys Ala Asn  
165

(2) INFORMATION FOR SEQ ID NO:2935:

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- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 108 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..108  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574841  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2935:

Ile Pro Phe Gln Ile Arg Ser Pro Gln Thr Arg Val Glu Ala Gly His  
1                  5                  10                  15  
Arg Gln Glu Glu Lys Pro Met Ala Leu Ser Leu Ser Leu Ala Arg Pro  
                  20                  25                  30  
Ala Pro Leu Ala Val Ser Ala Gly Ala Gly Ala Arg Lys Leu Pro Ala  
                  35                  40                  45  
Ala Ser Leu Ala Phe Pro Ala Lys Ser Phe Phe Gly Ala Pro Leu Ala  
                  50                  55                  60  
Ala Thr Ala Ala Ser Val Ala Ser Pro Leu Pro Arg Lys Pro Ala Thr  
65                  70                  75                  80  
Ser Thr Thr Ser Leu Glu Val Val Ala Ala Gly Lys Lys Gly Tyr Lys  
                  85                  90                  95  
Met Lys Thr His Lys Ala Ser Ala Asn Gly Ser Gly  
                  100                  105

(2) INFORMATION FOR SEQ ID NO:2936:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 743 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..743  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574842  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2936:

acaggcgaaa aaaaaaactg tttgttagcg tgacgtgcgt raggagtctg gagtcggacg          60  
gaatcgaaaa ggcgaaaact cagtgtctcg agtttcctcg gwnncgaggc gatggctggg          120  
aagggaggga aaggcttgct cgccgcgaag actacggcgg ccaagtccgc cgagaaggac          180  
aaggggaaga aggccccaat ctacgcgtcc tcccgcgccg gcctccagtt ccctgttggg          240  
cgtatccacc gtcagctgaa gcaaaggact caggcaaatt gtcgcgttg tgccaccgca          300  
gccgtctact ccgctgccat cctggagtag ttgactgccg aggttctKgg agctggcgaa          360  
tgctagcaag gatctgaagk tgaagcgtat cacccttcgc catttgacagc tagccattcg          420  
tgagagacgag gagctggaca ccctcatcaa gggcaccatc gcaggcggag gtgtcatccc          480  
gcacattcac aagtcacctga tcaacaagtc ctccaaggag tgaagactag gggatgtgca          540  
tctttagttt aaactagact tctgtgcgct cctcggcgag tccttgatcat cctgtagggt          600  
ttagttgagc tgtcaggttg gagctcctct gtgtaacgct tgccctgtac tgcttcatca          660  
gttatttggt tattgtgttt gtgttgagtt gtttaacttca ggggtgcaaa cctggatgct          720  
tatttagtta tgtgactact gct

(2) INFORMATION FOR SEQ ID NO:2937:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 124 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..124  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2937:

Arg Arg Lys Lys Lys Leu Phe Val Ser Val Thr Cys Xaa Arg Ser Leu  
1 5 10 15  
Glu Ser Asp Gly Ile Glu Lys Ala Lys Thr Gln Cys Leu Glu Phe Pro  
20 25 30  
Arg Xaa Xaa Gly Asp Gly Trp Glu Gly Arg Glu Arg Leu Ala Arg Arg  
35 40 45  
Glu Asp Tyr Gly Gly Gln Val Arg Arg Glu Gly Gln Gly Glu Glu Gly  
50 55 60  
Pro Asn Leu Thr Leu Leu Pro Arg Arg Pro Pro Val Pro Cys Trp Ala  
65 70 75 80  
Tyr Pro Pro Ser Ala Glu Ala Lys Asp Ser Gly Lys Trp Ser Arg Trp  
85 90 95  
Cys His Arg Ser Arg Leu Leu Arg Cys His Pro Gly Val Leu Asp Cys  
100 105 110  
Arg Gly Ser Xaa Ser Trp Arg Met Leu Ala Arg Ile  
115 120

(2) INFORMATION FOR SEQ ID NO:2938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2938:

Met Ala Gly Lys Gly Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala  
1 5 10 15  
Ala Lys Ser Ala Glu Lys Asp Lys Gly Lys Lys Ala Pro Ile Ser Arg  
20 25 30  
Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Ile His Arg Gln  
35 40 45  
Leu Lys Gln Arg Thr Gln Ala Asn Gly Arg Val Gly Ala Thr Ala Ala  
50 55 60  
Val Tyr Ser Ala Ala Ile Leu Glu Tyr Leu Thr Ala Glu Val Xaa Gly  
65 70 75 80  
Ala Gly Glu Cys

(2) INFORMATION FOR SEQ ID NO:2939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..739
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2939:

atgttctctg gcaaacacac acacacacac acacacacac acacacacac 60  
acacatcgTt ttgctgttgc aacaaagctc tacacgggaa gacaggctgc ttctttcttg 120  
cagtctctgg tccagaagcc tgaagaaatg gcgtcaccca acgtcacatt ccttgccttc 180  
ttcgtggccc tcgcactatc ggcgcttcac accgacgcag cggcggcggT cagaaacctt 240  
gcacyatagg agcgacacat ggtgcgtggc caagccgtcg acgcaggagg cggcgctgcg 300  
gggcaacctg gagttcgctt gctccgagag cgactgcggc gccatccagg gcaccggcgt 360  
gcgcccagcc cgacagcctg ctgtcgcggg cgtcggtggc catgaacgcc tactaccagg 420  
cccgggggag gaactcgtgg aactgcttct tcaacggcac cggcataatc accatcactg 480

```
accccagcct tggcacctgc aaatatgctt gacacgacgg gctgctctgc tgctgctgtg 540
ctcaacggac gatgaataag gctgtagggg aatgatgcat cttttccttc tctttgtttt 600
gttattgtgt ctgtgtgagt gacgaggag tatccttgca gaaccaacca gtatcatgtc 660
tgagcactgt agagagaatt tccgtgcttt tatttcccaa atacagttct actccaggcc 720
agtggctgga ggggagttt
```

(2) INFORMATION FOR SEQ ID NO:2940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2940:

```
Met Phe Ser Gly Lys His Thr His Thr His Thr His Thr His Thr His
1 5 10 15
Thr His Thr His Thr His Arg Phe Ala Val Ala Thr Lys Leu Tyr Thr
20 25 30
Gly Arg Gln Ala Ala Ser Phe Leu Gln Ser Leu Val Gln Lys Pro Glu
35 40 45
Glu Met Ala Ser Pro Asn Val Thr Phe Leu Ala Phe Phe Val Ala Leu
50 55 60
Ala Leu Ser Ala Leu His Thr Asp Ala Ala Ala Val Arg Asn Leu
65 70 75 80
Ala Xaa
```

(2) INFORMATION FOR SEQ ID NO:2941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2941:

```
Cys Ser Leu Ala Asn Thr His Thr His Thr His Thr His Thr His Thr
1 5 10 15
His Thr His Thr His Ile Val Leu Leu Leu Gln Gln Ser Ser Thr Arg
20 25 30
Glu Asp Arg Leu Leu Leu Ser Cys Ser Leu Trp Ser Arg Ser Leu Lys
35 40 45
Lys Trp Arg His Pro Thr Ser His Ser Leu Pro Ser Ser Trp Pro Ser
50 55 60
His Tyr Arg Arg Phe Thr Pro Thr Gln Arg Arg Arg Ser Glu Thr Leu
65 70 75 80
His Xaa Arg Ser Asp Thr Trp Cys Val Ala Lys Pro Ser Thr Gln Glu
85 90 95
Ala Ala Leu Arg Gly Asn Leu Glu Phe Ala Cys Ser Glu Ser Asp Cys
100 105 110
Gly Ala Ile Gln Gly Thr Gly Val Arg Pro Ala Arg Gln Pro Ala Val
115 120 125
Ala Gly Val Gly Gly His Glu Arg Leu Leu Pro Gly Pro Gly Glu Glu
130 135 140
Leu Val Glu Leu Leu Leu Gln Arg His Arg His Asn His His His
145 150 155
```

(2) INFORMATION FOR SEQ ID NO:2942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2942:

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| agctcaccgc  | cacctccacg  | ctcgaagctc | ctcccgaacc  | ggccgcatcg | tcgccatggc  | 60   |
| agccgcccgt  | cttgcaagct  | ccgtgaagga | agtgcctgccg | tctcccctga | cctccgcctc  | 120  |
| cgagccccct  | Cccccctttc  | gatggcacca | ccagggttgta | cgtggcctat | ctttgcccgt  | 180  |
| tcgcgcagcg  | cttggtattgc | tagaaactac | aagggctctgc | aggacaagat | taagatagtt  | 240  |
| gccatcgatc  | tcgctgacag  | gccagcgtgg | tacaaggaga  | aggtttatcc | agaaaacaag  | 300  |
| gtgcctttctc | tagagcacga  | caaccaggtg | aaaggagaga  | gcttggtatt | ggttaagtac  | 360  |
| atcgacaaca  | acttcgaagg  | tccatcgttg | ctccccgagg  | atcatgcaaa | gcagcagttc  | 420  |
| gctgaggagc  | tgctcggata  | cactgacgca | ttcaacaaag  | cattttactc | atgttttagtc | 480  |
| gacagggaag  | atgtgtctga  | ggaagccgtt | gctgccttgg  | acaaaataga | agacgccctg  | 540  |
| gggaaattca  | acgacggccc  | gttcttcctt | ggccagttca  | gtctggtgga | cgttgcgat   | 600  |
| gtaccgttca  | tcgagaggtt  | tcagatactc | tattccaata  | taaagaacta | tgacatcaca  | 660  |
| aagggcagac  | ccagccttca  | gaaattcatc | gaggaagtga  | acaagatcga | tgcgtacaca  | 720  |
| cagactaaac  | tggaccgcga  | gtttttgctt | gagcaaacaa  | agaagcggct | tgggattgct  | 780  |
| taaagcctgt  | gaccaaggac  | gagactttcg | ccagaagcac  | cagcgtagta | gatcggagct  | 840  |
| cgttttagta  | ggttggtgtg  | ttggatatta | cgtctggtct  | tcaataaggc | atggccttct  | 900  |
| ttaatggctg  | tgcttctgaa  | aataaataaa | ctagttgtcc  | aggtattatc | gttgctttgg  | 960  |
| tgacgtgtcg  | atgtcactgt  | atatatatga | atgggtggga  | aaGgaatgat | gatgtgcagt  | 1020 |
| gtgttctgtg  | caaatatgtc  | cgagatgaag | gatcagtatc  | catgtagaca | ttcatatatt  | 1080 |
| gctcatattg  | tgacacggcg  | catgaaagac | atggtttcgg  | cccctaccac | gc          |      |

(2) INFORMATION FOR SEQ ID NO:2943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2943:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Pro | Pro | Pro | Pro | Arg | Ser | Lys | Leu | Leu | Pro | Asn | Arg | Pro | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | His | Gly | Ser | Arg | Arg | Phe | Cys | Lys | Leu | Arg | Glu | Gly | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Ser | Pro | Asp | Leu | Arg | Leu | Arg | Ala | Pro | Ser | Pro | Phe | Ser | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Pro | Pro | Gly | Cys | Thr | Trp | Pro | Ile | Phe | Ala | Arg | Ser | Arg | Ser | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Trp | Ile | Ala | Arg | Asn | Tyr | Lys | Gly | Leu | Gln | Asp | Lys | Ile | Lys | Ile | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ile | Asp | Leu | Ala | Asp | Arg | Pro | Ala | Trp | Tyr | Lys | Glu | Lys | Val | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Glu | Asn | Lys | Val | Pro | Ser | Leu | Glu | His | Asp | Asn | Gln | Val | Lys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ser | Leu | Asp | Leu | Val | Lys | Tyr | Ile | Asp | Asn | Asn | Phe | Glu | Gly | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Leu | Leu | Pro | Glu | Asp | His | Ala | Lys | Gln | Gln | Phe | Ala | Glu | Glu | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |



(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..747  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2945:

|          |             |                |             |            |             |     |
|----------|-------------|----------------|-------------|------------|-------------|-----|
| aaaaaacc | aaagcagagg  | gaaagtgccg     | tccggtctga  | ctcttgggca | cttgggctgac | 60  |
| gaccogtt | ctctctgcaa  | ctgcaactgc     | aacgcaccaa  | gaaactgccg | gcgatcgatc  | 120 |
| ggggaagg | ataaacatgg  | tgcacgggaa     | gctggargtc  | ctcctcgtct | ccgccaaagg  | 180 |
| actcgagg | accgatttcc  | tcaataacat     | ggaccccttc  | gtgatcctta | cctgccgcac  | 240 |
| ccaagagc | aaaagcagcg  | tgcgaaatgg     | agcaggaagc  | gagcccgaat | ggaacgagac  | 300 |
| cttcgtct | accgtctccg  | acgacacccc     | gcagctgcac  | ctcaagatca | tggacagcga  | 360 |
| cctcacc  | aacgatttccg | tccggcgaag     | Caaccatcccc | ctggaggccg | tgtttcagga  | 420 |
| aggcagc  | cttccccggc  | gttaccgcgt     | cgtcaaggag  | gagaagtact | gcggagaggt  | 480 |
| caagctcg | ctcacctt    | ccagcagcgg     | aaactcgccg  | ccctgatgac | aacgaggagg  | 540 |
| ggccgcct | tta cagcag  | ctgtgg agttgat | ctatcttgcc  | atggatgc   | atcatatata  | 600 |
| ccaccaag | agagaggat   | aattaattaa     | tctactcaag  | agaagaatca | gtgttgctgt  | 660 |
| tatgcgac | ccctctatc   | tatatatatg     | tgcttaattt  | gtcataacga | ctgccaatat  | 720 |
| aaaataaa | act attcag  | agttgttgcc     |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2946:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | His | Gly | Lys | Leu | Xaa | Val | Leu | Leu | Val | Ser | Ala | Lys | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asp | Thr | Asp | Phe | Leu | Asn | Asn | Met | Asp | Pro | Phe | Val | Ile | Leu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Arg | Thr | Gln | Glu | Gln | Lys | Ser | Val | Ala | Asn | Gly | Ala | Gly | Ser |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Pro | Glu | Trp | Asn | Glu | Thr | Phe | Val | Phe | Thr | Val | Ser | Asp | Asp | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Gln | Leu | His | Leu | Lys | Ile | Met | Asp | Ser | Asp | Leu | Thr | Asn | Asp | Asp |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Phe | Val | Gly | Glu | Ala | Thr | Ile | Pro | Leu | Glu | Ala | Val | Phe | Gln | Glu | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Leu | Pro | Pro | Ala | Val | His | Pro | Val | Lys | Glu | Glu | Lys | Tyr | Cys |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gly | Glu | Val | Lys | Leu | Ala | His | Leu | His | Ser | Ser | Ser | Gly | Asn | Ser | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..105  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2947:  
Met Asp Pro Phe Val Ile Leu Thr Cys Arg Thr Gln Glu Gln Lys Ser  
1 5 10 15  
Ser Val Ala Asn Gly Ala Gly Ser Glu Pro Glu Trp Asn Glu Thr Phe  
20 25 30  
Val Phe Thr Val Ser Asp Asp Thr Pro Gln Leu His Leu Lys Ile Met  
35 40 45  
Asp Ser Asp Leu Thr Asn Asp Asp Phe Val Gly Glu Ala Thr Ile Pro  
50 55 60  
Leu Glu Ala Val Phe Gln Glu Gly Ser Leu Pro Pro Ala Val His Pro  
65 70 75 80  
Val Val Lys Glu Glu Lys Tyr Cys Gly Glu Val Lys Leu Ala His Leu  
85 90 95  
His Ser Ser Ser Gly Asn Ser Pro Pro  
100 105

(2) INFORMATION FOR SEQ ID NO:2948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2948:

Met Glu Arg Asp Leu Arg Leu His Arg Leu Arg Arg His Pro Ala Ala  
1 5 10 15  
Ala Pro Gln Asp His Gly Gln Arg Pro His Gln Arg Arg Phe Arg Arg  
20 25 30  
Arg Ser Asn His Pro Pro Gly Gly Arg Val Ser Gly Arg Gln Pro Ser  
35 40 45  
Pro Gly Gly Ser Pro Gly Arg Gln Gly Gly Glu Val Leu Arg Arg Gly  
50 55 60  
Gln Ala Arg Ser Pro Ser Leu Gln Gln Arg Lys Leu Ala Ala Leu Met  
65 70 75 80  
Thr Thr Arg Arg Gly Arg Leu Thr Ala Ala Gly Val Asp Leu Ser Ala  
85 90 95  
Met Gly Cys Met His His Ile Tyr Pro Pro Arg Glu Glu Arg Ile Ile  
100 105 110  
Asn

(2) INFORMATION FOR SEQ ID NO:2949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..935
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2949:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agtttatggg ctggaatggg ccgctcaaac tggcccgtta cgtgaatttr gcggggctgc  | 60  |
| cgctgggatc cgagacgtgg tggctgcaca ggcacgtccg trggagcrgg cgggcgactg  | 120 |
| caggcagagg gtttcgtccg aaccctagtg tctccacac gccgtcgcca tggccgccgc   | 180 |
| ccgcgccgcc ctccgcctgc agcgccagtg cctcgccgcc aaccctttc tcttctccgg   | 240 |
| gcatggcctc cgctaccgca agcttgaggt catcctcacc acgactattg ataagctggg  | 300 |
| gaaagcaggc gaggtgggtca aggtggcgcc tggccacttc cgcaaccacc ttatgcccac | 360 |

gatgctcgca gtcccgaacc tggacaaatt cgccatacta atccgagagc agcgcaagCt 420  
ctatcaacgc gaagaggagg tcgcggtgaa acaagtcacg gagaaagatg atgatgcacg 480  
gctacaggaa gaaagaatga agcagtacca aacggcagca aagcggctag ataacgcact 540  
cttggtgttg aggaggttca tctcgactgg aaacgagctg cgtactcctg taacaaaaga 600  
cgaaattggt tccgaggtgg cgaggcagct caacatcaac atccatccgg agaacctgca 660  
totgcagtca cctttggcgt cgctcggcga atttgagttg cccctccggt taccgcagaa 720  
cataccgtgc ccagaaggta agctccagtg gactctgaag gtgaagatca ggagaaaatg 780  
agcgcaggaa ctggggaagt ttcttttgcc cccccacaat ctggtgtatg gtaccaaacc 840  
attgttagct ccgaaacaat ggtaccaaac cattggttat gcaagtttag ctccgaaaca 900  
tttttttctg atgtataata aaagagtaag gttgc

(2) INFORMATION FOR SEQ ID NO:2950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1574881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2950:

Met Ala Ala Ala Arg Ala Ala Leu Arg Leu Gln Arg Gln Cys Leu Ala  
1 5 10 15  
Ala Asn Pro Phe Leu Phe Ser Gly His Gly Leu Arg Tyr Arg Lys Leu  
20 25 30  
Glu Val Ile Leu Thr Thr Thr Ile Asp Lys Leu Gly Lys Ala Gly Glu  
35 40 45  
Val Val Lys Val Ala Pro Gly His Phe Arg Asn His Leu Met Pro Lys  
50 55 60  
Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu Ile Arg Glu  
65 70 75 80  
Gln Arg Lys Leu Tyr Gln Arg Glu Glu Glu Val Ala Val Lys Gln Val  
85 90 95  
Thr Glu Lys Asp Asp Asp Ala Arg Leu Gln Glu Glu Arg Met Lys Gln  
100 105 110  
Tyr Gln Thr Ala Ala Lys Arg Leu Asp Asn Ala Leu Leu Val Leu Arg  
115 120 125  
Arg Phe Ile Ser Thr Gly Asn Glu Leu Arg Thr Pro Val Thr Lys Asp  
130 135 140  
Glu Ile Val Ser Glu Val Ala Arg Gln Leu Asn Ile Asn Ile His Pro  
145 150 155 160  
Glu Asn Leu His Leu Gln Ser Pro Leu Ala Ser Leu Gly Glu Phe Glu  
165 170 175  
Leu Pro Leu Arg Leu Pro Gln Asn Ile Pro Cys Pro Glu Gly Lys Leu  
180 185 190  
Gln Trp Thr Leu Lys Val Lys Ile Arg Arg Lys  
195 200

(2) INFORMATION FOR SEQ ID NO:2951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1574882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2951:

Met Pro Lys Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu

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(2) INFORMATION FOR SEO ID NO:2952:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(IX) FEATURE:  
(A) NAME

(A) NAME/REF: peptide  
(B) LOCATION: 1 139

(B) LOCATION: 1..139  
(D) OTHER INFORMATION:

(D) OTHER INFORMATION: 7 Ceres Seq. ID 1574889  
SEQUENCE DESCRIPTION: SEQ ID NO:2952:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2932:  
Leu Ala Val Pro Asp Leu Asp Lys Phe Ala Il

(2) INFORMATION FOR SEQ ID NO.2935:  
(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(1X) FEATURE:  
(7) NAME

(A) NAME/KEY: -  
(B) LOCATION: 1

(B) LOCATION: 1..938  
(D) OTHER INFORMATION:

(D) OTHER INFORMATION: / Ceres Seq. ID 1574898  
SEQUENCE DESCRIPTION: SEQ ID NO:2953:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2995:  
ggagtg gaggagatga gggcccgagaa aaaagtccga ac

gccaggagtc caggacatca ggccccagaa aaaagtccga acgcattctt tttttctact  
ttcttgtaac ccaagacgaa ctcggtgaac tctttctcct cgcgcasacc ggagcacaat

60  
120

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| caaggattcc | agtcaggtcc | tgccaatgga | gtgcgttttg | ggcttggttg | gccgcgactt | 180 |
| cgcggtggtg | gcggccgaca | cctccgccgt | gcagagtatc | ctcgtccaca | agactgacga | 240 |
| ggacaaagta | atggtcctcg | actcgcacaa | gctgttgggc | gcttcarggg | agcctggtga | 300 |
| ccgggtgcag | tttacggagt | tcatacagaa | gaacctccac | ctgtaccagt | tccgcaacac | 360 |
| catcccgtcg | tcaaccgccg | Ctgccgccaa | cttcacacgc | ggcgagctcg | ccacagccct | 420 |
| togtaagaat | ccatacatgg | tcaatgttat | tctcgggtgt | tacgataagg | atgttggcgc | 480 |
| ctcactgtac | tacatcgact | acattgcgac | cttgacaaag | atcgacaagg | gcgcttttgg | 540 |
| gtacggatcg | tatttctgcc | tgtctctgat | ggacaagctg | taccgcccgg | acatgaccgt | 600 |
| tgaggaascg | gtagacctcg | ttgataagtg | cattaaggag | atccggctgc | ggctggttgt | 660 |
| ggcgccccag | aacttcgtga | tcaagatcgt | cgacaaggac | ggggccaggg | agtacgcgag | 720 |
| gcgtgaactc | gtcggcgaca | gtgcacctgc | tgaagctgca | gctacggttg | ccgcctgagg | 780 |
| catgaaactt | gtttgtgtta | gttgtttgtt | tctcagcgag | gctactatgt | aatcaaattg | 840 |
| atactggtgg | gggtcccaca | gctgtttttt | aatcaatttt | agcccagaca | tgtattctgt | 900 |
| tttctgcact | aattcatgtc | ttcgccgagt | acaagttg   |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1574897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2954:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Cys | Val | Leu | Gly | Leu | Val | Gly | Arg | Asp | Phe | Ala | Val | Val | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Asp | Thr | Ser | Ala | Val | Gln | Ser | Ile | Leu | Val | His | Lys | Thr | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Asp | Lys | Val | Met | Val | Leu | Asp | Ser | His | Lys | Leu | Leu | Gly | Ala | Ser | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Pro | Gly | Asp | Arg | Val | Gln | Phe | Thr | Glu | Phe | Ile | Gln | Lys | Asn | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Leu | Tyr | Gln | Phe | Arg | Asn | Thr | Ile | Pro | Leu | Ser | Thr | Ala | Ala | Ala |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Asn | Phe | Thr | Arg | Gly | Glu | Leu | Ala | Thr | Ala | Leu | Arg | Lys | Asn | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Met | Val | Asn | Val | Ile | Leu | Gly | Gly | Tyr | Asp | Lys | Asp | Val | Gly | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Leu | Tyr | Tyr | Ile | Asp | Tyr | Ile | Ala | Thr | Leu | His | Lys | Ile | Asp | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Phe | Gly | Tyr | Gly | Ser | Tyr | Phe | Cys | Leu | Ser | Leu | Met | Asp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Tyr | Arg | Pro | Asp | Met | Thr | Val | Glu | Glu | Xaa | Val | Asp | Leu | Val | Asp |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Lys | Cys | Ile | Lys | Glu | Ile | Arg | Leu | Arg | Leu | Val | Val | Ala | Pro | Gln | Asn |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |
| Phe | Val | Ile | Lys | Ile | Val | Asp | Lys | Asp | Gly | Ala | Arg | Glu | Tyr | Ala | Arg |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Arg | Glu | Leu | Val | Gly | Asp | Ser | Ala | Pro | Ala | Glu | Ala | Ala | Ala | Thr | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Ala | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1574898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2955:

```
Met Val Leu Asp Ser His Lys Leu Leu Gly Ala Ser Xaa Glu Pro Gly
1 5 10 15
Asp Arg Val Gln Phe Thr Glu Phe Ile Gln Lys Asn Leu His Leu Tyr
 20 25 30
Gln Phe Arg Asn Thr Ile Pro Leu Ser Thr Ala Ala Ala Asn Phe
 35 40 45
Thr Arg Gly Glu Leu Ala Thr Ala Leu Arg Lys Asn Pro Tyr Met Val
 50 55 60
Asn Val Ile Leu Gly Gly Tyr Asp Lys Asp Val Gly Ala Ser Leu Tyr
65 70 75 80
Tyr Ile Asp Tyr Ile Ala Thr Leu His Lys Ile Asp Lys Gly Ala Phe
 85 90 95
Gly Tyr Gly Ser Tyr Phe Cys Leu Ser Leu Met Asp Lys Leu Tyr Arg
 100 105 110
Pro Asp Met Thr Val Glu Glu Xaa Val Asp Leu Val Asp Lys Cys Ile
 115 120 125
Lys Glu Ile Arg Leu Arg Leu Val Val Ala Pro Gln Asn Phe Val Ile
 130 135 140
Lys Ile Val Asp Lys Asp Gly Ala Arg Glu Tyr Ala Arg Arg Glu Leu
145 150 155 160
Val Gly Asp Ser Ala Pro Ala Glu Ala Ala Ala Thr Val Ala Ala
 165 170 175
```

(2) INFORMATION FOR SEQ ID NO:2956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1574899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2956:

```
Met Val Asn Val Ile Leu Gly Gly Tyr Asp Lys Asp Val Gly Ala Ser
1 5 10 15
Leu Tyr Tyr Ile Asp Tyr Ile Ala Thr Leu His Lys Ile Asp Lys Gly
 20 25 30
Ala Phe Gly Tyr Gly Ser Tyr Phe Cys Leu Ser Leu Met Asp Lys Leu
 35 40 45
Tyr Arg Pro Asp Met Thr Val Glu Glu Xaa Val Asp Leu Val Asp Lys
 50 55 60
Cys Ile Lys Glu Ile Arg Leu Arg Leu Val Val Ala Pro Gln Asn Phe
65 70 75 80
Val Ile Lys Ile Val Asp Lys Asp Gly Ala Arg Glu Tyr Ala Arg Arg
 85 90 95
Glu Leu Val Gly Asp Ser Ala Pro Ala Glu Ala Ala Ala Thr Val Ala
 100 105 110
Ala
```

(2) INFORMATION FOR SEQ ID NO:2957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..907

(D) OTHER INFORMATION: / Ceres Seq. ID 1574910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2957:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| atccatccaa | ctcttcataa  | caggcgacct | gagagcagag | cagacagaga | gcgtttctggc | 60  |
| agccgttgcg | gasttgaacc  | tctgcaacca | ccaacagcta | aactaaaagc | agcrgcggac  | 120 |
| ggcgcgcggt | actggaacgac | cggccgacga | tggctacgcc | ggcgcasagc | agggtgacca  | 180 |
| gcaccagccg | aggctgcaga  | aggatgatgg | ggctgtagac | gagagcgagt | gcagccggca  | 240 |
| cgcgctggag | tgggcgctgc  | ggaacctggc | gcccacgctg | gccccaccgc | tactggtgct  | 300 |
| caccgtgcag | ccgcacttcc  | cgtctcgata | cgtctccgcc | gcgtcCttcg | gcgcaccctt  | 360 |
| gggcaccgtc | cctccggttg  | ctccggagct | catcaggtcg | atgcaggagc | agcagagggg  | 420 |
| gCtcacgcag | gagctcctcg  | acaaggccag | ggccatctgc | gccgagcaag | gggttgctgt  | 480 |
| agaggcaatt | gtcgaggtcg  | gagatgcaaa | ggaggtgata | tgtgaagtgg | ctgagaagaa  | 540 |
| aaatgtcgat | ctgctggttc  | ttggaagcca | cagtcgtggg | ccaatacaga | ggttgttctt  | 600 |
| tgggagcgtc | agtaactact  | gtgtacatca | ttctaagtgt | ccagttcttg | tggatgaagaa | 660 |
| ccaaggctga | tgaaggattc  | aactcccagc | tgctagtcct | aatcatgttc | gggtatttgt  | 720 |
| caacgtattt | gtaatgtgta  | gtacttgctt | tagccaaacg | cattggccaa | taaagtagct  | 780 |
| tgctttgctt | cttggaagg   | ccgaggctgg | actggaggag | agttcttttt | ctttttcttt  | 840 |
| tttctggtca | gtgtgccttt  | gctccggaat | ggcagagttg | taaataagaa | ctacgaactt  | 900 |
| tgtgcgc    |             |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1574911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2958:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1574912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2959:

```
Met Gln Glu Gln Gln Arg Glu Leu Thr Gln Glu Leu Leu Asp Lys Ala
1 5 10 15
Arg Ala Ile Cys Ala Glu His Gly Val Ala Val Glu Ala Ile Val Glu
20 25 30
Val Gly Asp Ala Lys Glu Val Ile Cys Glu Val Ala Glu Lys Lys Asn
35 40 45
Val Asp Leu Leu Val Leu Gly Ser His Ser Arg Gly Pro Ile Gln Arg
50 55 60
Leu Phe Leu Gly Ser Val Ser Asn Tyr Cys Val His His Ser Lys Cys
65 70 75 80
Pro Val Leu Val Val Lys Asn Gln Gly
85
```

(2) INFORMATION FOR SEQ ID NO:2960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..846

(D) OTHER INFORMATION: / Ceres Seq. ID 1574947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2960:

```
gccatcggttc cctcctctgc acccccacac ctccgacatc ctgcctgca gcagaccctc 60
ctctggtgcg cgtgcgccac cggcgagatg tcgaagaaaa tcgtggtgaa cgtgcacctg 120
caggacaaca aggacaagca gaaggccatg aaggctgtct cggcgctcac cggcatcgac 180
gagatatccg cggacatggc gtgcacaaag atgacggttg tcggcatggt ggaccccggt 240
agcgtggtga gcaagctgcg caaggcgctg tggtcggcga ccatcgagtc cgtcggccct 300
gccaccgccg ccgcccgcgc gcgcacaaa ctgtcaccgt cgctatggcc cgtatcaagg 360
tgacagagct ccgggggaag agcaagacgg acctgcaggc gcaGctcaag gagctgaagt 420
ctgagctctc cctcctccgc gtaGccaagg tcaccggcgg cgcacccaac aagctctcca 480
agatcaagggt ggtgcgcacc tcgatcgcg cgtgtctcac agtgatctcg cagaagcaga 540
agtcggcggt gcgggaggcg tacaagaaga agaacctgct cccctcgac ctccgcccta 600
agaagaccgg tgccatccgc cgcgctctga ccaagcacca gctttctctg aagaccgaga 660
gggaaaagaa gcggtgagaag tacttcccca tgaggaagta tgctatcaag gcctaggtca 720
gaactgtgag atgctgtgct tagcatatca tcggctgtgt tttaattttt ggtttgtatg 780
gacatttggt gaagtaogat gtattcctct gtttccatat aaatggctag attggtttga 840
ctggct
```

(2) INFORMATION FOR SEQ ID NO:2961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1574948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2961:

```
Ala Ile Val Pro Ser Ser Ala Pro Pro Ile Leu Gly His Pro Arg Leu
1 5 10 15
Gln Gln Thr Leu Leu Trp Cys Ala Cys Ala Thr Gly Glu Met Ser Lys
20 25 30
Lys Ile Val Val Lys Leu His Leu Gln Asp Asn Lys Asp Lys Gln Lys
```

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(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..123
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1574950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2963:

Met Ala Arg Ile Lys Val His Glu Leu Arg Gly Lys Ser Lys Thr Asp  
1 5 10 15  
Leu Gln Ala Gln Leu Lys Glu Leu Lys Ser Glu Leu Ser Leu Leu Arg  
20 25 30  
Val Ala Lys Val Thr Gly Gly Ala Pro Asn Lys Leu Ser Lys Ile Lys  
35 40 45  
Val Val Arg Thr Ser Ile Ala Arg Val Leu Thr Val Ile Ser Gln Lys  
50 55 60  
Gln Lys Ser Ala Leu Arg Glu Ala Tyr Lys Lys Lys Asn Leu Leu Pro  
65 70 75 80  
Leu Asp Leu Arg Pro Lys Lys Thr Arg Ala Ile Arg Arg Arg Leu Thr  
85 90 95  
Lys His Gln Leu Ser Leu Lys Thr Glu Arg Glu Lys Lys Arg Glu Lys  
100 105 110  
Tyr Phe Pro Met Arg Lys Tyr Ala Ile Lys Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:2964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1052
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2964:

taagaatgat gtgatcaaatt tttgccaaga gaacaatttt cattctggtt tctttgatgg 60  
aactgaaaac aacatggttag ctgatgccta tgaattgaag gtgcgtcttg aacacatcat 120  
tgaaaggata gccttgattt ctgatgctgc aaatacagaa cgaccttctc ttgttgctcaa 180  
caacttggtc ataggtgggg ctctggctgc aaggtctaag tacaccctac agcatttggg 240  
cattacccat gtactctgtt tgtgttcaaa tgagattggt caatccgatt cccaatttcc 300  
cgatcttttt gaatacaaga acttttcaat tagcgatgat gatgatgcaa acatcagtga 360  
tctttttgag gaagcatcag acttcattga tcatgtggat catgttgggg gcaaggttct 420  
agttcattgc tttgaaggga aaagtcggag tgccacagtc gtacttgctt atcttatgct 480  
tagagagggc tttactcttg caaaagcctg gaacttactg aagaaagtac accgtcgagc 540  
gcaGccaaac gacggttcgc aaaggctctc ctggcccttg acaagaggct gcatggcaag 600  
gtatctatgg actggcaaca caagcggcc aaatgaagg tgtgtccaat ctgcagcaag 660  
aatgtttggtc taagtacgag ttactcaag ctgcacctgc agaaggcaca caagcgtcta 720  
tctgcaggca gtgtcgacag cgccatgacc atgaagatcc aaaaatcgat cgagtcactc 780  
cagatcagcc gaggaggaag cctgagcccg tcccagaagc tgaccaaggt gttcagcaat 840  
gagctgagct tctgatctgt tttcctgtac tatagatgag gcaatgtact tggctcacat 900  
tgtaataaact tgtactatca gactgaactt gtgactgtag gtttagttca cagcctata 960  
tgattagcac acgaatgttc aggtgtgaag ggtgcaacac taaagaatgt tcaggctctg 1020  
tatttggtgc ctgcagtatg cagttttctt ct

(2) INFORMATION FOR SEQ ID NO:2965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1574982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2965:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Asn | Asp | Val | Ile | Lys | Phe | Cys | Gln | Glu | Asn | Asn | Phe | His | Ser | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Phe | Asp | Gly | Thr | Glu | Asn | Asn | Met | Val | Ala | Asp | Ala | Tyr | Glu | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Val | Arg | Leu | Glu | His | Ile | Ile | Glu | Arg | Ile | Ala | Leu | Ile | Ser | Asp |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Ala | Asn | Thr | Glu | Arg | Pro | Ser | Leu | Val | Val | Asn | Asn | Leu | Phe | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Gly | Ala | Leu | Ala | Ala | Arg | Ser | Lys | Tyr | Thr | Leu | Gln | His | Leu | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Thr | His | Val | Leu | Cys | Leu | Cys | Ser | Asn | Glu | Ile | Gly | Gln | Ser | Asp |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Gln | Phe | Pro | Asp | Leu | Phe | Glu | Tyr | Lys | Asn | Phe | Ser | Ile | Ser | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Asp | Asp | Ala | Asn | Ile | Ser | Asp | Leu | Phe | Glu | Glu | Ala | Ser | Asp | Phe |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Asp | His | Val | Asp | His | Val | Gly | Gly | Lys | Val | Leu | Val | His | Cys | Phe |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Gly | Lys | Ser | Arg | Ser | Ala | Thr | Val | Val | Leu | Ala | Tyr | Leu | Met | Leu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Arg | Glu | Gly | Phe | Thr | Leu | Ala | Lys | Ala | Trp | Asn | Leu | Leu | Lys | Lys | Val |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| His | Arg | Arg | Ala | Gln | Pro | Asn | Asp | Gly | Ser | Gln | Arg | Leu | Ser | Trp | Pro |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Thr | Arg | Gly | Cys | Met | Ala | Arg | Tyr | Leu | Trp | Thr | Gly | Asn | Thr | Ser |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gly | Gln | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1574983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2966:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Ala | Asp | Ala | Tyr | Glu | Leu | Lys | Val | Arg | Leu | Glu | His | Ile | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Arg | Ile | Ala | Leu | Ile | Ser | Asp | Ala | Ala | Asn | Thr | Glu | Arg | Pro | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Val | Val | Asn | Asn | Leu | Phe | Ile | Gly | Gly | Ala | Leu | Ala | Ala | Arg | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Tyr | Thr | Leu | Gln | His | Leu | Gly | Ile | Thr | His | Val | Leu | Cys | Leu | Cys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Asn | Glu | Ile | Gly | Gln | Ser | Asp | Ser | Gln | Phe | Pro | Asp | Leu | Phe | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Tyr | Lys | Asn | Phe | Ser | Ile | Ser | Asp | Asp | Asp | Ala | Asn | Ile | Ser | Asp |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Leu | Phe | Glu | Glu | Ala | Ser | Asp | Phe | Ile | Asp | His | Val | Asp | His | Val | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Lys | Val | Leu | Val | His | Cys | Phe | Glu | Gly | Lys | Ser | Arg | Ser | Ala | Thr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Val | Leu | Ala | Tyr | Leu | Met | Leu | Arg | Glu | Gly | Phe | Thr | Leu | Ala | Lys |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |

Ala Trp Asn Leu Leu Lys Lys Val His Arg Arg Ala Gln Pro Asn Asp  
145 150 155 160  
Gly Ser Gln Arg Leu Ser Trp Pro Leu Thr Arg Gly Cys Met Ala Arg  
165 170 175  
Tyr Leu Trp Thr Gly Asn Thr Ser Gly Gln Lys  
180 185

(2) INFORMATION FOR SEQ ID NO:2967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..948
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2967:

ctycgtyccc ctctcgvt cctcgcgatc cttctttact gcccgagagt tctgactagc 60  
cacatccagt caagcagtaa aggcgcacca tggaggcggc gccggagaat aaggaggccg 120  
agcaggagga gcagcagcta ccgcacgcgc agaaggataa cgcgcccgcc gccgccgagg 180  
aagacgaagc ggattcggag gagaccgagc gccgcaaccg cgacctcaag tccggccttc 240  
accccttag gcacaaactc gtgctctggt aactcgccg gacgcctgga gcgaggctgc 300  
agtcgtacga ggacaacatc aagaagatca tcgatttcag cacagtcgaa tcgttctggg 360  
tttgctactg ccaccttgcg cgccttctt cctgcccag cccactgac cttcatctct 420  
tcaaggatgg catccgtccc ctctggGagg atcctgcaaa ccagaatggt ggcaagtgga 480  
taattagatt caaaaaggca gtttcaggct gattttggga ggatttggtg ctagtggtag 540  
taggcgacca gcttgagtat agcgatgatg tctgtggtgt tgtgcttagt gtccgtttca 600  
atgaagacat tctgagcgtc tggaaccgga acgcatcaga ccatcaggct gtgatggcat 660  
tgagggattc tatcaagagg cacctcaagc tgccgcacag ctatctgatg gagtacaaac 720  
cccatgatst tcgcggcgtg acaactcgtc ctacaggaac acatggctga gaggatagat 780  
aaacctcatg atactcgga gcttactgac gacggttctg aagcaaagag actcttttat 840  
gtaccaagaa cgcagactat tatgcaatgt agtactacta ctactactac tcaaaagccc 900  
ctacaatgtg acgcgcaaca attttactat ctaatgtgtt ttttttgc

(2) INFORMATION FOR SEQ ID NO:2968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2968:

Xaa Arg Xaa Pro Pro Xaa Leu Leu Ala Ile Leu Leu Tyr Cys Pro Arg  
1 5 10 15  
Val Leu Thr Ser His Ile Gln Ser Ser Ser Lys Gly Ala Pro Trp Arg  
20 25 30  
Arg Arg Arg Arg Ile Arg Arg Pro Ser Arg Arg Ser Ser Ser Tyr Arg  
35 40 45  
Thr Arg Arg Arg Ile Thr Arg Pro Pro Pro Pro Arg Lys Thr Lys Arg  
50 55 60  
Ile Arg Arg Arg Pro Ser Ala Ala Thr Ala Thr Ser Ser Pro Ala Phe  
65 70 75 80  
Thr Pro Leu Gly Thr Asn Ser Cys Ser Gly Thr Leu Ala Gly Arg Leu  
85 90 95  
Glu Arg Gly Arg Ser Arg Thr Arg Thr Thr Ser Arg Arg Ser Ser Ile  
100 105 110  
Ser Ala Gln Ser Asn Arg Ser Gly Phe Ala Thr Ala Thr Leu Arg Ala

(2) INFORMATION FOR SEQ ID NO:2969:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1574986

[illegible]

(2) INFORMATION FOR SEQ ID NO:2970:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 965 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..965

(D) OTHER INFORMATION: / Ceres Seq. ID 1574999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2970:

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| agaccagcaa | tcaacattca  | agccatggca  | ctgttcaagt  | gcatgtgcat | cttcttagtc  | 60  |
| tcgcttctac | tcgccctcac  | cttcaccaat  | gcccaggaag  | aatcttcaca | tcggactctc  | 120 |
| ccaccgttcc | cctgcatccc  | aggccagcca  | cggcccccgc  | ggttgccacc | ttgcccgccg  | 180 |
| gcaccaaccg | agtgtctacac | gtcgtgtgctg | ggaatgatgc  | cgtgogcgga | cttcctcacc  | 240 |
| cacaacgagg | tgccaccgat  | gccaccacg   | gtcgccctgtt | gtGgatggtc | tcagggtcact | 300 |
| cgtcaccaac | gcgtccatct  | gtctatgcc   | tatcgtcaac  | ggtaacatca | acaagctcct  | 360 |
| accggcgccc | atgatacccg  | tgcgcatggt  | ggcgctcccc  | cgtttttgtg | ttgtccgctt  | 420 |
| cccacgagcc | atacttcgcc  | ggtgtatcag  | agggcatttg  | ccaccgatga | accctccgcc  | 480 |
| tccaccagag | gcatcaccgt  | cggaaccacc  | atctacatcg  | ccagcagcat | caccatcgga  | 540 |
| atcaccacca | gcagcatcgc  | caccagaatc  | gccgtcgaca  | ccaccaccag | agtcggtcga  | 600 |
| ctacaccgcc | gacaccagca  | gcagcaccac  | cgaaatcacc  | gtctgatcca | ccaccagcta  | 660 |
| cgtcaccaga | atcatcatct  | gatccaccgt  | cgacaccagc  | agctacacca | acggcgactc  | 720 |
| catccccatc | atcttaatat  | cgaaagatat  | ttcaaaaagca | gtagtagttt | agtcaaatta  | 780 |
| gatatgcgtt | ttaggattct  | agttgatatg  | cgtccattat  | tttgttcaca | tcgaatgcag  | 840 |
| tagtgtgtta | gctatgtagt  | tgcataccta  | tcataactaa  | gtctattaga | agtatctcta  | 900 |
| ataatattta | ggatctgtca  | tcaataaaat  | gtatgcaaca  | atacgactat | tgtattattt  | 960 |
| tgtct      |             |             |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2971:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Ala | Ile | Asn | Ile | Gln | Ala | Met | Ala | Leu | Phe | Lys | Cys | Met | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Phe | Leu | Val | Ser | Leu | Leu | Leu | Ala | Leu | Thr | Phe | Thr | Asn | Ala | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Ser | Ser | His | Arg | Thr | Leu | Pro | Pro | Phe | Pro | Cys | Ile | Pro | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Pro | Arg | Pro | Pro | Arg | Leu | Pro | Pro | Cys | Pro | Pro | Ala | Pro | Thr | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Tyr | Thr | Ser | Leu | Ser | Gly | Met | Met | Pro | Cys | Ala | Asp | Phe | Leu | Thr |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Asn | Glu | Val | Pro | Pro | Met | Pro | Pro | Thr | Val | Ala | Cys | Cys | Gly | Trp |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gln | Val | Thr | Arg | His | Gln | Arg | Val | His | Leu | Ser | Met | Pro | Tyr | Arg |
|     |     |     |     |     | 100 |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2972:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Asn | Gln | His | Ser | Ser | His | Gly | Thr | Val | Gln | Val | His | Val | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Leu | Ser | Leu | Ala | Ser | Thr | Arg | Pro | His | Leu | His | Gln | Cys | Pro | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |

Arg Ile Phe Thr Ser Asp Ser Pro Thr Val Pro Leu His Pro Arg Pro  
35 40 45  
Ala Thr Ala Pro Ala Val Ala Thr Leu Pro Ala Gly Thr Asn Arg Val  
50 55 60  
Leu His Val Ala Val Gly Asn Asp Ala Val Arg Gly Leu Pro His Pro  
65 70 75 80  
Gln Arg Gly Ala Thr Asp Ala Thr His Gly Arg Leu Leu Trp Met Val  
85 90 95  
Ser Gly His Ser Ser Pro Thr Arg Pro Ser Val Tyr Ala Ile Ser Ser  
100 105 110  
Thr Val Thr Ser Thr Ser Ser Tyr Arg Arg Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:2973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2973:

Met Ala Leu Phe Lys Cys Met Cys Ile Phe Leu Val Ser Leu Leu Leu  
1 5 10 15  
Ala Leu Thr Phe Thr Asn Ala Gln Glu Glu Ser Ser His Arg Thr Leu  
20 25 30  
Pro Pro Phe Pro Cys Ile Pro Gly Gln Pro Arg Pro Pro Arg Leu Pro  
35 40 45  
Pro Cys Pro Pro Ala Pro Thr Glu Cys Tyr Thr Ser Leu Ser Gly Met  
50 55 60  
Met Pro Cys Ala Asp Phe Leu Thr His Asn Glu Val Pro Pro Met Pro  
65 70 75 80  
Pro Thr Val Ala Cys Cys Gly Trp Ser Gln Val Thr Arg His Gln Arg  
85 90 95  
Val His Leu Ser Met Pro Tyr Arg Gln Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:2974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2974:

aagaagaact cggtcggggt catcctgcc aacctggagg tgaagttcgt cgaccccgac 60  
acgggcccgt cgctgcccaa gaacacgccc ggggagatct gcgtccggag tcaggccgtg 120  
atgcaggGct actacaggaa gaaggaggag acggagcgca ccatcgatgc caaggggtgg 180  
ctccataccg gcgacgtcgg ctacatcgac gacgacggcg acgtgttcac cgtcgaccgg 240  
atcaaggagc tcatcaagta caagggttc caggtcgctc ctgccgagct ggaggccatt 300  
ctcctgtccc acccgtcggt ccaagatgcg gccgtcttcg gcctgccgga cgaggaggct 360  
ggcgagatcc cgggtgctgt cgtggtgcgg cgggtgtggc cgctcgagag cgaagCggaN 420  
catcatggcg tacgtggcgg gccgcgtggc gtcgtacaag aagctccggc tgctgcagtt 480  
cgtggacgtc atccacaagt cgggtgcagg caagatcctg cggcggcagc tccgggacga 540  
gttcgttagc aggacaaaaa cggcggcagc ctagctctag cgagagctag acagtccaat 600  
atgccagtta catacttaca ttgcacacgt acatcaaacg aataaatgtc aagctattct 660



(2) INFORMATION FOR SEQ ID NO:2975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2975:

Lys Lys Asn Ser Val Gly Phe Ile Leu Pro Asn Leu Glu Val Lys Phe  
1 5 10 15  
Val Asp Pro Asp Thr Gly Arg Ser Leu Pro Lys Asn Thr Pro Gly Glu  
20 25 30  
Ile Cys Val Arg Ser Gln Ala Val Met Gln Gly Tyr Tyr Arg Lys Lys  
35 40 45  
Glu Glu Thr Glu Arg Thr Ile Asp Ala Lys Gly Trp Leu His Thr Gly  
50 55 60  
Asp Val Gly Tyr Ile Asp Asp Gly Asp Val Phe Ile Val Asp Arg  
65 70 75 80  
Ile Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu  
85 90 95  
Leu Glu Ala Ile Leu Leu Ser His Pro Ser Val Gln Asp Ala Ala Val  
100 105 110  
Phe Gly Leu Pro Asp Glu Glu Ala Gly Glu Ile Pro Val Ser Cys Val  
115 120 125  
Val Arg Arg Cys Gly Ala Ser Glu Ser Glu Ala Xaa His His Gly Val  
130 135 140  
Arg Gly Gly Pro Arg Gly Val Val Gln Glu Ala Pro Ala Ala Ala Val  
145 150 155 160  
Arg Gly Arg His Pro Gln Val Gly Val Arg Gln Asp Pro Ala Ala Ala  
165 170 175  
Ala Pro Gly Arg Val Arg  
180

(2) INFORMATION FOR SEQ ID NO:2976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2976:

Glu Glu Leu Gly Arg Val His Pro Ala Gln Pro Gly Gly Glu Val Arg  
1 5 10 15  
Arg Pro Arg His Gly Pro Val Ala Ala Gln Glu His Ala Arg Gly Asp  
20 25 30  
Leu Arg Pro Glu Ser Gly Arg Asp Ala Gly Leu Leu Gln Glu Glu Gly  
35 40 45  
Gly Asp Gly Ala His His Arg Cys Gln Gly Val Ala Pro Tyr Arg Arg  
50 55 60  
Arg Arg Leu His Arg Arg Arg Arg Arg Val His Arg Arg Pro Asp  
65 70 75 80  
Gln Gly Ala His Gln Val Gln Gly Leu Pro Gly Arg Ser Cys Arg Ala  
85 90 95

Gly Gly His Ser Pro Val Pro Pro Val Gly Pro Arg Cys Gly Arg Leu  
100 105 110  
Arg Pro Ala Gly Arg Gly Gly Trp Arg Asp Pro Gly Val Val Arg Gly  
115 120 125  
Ala Ala Val Trp Arg Val Gly Glu Arg Ser Gly Xaa Ser Trp Arg Thr  
130 135 140  
Trp Arg Ala Ala Trp Arg Arg Thr Arg Ser Ser Gly Cys Cys Ser Ser  
145 150 155 160  
Trp Thr Ser Ser Thr Ser Arg Cys Gln Ala Arg Ser Cys Gly Gly Ser  
165 170 175  
Ser Gly Thr Ser Ser Leu Ala Gly Pro Lys Arg Arg Gln Pro Ser Ser  
180 185 190  
Ser Glu Ser  
195

(2) INFORMATION FOR SEQ ID NO:2977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2977:

Met Gln Gly Tyr Tyr Arg Lys Lys Glu Glu Thr Glu Arg Thr Ile Asp  
1 5 10 15  
Ala Lys Gly Trp Leu His Thr Gly Asp Val Gly Tyr Ile Asp Asp  
20 25 30  
Gly Asp Val Phe Ile Val Asp Arg Ile Lys Glu Leu Ile Lys Tyr Lys  
35 40 45  
Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Ile Leu Leu Ser His  
50 55 60  
Pro Ser Val Gln Asp Ala Ala Val Phe Gly Leu Pro Asp Glu Glu Ala  
65 70 75 80  
Gly Glu Ile Pro Val Ser Cys Val Val Arg Arg Cys Gly Ala Ser Glu  
85 90 95  
Ser Glu Ala Xaa His His Gly Val Arg Gly Gly Pro Arg Gly Val Val  
100 105 110  
Gln Glu Ala Pro Ala Ala Ala Val Arg Gly Arg His Pro Gln Val Gly  
115 120 125  
Val Arg Gln Asp Pro Ala Ala Ala Ala Pro Gly Arg Val Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2978:

gactccacgc cgccagtcac gaccacgccg cgcctccgcc tggaaccctt tagccgagcg 60  
gagCaaggga agaaatgggg aagggtacgg gcagcttcgg caagcgccgg aacaagacgc 120  
acacgctctg catccgctgc ggccgcgcga gcttcacct ccagaagagc acctgctcct 180  
cctgcggtta ccccgccgcc cgcatacgca agtataactg gagtgtgaaa gccatcaggc 240  
gtaagacaac tggtagcgga aggatgaggt acatgcgaca cgttcctcgc cgttttcaaga 300

gcaacttcag agaagggact gaggtgccc caaagaaggg tgttgctgct gccaaactaag 360  
tgtggtcttg ctgccatcaa gaagtgctag aacttgagac tttttgattg aattgtactt 420  
ctgaactctt tagcccataa tactatgctt gaattaattt cagacgccct ggagaggtat 480  
gatatgt

(2) INFORMATION FOR SEQ ID NO:2979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2979:

Asp Ser Thr Pro Pro Val Thr Thr Thr Pro Arg Leu Arg Leu Glu Pro  
1 5 10 15  
Phe Ser Arg Ala Glu Gln Gly Lys Lys Trp Gly Arg Val Arg Ala Ala  
20 25 30  
Ser Ala Ser Ala Gly Thr Arg Arg Thr Arg Ser Ala Ser Ala Ala Ala  
35 40 45  
Ala Ala Ala Ser Thr Ser Arg Arg Ala Pro Ala Pro Pro Ala Ala Thr  
50 55 60  
Pro Pro Pro Ala Ser Ala Ser Ile Thr Gly Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2980:

Thr Pro Arg Arg Gln Ser Arg Pro Arg Ala Ser Ala Trp Asn Pro  
1 5 10 15  
Leu Ala Glu Arg Ser Lys Gly Arg Asn Gly Glu Gly Tyr Gly Gln Leu  
20 25 30  
Arg Gln Ala Pro Glu Gln Asp Ala His Ala Leu His Pro Leu Arg Pro  
35 40 45  
Pro Gln Leu Pro Pro Pro Glu His Leu Leu Leu Arg Leu Pro  
50 55 60  
Arg Arg Pro His Pro Gln Val  
65 70

(2) INFORMATION FOR SEQ ID NO:2981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2981:

Met Gly Lys Gly Thr Gly Ser Phe Gly Lys Arg Arg Asn Lys Thr His

U.S. PAT. & TM. OFF.

```

1 5 10 15
Thr Leu Cys Ile Arg Cys Gly Arg Arg Ser Phe His Leu Gln Lys Ser
 20 25 30
Thr Cys Ser Ser Cys Gly Tyr Pro Ala Ala Arg Ile Arg Lys Tyr Asn
 35 40 45
Trp Ser Val Lys Ala Ile Arg Arg Lys Thr Thr Gly Thr Gly Arg Met
 50 55 60
Arg Tyr Met Arg His Val Pro Arg Arg Phe Lys Ser Asn Phe Arg Glu
 65 70 75 80
Gly Thr Glu Ala Ala Pro Lys Lys Gly Val Ala Ala Ala Asn
 85 90
```

(2) INFORMATION FOR SEQ ID NO:2982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..670
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2982:

```

gagcctcgaa ccctaaccac caccacgtaa ctcttggaa ttaccgaaat gccactcttc 60
ttctccaaat tcgcaccatt ggtcccccgc gtcgcgcgcc tttccatcgc cgcggcgaca 120
gccggcgang sgaccctaag ctgtctcgaa tcgcggatga gtcctcgcgc ctatcccccgc 180
ccgagctgga cgactatgcg gcgctcctgc gCctcaagct ccgcctgtcg ctcacctcca 240
gcgcagbcnt Tggagcctct ccggccggggg ccgggggacgc cgcggctgca gccgtggagg 300
Ccgcgcgggc kgtgaagacg gcgttcgact tgaagatcga gaagtacgag gccgcggcga 360
agattaagat catcaaggag gtgcgcgcga tgacggacct gggctctgaag gaggcaaagg 420
agctcgtgga gaaggcgccc atagtgggtc gcgcgggggt gcctaaagag gaggccgagg 480
cgctcgccgc taagctcaag gccgcgggtg ccgctgttgc actcgagtga tcccacgaag 540
gtgtcgcttc tttttttttt gttcctagtg ttcttagacg atgcaacgta tctttgcgcc 600
ttaatttggt tgtaatggaa ttcaatagat tggatatggg tataaagagg atgcaacgct 660
taagaacact
```

(2) INFORMATION FOR SEQ ID NO:2983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2983:

```

Ala Ser Asn Pro Asn Pro His His Val Thr Pro Trp Asn Tyr Arg Asn
1 5 10 15
Ala Thr Leu Leu Leu Gln Ile Arg Thr Ile Gly Pro Pro Arg Pro Pro
 20 25 30
Pro Phe His Arg Arg Gly Asp Ser Arg Arg Xaa Asp Pro Lys Leu Ser
 35 40 45
Arg Ile Ala Asp Glu Leu Leu Ala Leu Ser Pro Ala Glu Leu Asp Asp
 50 55 60
Tyr Ala Ala Leu Leu Arg Leu Lys Leu Arg Leu Ser Leu Thr Ser Ser
 65 70 75 80
Ala Xaa Xaa Gly Ala Ser Pro Ala Gly Ala Gly Asp Ala Ala Ala Ala
 85 90 95
Ala Val Glu Ala Ala Ala Xaa Val Lys Thr Ala Phe Asp Leu Lys Ile
 100 105 110
```

Glu Lys Tyr Glu Ala Ala Ala Lys Ile Lys Ile Ile Lys Glu Val Arg  
115 120 125  
Ala Met Thr Asp Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys  
130 135 140  
Ala Pro Ile Val Val Arg Ala Gly Leu Pro Lys Glu Glu Ala Glu Ala  
145 150 155 160  
Leu Ala Ala Lys Leu Lys Ala Ala Gly Ala Ala Val Ala Leu Glu  
165 170 175

(2) INFORMATION FOR SEQ ID NO:2984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1575019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2984:

Met Pro Leu Phe Phe Ser Lys Phe Ala Pro Leu Val Pro Arg Val Arg  
1 5 10 15  
Arg Leu Ser Ile Ala Ala Ala Thr Ala Gly Xaa Xaa Thr Leu Ser Cys  
20 25 30  
Leu Glu Ser Arg Met Ser Ser Ser Pro Tyr Pro Pro Pro Ser Trp Thr  
35 40 45  
Thr Met Arg Arg Ser Cys Ala Ser Ser Ser Ala Cys Arg Ser Pro Pro  
50 55 60  
Ala Gln Xaa Leu Glu Pro Leu Arg Pro Gly Pro Gly Thr Pro Arg Leu  
65 70 75 80  
Gln Pro Trp Arg Pro Pro Arg Xaa  
85

(2) INFORMATION FOR SEQ ID NO:2985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1109

(D) OTHER INFORMATION: / Ceres Seq. ID 1575027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2985:

gttcggttcc ttctcgtaacc gagcgcgagg tagccagcca accgccgacg cakycacaag 60  
cgatgaagcg cttcttccag ccagtgcaca aggacggctc cccgtccaag aagcggctag 120  
cggngtgctg ctgaaccggg cgacggcccc acatcagccg gtgccgccac cgGCgcctgg 180  
cggggatgta gaggggaggg ccaccgagga gccgttcaag ttcttgacgt ggaacgcca 240  
cagcctgctc ctccggatga agagcgactg gctgtcttc tcgcagctcg tcgccgcct 300  
tgaccccgac gtcatcttggt tccaggaagt gcggatgcgg gcagctgggt ccaaaggggc 360  
acctaaaaac cccagtgaac taaaagatga cacaagcttg tcacgggatg aaaagcaggt 420  
agttctacgt gctttgtcag cttcaccttt caaagactac cgtgtctggt ggtctctttc 480  
agattcaaaa tatgctggga castatgttt ataaagaaaa agtttgagcc taagaaggtg 540  
tctttcaact tggatagaac atcttotaag catgaagccg atgggcgtgt tataattgcg 600  
gaatttgaat cattcctttt tactgaacac ttattctcca aacaatggat ggaaggagga 660  
ggaaaatgca tttcaaagaa gacgtaagtg ggacaagagg atgctagaat ttgttcaaca 720  
cgtggataaa cccttaatct ggtgtgggga cttgaatgtc agtcatgaag aaatcgacgt 780  
cagccatcct gatttcttta gcagcgctaa gctgaatgga tacacccac ccaataaaga 840  
ggactgtgga cagccaggat tcaccccgag agagagacgg cgttttgga acatattatt 900  
ccaaggaaa ctggttagat cttacaggca cctgcacaaa gaaaaggaca tagacgggtg 960  
cttctcttgg tccggtcatc caattggcaa gtaccgagga aagagaatga ggatcgacta 1020

cttccttgtt tcggaacagt taaaggacag aatagtttca tgtgaaatgc atggccgtgg 1080  
cattgaattg gatggatttt atggaagtg

(2) INFORMATION FOR SEQ ID NO:2986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1575028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2986:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Gly | Ser | Phe | Ser | Tyr | Arg | Ala | Ala | Gly | Ser | Gln | Pro | Thr | Ala | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Xaa | Thr | Ser | Asp | Glu | Ala | Leu | Leu | Pro | Ala | Ser | Ala | Gln | Gly | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Pro | Val | Gln | Glu | Ala | Ala | Ser | Xaa | Val | Leu | Leu | Asn | Arg | Ala | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Pro | His | Gln | Pro | Val | Pro | Pro | Pro | Ala | Pro | Gly | Gly | Asp | Val | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Arg | Pro | Thr | Glu | Glu | Pro | Phe | Lys | Phe | Leu | Thr | Trp | Asn | Ala | Asn |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Leu | Leu | Leu | Arg | Met | Lys | Ser | Asp | Trp | Pro | Ala | Phe | Ser | Gln | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ala | Arg | Leu | Asp | Pro | Asp | Val | Ile | Cys | Val | Gln | Glu | Val | Arg | Met |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Ala | Ala | Gly | Ser | Lys | Gly | Ala | Pro | Lys | Asn | Pro | Ser | Glu | Leu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Asp | Asp | Thr | Ser | Leu | Ser | Arg | Asp | Glu | Lys | Gln | Val | Val | Leu | Arg | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Ala | Ser | Pro | Phe | Lys | Asp | Tyr | Arg | Val | Trp | Trp | Ser | Leu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ser | Lys | Tyr | Ala | Gly | Thr | Xaa | Cys | Leu |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1575029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2987:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Asp | Trp | Pro | Ala | Phe | Ser | Gln | Leu | Val | Ala | Arg | Leu | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Asp | Val | Ile | Cys | Val | Gln | Glu | Val | Arg | Met | Pro | Ala | Ala | Gly | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Lys | Gly | Ala | Pro | Lys | Asn | Pro | Ser | Glu | Leu | Lys | Asp | Asp | Thr | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ser | Arg | Asp | Glu | Lys | Gln | Val | Val | Leu | Arg | Ala | Leu | Ser | Ala | Ser | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Lys | Asp | Tyr | Arg | Val | Trp | Trp | Ser | Leu | Ser | Asp | Ser | Lys | Tyr | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Thr | Xaa | Cys | Leu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2988:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Phe | Val | Gln | His | Val | Asp | Lys | Pro | Leu | Ile | Trp | Cys | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Asn | Val | Ser | His | Glu | Glu | Ile | Asp | Val | Ser | His | Pro | Asp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ser | Ser | Ala | Lys | Leu | Asn | Gly | Tyr | Thr | Pro | Pro | Asn | Lys | Glu | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Gly | Gln | Pro | Gly | Phe | Thr | Pro | Ala | Glu | Arg | Arg | Arg | Phe | Gly | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Phe | Gln | Gly | Lys | Leu | Val | Asp | Ala | Tyr | Arg | His | Leu | His | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Lys | Asp | Ile | Asp | Gly | Gly | Phe | Ser | Trp | Ser | Gly | His | Pro | Ile | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Tyr | Arg | Gly | Lys | Arg | Met | Arg | Ile | Asp | Tyr | Phe | Leu | Val | Ser | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Leu | Lys | Asp | Arg | Ile | Val | Ser | Cys | Glu | Met | His | Gly | Arg | Gly | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Leu | Asp | Gly | Phe | Tyr | Gly | Ser |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1575038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2989:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atctctcact  | caaccgcgcg | cgaagCacac | gagatagagc | tgctagaggc | tagagcagta | 60  |
| gagctagaag  | aggaggacaa | caaccatgga | tgcggcggcg | gcggcgggcg | cgaggggaga | 120 |
| tacgaagaag  | aagaagatgc | ttgccaccct | ggtgggctgc | aactacgccg | gcacgccgta | 180 |
| cgagctgcag  | ggtgcctca  | acgacgtcca | cgccatgcgc | gccgtcctcc | tcgcccgctt | 240 |
| cggCtttcgcg | cctgccgaag | tcaccgtgct | caccgacgac | cagcacgggc | gcggcgggcg | 300 |
| cgcgcgctg   | ctcccg     |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1575039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2990:

Ile Ser His Ser Thr Ala Arg Glu Ala His Glu Ile Glu Leu Leu Glu  
1 5 10 15

Ala Arg Ala Val Glu Leu Glu Glu Glu Asp Asn Asn His Gly Cys Gly  
20 25 30  
Gly Gly Gly Gly Glu Gly Arg Tyr Glu Glu Glu Glu Asp Ala Cys  
35 40 45  
His Pro Gly Gly Leu Gln Leu Arg Arg His Ala Val Arg Ala Ala Gly  
50 55 60  
Leu His Gln Arg Arg Pro Arg His Ala Arg Arg Pro Pro Arg Pro Leu  
65 70 75 80  
Arg Leu Arg Ala Cys Arg Arg His Arg Ala His Arg Arg Pro Ala Arg  
85 90 95  
Ala Arg Arg Arg Arg Arg Ala Pro  
100 105

(2) INFORMATION FOR SEQ ID NO:2991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2991:

Met Asp Ala Ala Ala Ala Ala Ala Arg Gly Asp Thr Lys Lys Lys  
1 5 10 15  
Lys Met Leu Ala Thr Leu Val Gly Cys Asn Tyr Ala Gly Thr Pro Tyr  
20 25 30  
Glu Leu Gln Gly Cys Ile Asn Asp Val His Ala Met Arg Ala Val Leu  
35 40 45  
Leu Ala Arg Phe Gly Phe Ala Pro Ala Asp Val Thr Val Leu Thr Asp  
50 55 60  
Asp Gln His Gly Arg Gly Gly Gly Gly Gly Val Leu Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2992:

Met Arg Arg Arg Arg Arg Arg Gly Glu Ile Arg Arg Arg Arg  
1 5 10 15  
Cys Leu Pro Pro Trp Trp Ala Ala Thr Thr Pro Ala Arg Arg Thr Ser  
20 25 30  
Cys Arg Ala Ala Ser Thr Thr Ser Thr Pro Cys Ala Pro Ser Ser Ser  
35 40 45  
Pro Ala Ser Ala Ser Arg Leu Pro Thr Ser Pro Cys Ser Pro Thr Thr  
50 55 60  
Ser Thr Gly Ala Ala Ala Ala Ala Cys Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..928  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2993:

```
agggccttgc attttttcct ccgcttttgc ttccccgatt acgttccctc gctactcgct 60
agtcgccact tctcccgttg cccccccgcg tctctcttct cgttgcgacg actgggcgat 120
ccctgccgcc ccccgctctc cgctccccgc cgccaggtgc ccagggtgtc gccggggcct 180
tcgccggcga tgagcaccca acaggaggtt actgagaact acgcaaatcc taagacatgc 240
ttcttccatg ttctcttcaa ggcacgcgca ttggcgcttc acatactgtc cacactgttc 300
gtgaacaact tcgtcatcat ctttgtcatc actgtgctcc tcgcagcact tgacttctgg 360
gtcgtgaaga atgtcagcgg aaggatactg gttgggctgc ggtggtggaa tgagattaac 420
gatgagggag agagtgtctg gaagtttgag tgccttgatg gagagtcccC tggctaggat 480
gaataagaag gactcatggc tgttctgggt gactctatat ttgactgcgg ctgcatggat 540
tatacttggg atattctcgc tcatcagact tcaagctgat taccttctcg ttgttggagt 600
ttgcttgagc ctcagcattg caaatatwat kgsrtwcwcs rwwtgawtm wagatkcsaa 660
gaagaacatc caggattgga caaggaatgc acttctatca ggtagtgtca gatcgcatct 720
gcagtcagca tttgggtgtc gaacaataac ctatgacctt gttatacgtg tagtgctgta 780
taatttacag ataacatgat tggttactag agtgcgctcg tttttttttt tgttggctat 840
gtgcatcttg ctaggcagag tcggaagaac attttcagag ccgtgtatca actcgatgta 900
taatgcagtt tgaataaaat cttccttt
```

(2) INFORMATION FOR SEQ ID NO:2994:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 158 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..158  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2994:

```
Arg Ala Leu His Phe Phe Leu Arg Phe Ala Phe Pro Asp Tyr Val Pro
1 5 10 15
Ser Leu Leu Ala Ser Arg His Phe Ser Arg Cys Pro Pro Ala Ser Leu
20 25 30
Phe Ser Leu Arg Arg Leu Gly Asp Pro Cys Arg Pro Pro Ser Pro Ala
35 40 45
Pro Arg Arg Gln Val Pro Arg Leu Ser Pro Gly Pro Ser Pro Ala Met
50 55 60
Ser Thr Gln Gln Glu Val Thr Glu Asn Tyr Ala Asn Pro Lys Thr Cys
65 70 75 80
Phe Phe His Val Leu Phe Lys Ala Ser Ala Leu Ala Phe Tyr Ile Leu
85 90 95
Ser Thr Leu Phe Val Asn Asn Phe Val Ile Ile Phe Val Ile Thr Val
100 105 110
Leu Leu Ala Ala Leu Asp Phe Trp Val Val Lys Asn Val Ser Gly Arg
115 120 125
Ile Leu Val Gly Leu Arg Trp Trp Asn Glu Ile Asn Asp Glu Gly Glu
130 135 140
Ser Val Trp Lys Phe Glu Cys Leu Asp Gly Glu Ser Pro Gly
145 150 155
```

(2) INFORMATION FOR SEQ ID NO:2995:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 123 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1575058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2995:

Met Ser Ala Glu Gly Tyr Trp Leu Gly Cys Gly Gly Gly Met Arg Leu  
1 5 10 15  
Thr Met Arg Glu Arg Val Ser Gly Ser Leu Ser Ala Leu Met Glu Ser  
20 25 30  
Pro Leu Ala Arg Met Asn Lys Lys Asp Ser Trp Leu Phe Trp Trp Thr  
35 40 45  
Leu Tyr Leu Thr Ala Ala Ala Trp Ile Ile Leu Gly Ile Phe Ser Leu  
50 55 60  
Ile Arg Leu Gln Ala Asp Tyr Leu Leu Val Val Gly Val Cys Leu Ser  
65 70 75 80  
Leu Ser Ile Ala Asn Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Asp Xaa  
85 90 95  
Lys Lys Asn Ile Gln Asp Trp Thr Arg Asn Ala Leu Leu Ser Gly Ser  
100 105 110  
Val Arg Ser His Leu Gln Ser Ala Phe Gly Val  
115 120

(2) INFORMATION FOR SEQ ID NO:2996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1575059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2996:

Met Arg Leu Thr Met Arg Glu Arg Val Ser Gly Ser Leu Ser Ala Leu  
1 5 10 15  
Met Glu Ser Pro Leu Ala Arg Met Asn Lys Lys Asp Ser Trp Leu Phe  
20 25 30  
Trp Trp Thr Leu Tyr Leu Thr Ala Ala Trp Ile Ile Leu Gly Ile  
35 40 45  
Phe Ser Leu Ile Arg Leu Gln Ala Asp Tyr Leu Leu Val Val Gly Val  
50 55 60  
Cys Leu Ser Leu Ser Ile Ala Asn Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa  
65 70 75 80  
Xaa Asp Xaa Lys Lys Asn Ile Gln Asp Trp Thr Arg Asn Ala Leu Leu  
85 90 95  
Ser Gly Ser Val Arg Ser His Leu Gln Ser Ala Phe Gly Val  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2997:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 887 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..887

(D) OTHER INFORMATION: / Ceres Seq. ID 1575067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2997:

ataaataact tatgaggcca aactaaagar ggcagggcag gcgaatcgaa ggaaaagtag

tcaggagagg cgtttccctc gcaatcgacc atcacagatc aaatcgctgc aactagctag 120  
ggtttcgctc cctcatctct cgtcgatcca tcgatggcgt ccgagggcga aaacaagagg 180  
atgatcacgc tcaggagctc cgacttagag gagttcgagg tggaggaagc ggtggccatg 240  
gagtcgcaga ctctccgcca catgatcgag gacgactgcd ccgacaacgg catcccgtc 300  
cccaacgtca actccaggat cctctctaag gtcacgaGg tactgcaaca gtcacgtcca 360  
cgccgccgcc aaacccgctg actccgctgc ctccgagggc ggcgaggacc tcaagagctg 420  
ggacgcgaag ttcgtcaagg tggaccaGgc tacgtctctc gacctcatcc tggctgccaa 480  
ctatctgaac atcaagggat tgctggacct gacctgccag acggttgctg acatgatcaa 540  
gggcaagact ccggaggaga tccgcaagac attcagcatc aagaacgact tcacccaaga 600  
ggaggaggat gagatccgca tggagaacca gtgggccttc gagtgattgt tgtcttcctt 660  
tccctggtag tgggtggtgt tcttttacia gaacagatgg atgtctgcac tgcactctac 720  
aatgctagtc tatctactta cgaaatagta gtgaaatagt agtataatgg tcgtgatggg 780  
tgtatccttt tttggattga atgtatgtca agctgggtgg tgctagtctg tctgtctgga 840  
cttgttacta gttaatatct cataatacat atataaaagt ggatctt

(2) INFORMATION FOR SEQ ID NO:2998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2998:

Met Ala Ser Glu Gly Glu Asn Lys Arg Met Ile Thr Leu Arg Ser Ser  
1 5 10 15  
Asp Leu Glu Glu Phe Glu Val Glu Glu Ala Val Ala Met Glu Ser Gln  
20 25 30  
Thr Leu Arg His Met Ile Glu Asp Asp Cys Xaa Asp Asn Gly Ile Pro  
35 40 45  
Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val Ile Glu Val Leu  
50 55 60  
Gln Gln Ser Arg Pro Arg Arg Arg Gln Thr Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2999:

Met Ile Thr Leu Arg Ser Ser Asp Leu Glu Glu Phe Glu Val Glu Glu  
1 5 10 15  
Ala Val Ala Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp  
20 25 30  
Cys Xaa Asp Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu  
35 40 45  
Ser Lys Val Ile Glu Val Leu Gln Gln Ser Arg Pro Arg Arg Arg Gln  
50 55 60  
Thr Arg  
65

(2) INFORMATION FOR SEQ ID NO:3000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..47  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575070  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3000:

Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp Cys Xaa Asp  
1 5 10 15  
Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val  
20 25 30  
Ile Glu Val Leu Gln Gln Ser Arg Pro Arg Arg Arg Gln Thr Arg  
35 40 45

(2) INFORMATION FOR SEQ ID NO:3001:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 723 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..723  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575105  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3001:

gcggtttgcm ggcactvrca ggargagaga ccganarcrc gggcgcaggar gcgtcgagca 60  
gcgavgwgn ghrccggcgg cggcgagctg gacggaggag gggaccacaa gaagcggcgg 120  
ctgaccgacg agcaggtaga gatgctggar ctgagcttcc gggaggagcg gaagctggag 180  
accggccgga aggtgcacct ggccgcccag ctggggctcg accccaagca ggtcgccgctc 240  
tggtttccaga accgcccgcg ccgccacaag agcaagctgc tcgaggagga gttcgccaag 300  
ctcaagcagg cacacgacgc cgccatcctc cacaaatgcc accttgagaa cgaggtgatg 360  
agRgctgaag gacaagctgg tgctgcgccg ggaggaGGct gacgcgtttc agatccgcgg 420  
gcaaccacgc ggtctccggt gacggcggag acgtcatggc ccgtgccgctc tgcagcggga 480  
gcccagactc atcgttctcg actggcacct gccagcagcc cggaggaggc ggccggcggcg 540  
gcgatcacct gggggacgac gacctgctct atgttctctga ctatgcctac gctgacagca 600  
gcgtggctga gtggtttagc ctgtatggac tgatgtaatc gatggtatgg tatgccatcg 660  
tcgtcggcag attaattcta gctagctact catcgtagcg tgtcattgct gtgstgaatt 720  
gct

(2) INFORMATION FOR SEQ ID NO:3002:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..133  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575106  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3002:

Ala Val Cys Xaa His Xaa Gln Xaa Glu Arg Pro Xaa Xaa Arg Arg Arg  
1 5 10 15  
Xaa Arg Arg Ala Ala Xaa Xaa Xaa Xaa Gly Gly Gly Glu Leu Asp Gly  
20 25 30  
Gly Gly Asp His Lys Lys Arg Arg Leu Thr Asp Glu Gln Val Glu Met  
35 40 45  
Leu Xaa Leu Ser Phe Arg Glu Glu Arg Lys Leu Glu Thr Gly Arg Lys  
50 55 60  
Val His Leu Ala Ala Glu Leu Gly Leu Asp Pro Lys Gln Val Ala Val

(2) INFORMATION FOR SEQ ID NO:3003:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1575107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3003:

(2) INFORMATION FOR SEQ ID NO:3004:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1575108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3004:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3005:

(2) INFORMATION FOR SEQ ID NO:3006:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3006:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3007:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1575126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3007:

Met Pro Pro Pro Gln Ser Gly Met Thr Leu Cys Arg Leu Pro Lys Ala  
1 5 10 15  
Thr Leu Gly Leu Pro Leu Ser Leu Pro Ser Leu Leu Tyr Arg Pro Ser  
20 25 30  
Leu Ser Leu Ala Ala Arg Arg Thr Lys Ala Val Ser Ala Arg Ala Ser  
35 40 45  
Ser Ser Ser Pro Ser Pro Asp Ser Ser Phe Gly Ser Arg Met Glu Asp  
50 55 60  
Ser Val Lys Lys Thr Val Ala Asp Asn Pro Val Val Ile Tyr Ser Lys  
65 70 75 80  
Ser Trp Cys Ser Tyr Ser Met Glu Val Lys Ser Leu Phe Lys Arg Ile  
85 90 95  
Gly Val Gln Pro His Val Ile Glu Leu Asp Asn Leu Gly Ala Gln Gly  
100 105 110  
Pro Gln Leu Gln Lys Val Leu Glu Arg Leu Thr Gly Gln Ser Thr Val  
115 120 125  
Pro Asn Val Phe Ile Gly Gly Lys His Val Gly Arg Cys Thr Asp Thr  
130 135 140  
Val Lys Ala Val Ser Gln Gly Gly Ala Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:3008:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1575127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3008:

Met Thr Leu Cys Arg Leu Pro Lys Ala Thr Leu Gly Leu Pro Leu Ser  
1 5 10 15  
Leu Pro Ser Leu Leu Tyr Arg Pro Ser Leu Ser Leu Ala Ala Arg Arg  
20 25 30  
Thr Lys Ala Val Ser Ala Arg Ala Ser Ser Ser Ser Pro Ser Pro Asp  
35 40 45  
Ser Ser Phe Gly Ser Arg Met Glu Asp Ser Val Lys Lys Thr Val Ala  
50 55 60  
Asp Asn Pro Val Val Ile Tyr Ser Lys Ser Trp Cys Ser Tyr Ser Met  
65 70 75 80  
Glu Val Lys Ser Leu Phe Lys Arg Ile Gly Val Gln Pro His Val Ile  
85 90 95  
Glu Leu Asp Asn Leu Gly Ala Gln Gly Pro Gln Leu Gln Lys Val Leu  
100 105 110  
Glu Arg Leu Thr Gly Gln Ser Thr Val Pro Asn Val Phe Ile Gly Gly  
115 120 125  
Lys His Val Gly Arg Cys Thr Asp Thr Val Lys Ala Val Ser Gln Gly

140

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Glu | Gln | Glu | Leu | Asp | Leu | Glu | Leu | Thr | Leu | Leu | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Trp | Ala | Thr | Gln | Glu | Glu | Ala | Pro | Gly | Phe | Phe | Leu | Cys | Thr | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Gly | Arg | Lys | Phe | Cys | Thr | Ser | Gln | Ala | Leu | Gly | Gly | His | Gln | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | His | Lys | Tyr | Glu | Arg | Ala | Leu | Ala | Lys | Arg | Arg | Arg | Asp | Ile | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Leu | Arg | Lys | His | Gly | Val | Pro | Val | Thr | Arg | Ala | Gly | Gln | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Ala | Gly | Ala | Ser | Pro | Ser | Ala | Arg | Ala | Thr | Ala | Gly | Val | Ala | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Glu | Arg | Pro | Asp | Ala | Gly | Arg | Glu | Arg | Pro | Val | Ala | Val | Asp | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gln | Gly | Ala | Pro | Ala | Pro | Trp | Gln | Ser | Gly | Gly | Pro | Ala | Pro | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Ala | His | Arg | Gly | Ala | Gly | Phe | Val | Pro | Arg | Pro | Val | Ile | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ala | Phe | Ser | Arg | Ser | Met | Tyr | His | Phe | His | Leu | Leu | Gly | Phe | Ala | Tyr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Asn | Cys | Tyr | Ile | His | Ala | Cys | Ile | Tyr | Asn | Val | Ile | Ala | Phe | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |



Pro Gln Arg Pro Glu Arg Leu  
180

(2) INFORMATION FOR SEQ ID NO:3011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..788
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3011:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atctccgaaa  | aaaaaacgcg  | aacgcagaac | gccgccggcc | cgctcgtcac | tcgtgtttcc  | 60  |
| cttctctccac | ttgccttcgt  | gttcgtgatt | cgtgatttcg | ccgccggaaa | gccgagggag  | 120 |
| agggagcgcg  | atgggggttcg | tccgagacac | gatggagtcg | atccgctcca | tgcagatCcg  | 180 |
| ccaagtgtct  | atgcagatca  | tcagcctcgg | tatgattgtt | acctctgcat | taatcatatg  | 240 |
| gaagggtttg  | atagttttca  | cggggagcga | gtcaccagtt | gtagtgggtc | tctcgggtag  | 300 |
| catggagcct  | ggatttaaaa  | ggggtgatat | cctgtttttg | catatgagca | aagatcctat  | 360 |
| tcgcacagga  | gaaatagttg  | ttttcaatat | cgatggtcgt | gagattccaa | ttgtccaccg  | 420 |
| agtgattaag  | gtccatgaac  | gtcaggacac | tgcagaagtg | gacatcctca | ccaaagggtga | 480 |
| caataatttt  | ggggatgacc  | gactattata | tgcacatggc | cagctttggc | tccagcaaca  | 540 |
| ccacattatg  | gggcgtgcgg  | tgggctacct | tccatattgt | ggctgggtta | caattatcat  | 600 |
| gactgagaaa  | ccatttatta  | agtacctgct | gattggcgca | ctgggcttgc | tggtcataac  | 660 |
| gtcgaaagat  | tagtgatgtc  | aaacttcagg | gccatgtaga | ttttgctctt | atggcgcaac  | 720 |
| agcagagatc  | actggctttg  | tggcgtttga | gagatgccgc | tatgttgccg | catgtatcaa  | 780 |

acgagrag

(2) INFORMATION FOR SEQ ID NO:3012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3012:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Val | Gly | Asp | Thr | Met | Glu | Ser | Ile | Arg | Ser | Met | Gln | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Gln | Val | Leu | Met | Gln | Ile | Ile | Ser | Leu | Gly | Met | Ile | Val | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ile | Ile | Trp | Lys | Gly | Leu | Ile | Val | Phe | Thr | Gly | Ser | Glu | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Val | Val | Val | Val | Leu | Ser | Gly | Ser | Met | Glu | Pro | Gly | Phe | Lys | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Gly | Asp | Ile | Leu | Phe | Leu | His | Met | Ser | Lys | Asp | Pro | Ile | Arg | Thr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ile | Val | Val | Phe | Asn | Ile | Asp | Gly | Arg | Glu | Ile | Pro | Ile | Val | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Val | Ile | Lys | Val | His | Glu | Arg | Gln | Asp | Thr | Ala | Glu | Val | Asp | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Lys | Gly | Asp | Asn | Asn | Phe | Gly | Asp | Asp | Arg | Leu | Leu | Tyr | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Gly | Gln | Leu | Trp | Leu | Gln | Gln | His | His | Ile | Met | Gly | Arg | Ala | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gly | Tyr | Leu | Pro | Tyr | Val | Gly | Trp | Val | Thr | Ile | Ile | Met | Thr | Glu | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Phe | Ile | Lys | Tyr | Leu | Leu | Ile | Gly | Ala | Leu | Gly | Leu | Leu | Val | Ile |

165 170 175  
Thr Ser Lys Asp  
180  
(2) INFORMATION FOR SEQ ID NO:3013:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..173  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575165  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3013:  
Met Glu Ser Ile Arg Ser Met Gln Ile Arg Gln Val Leu Met Gln Ile  
1 5 10 15  
Ile Ser Leu Gly Met Ile Val Thr Ser Ala Leu Ile Ile Trp Lys Gly  
20 25 30  
Leu Ile Val Phe Thr Gly Ser Glu Ser Pro Val Val Val Leu Ser  
35 40 45  
Gly Ser Met Glu Pro Gly Phe Lys Arg Gly Asp Ile Leu Phe Leu His  
50 55 60  
Met Ser Lys Asp Pro Ile Arg Thr Gly Glu Ile Val Val Phe Asn Ile  
65 70 75 80  
Asp Gly Arg Glu Ile Pro Ile Val His Arg Val Ile Lys Val His Glu  
85 90 95  
Arg Gln Asp Thr Ala Glu Val Asp Ile Leu Thr Lys Gly Asp Asn Asn  
100 105 110  
Phe Gly Asp Asp Arg Leu Leu Tyr Ala His Gly Gln Leu Trp Leu Gln  
115 120 125  
Gln His His Ile Met Gly Arg Ala Val Gly Tyr Leu Pro Tyr Val Gly  
130 135 140  
Trp Val Thr Ile Ile Met Thr Glu Lys Pro Phe Ile Lys Tyr Leu Leu  
145 150 155 160  
Ile Gly Ala Leu Gly Leu Leu Val Ile Thr Ser Lys Asp  
165 170

(2) INFORMATION FOR SEQ ID NO:3014:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 167 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..167  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575166  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3014:  
Met Gln Ile Arg Gln Val Leu Met Gln Ile Ile Ser Leu Gly Met Ile  
1 5 10 15  
Val Thr Ser Ala Leu Ile Ile Trp Lys Gly Leu Ile Val Phe Thr Gly  
20 25 30  
Ser Glu Ser Pro Val Val Val Val Leu Ser Gly Ser Met Glu Pro Gly  
35 40 45  
Phe Lys Arg Gly Asp Ile Leu Phe Leu His Met Ser Lys Asp Pro Ile  
50 55 60  
Arg Thr Gly Glu Ile Val Val Phe Asn Ile Asp Gly Arg Glu Ile Pro  
65 70 75 80  
Ile Val His Arg Val Ile Lys Val His Glu Arg Gln Asp Thr Ala Glu  
85 90 95

Val Asp Ile Leu Thr Lys Gly Asp Asn Asn Phe Gly Asp Asp Arg Leu  
100 105 110  
Leu Tyr Ala His Gly Gln Leu Trp Leu Gln Gln His His Ile Met Gly  
115 120 125  
Arg Ala Val Gly Tyr Leu Pro Tyr Val Gly Trp Val Thr Ile Ile Met  
130 135 140  
Thr Glu Lys Pro Phe Ile Lys Tyr Leu Leu Ile Gly Ala Leu Gly Leu  
145 150 155 160  
Leu Val Ile Thr Ser Lys Asp  
165

(2) INFORMATION FOR SEQ ID NO:3015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 961 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..961
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3015:

acgtacgtat agncmggcgg gaacgcgtac carghgccgg crgggcggcg ggacgggtcc 60  
gtgtcgcgcg cgtcggacac cagcaacctg ccgcgcgcga cggccaacgt cgcgcastca 120  
cgcagatctt cggcaccaag ggcctgacgc agaaggagat ggtcatcctg tcgggcgcg 180  
acaccatcgg ctctcgcac tgcagctnnt tcarcgccg gctgtcgggg tcggccacga 240  
cggcrggcgg gcaggaccgg accatggacc ccgcgtacgt rgcgcastgn gncrcggcag 300  
tgcccgcagg ggnchgaccc gctcgtgccc atgGaCtaog tctcccccaa cgccttcgac 360  
gaggGcttct acaaggcgt catggccaac cggggcctgc tgtcctcgga ccaggcgctg 420  
ctcagcgaca agaacaccgc cgtgcaggtc gtcacctaog ccaacgaccc ggccaccttc 480  
caggccgact tcgcccgcgc catggtcaag atgggctcog tcggcgtgct caccggcacc 540  
agcggcaagg tcagggccaa ctgcagagtc gcctgattca tcgtcatcac tcgtgtggag 600  
ttgtagattc attatattga ttgatttgga ccggacgacg tcgacgggat gctacatggc 660  
ctsttgcgca attgtatgta tgcctgtact tgcgcgtgta tgggtttcgc tgtgcaaatt 720  
ttcgttgtct cccccgattg attgaggcgt gtgtgcgtgt gtgtctcttc tgaatctgaa 780  
tggaatatct gtaacctgag ctaaaactgc tcgtgtacta cccaatagtt gcttcaaact 840  
acgatggatt tttattcaaa ctatcacttc caaacacgca caaatatgta ctcaatcaac 900  
tagggatcgg agaaactggg ttgtaaaggg aattttataa acacaagcta ttcagacatg 960  
t

(2) INFORMATION FOR SEQ ID NO:3016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3016:

Arg Thr Tyr Xaa Xaa Ala Gly Thr Arg Thr Xaa Xaa Arg Xaa Gly Gly  
1 5 10 15  
Gly Thr Gly Pro Cys Arg Ala Arg Arg Thr Pro Ala Thr Cys Arg Arg  
20 25 30  
Arg Arg Pro Thr Ser Arg Xaa His Ala Asp Leu Arg His Gln Gly Pro  
35 40 45  
Asp Ala Glu Gly Asp Gly His Pro Val Gly Arg Ala His His Arg Leu  
50 55 60  
Leu Ala Leu Gln Xaa Xaa Arg Pro Ala Val Gly Val Gly His Asp  
65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Gly | Xaa | Arg | Ala | Gly | Pro | Asp | His | Gly | Pro | Arg | Val | Arg | Xaa | Ala | Xaa |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Xaa | Xaa | Gly | Ser | Ala | Arg | Arg | Xaa | Xaa | Thr | Arg | Ser | Cys | Pro | Trp | Thr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Thr | Ser | Pro | Pro | Thr | Pro | Ser | Thr | Arg | Ala | Ser | Thr | Arg | Ala | Ser | Trp |  |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Pro | Thr | Gly | Ala | Cys | Cys | Pro | Arg | Thr | Arg | Arg | Cys | Ser | Ala | Thr | Arg |  |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Thr | Pro | Pro | Cys | Arg | Ser | Ser | Pro | Thr | Pro | Thr | Thr | Arg | Pro | Pro | Ser |  |  |
|     |     |     | 145 |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Arg | Pro | Thr | Ser | Pro | Pro | Pro | Trp | Ser | Arg | Trp | Ala | Pro | Ser | Ala | Cys |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Ser | Pro | Ala | Pro | Ala | Ala | Arg | Ser | Gly | Pro | Thr | Ala | Glu | Ser | Pro | Asp |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |  |
| Ser | Ser | Ser | Ser | Leu | Val | Trp | Ser | Cys | Arg | Phe | Ile | Ile | Leu | Ile | Asp |  |  |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |  |
| Leu | Asp | Arg | Thr | Thr | Ser | Thr | Gly | Cys | Tyr | Met | Ala | Xaa | Cys | Ala | Ile |  |  |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Val | Cys | Met | Pro | Val | Leu | Ala | Arg | Val | Trp | Val | Ser | Leu | Cys | Lys | Phe |  |  |
|     |     |     | 225 |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |  |
| Ser | Leu | Ser | Pro | Pro | Ile | Asp |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:3017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1575183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3017:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Arg | Ile | Xaa | Xaa | Arg | Glu | Arg | Val | Pro | Xaa | Ala | Gly | Xaa | Ala | Ala |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Gly | Arg | Val | Arg | Val | Ala | Arg | Val | Gly | His | Gln | Gln | Pro | Ala | Ala | Ala |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |
| Asp | Gly | Gln | Arg | Arg | Ala | Xaa | Thr | Gln | Ile | Phe | Gly | Thr | Lys | Gly | Leu |  |  |
|     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Thr | Gln | Lys | Glu | Met | Val | Ile | Leu | Ser | Gly | Ala | His | Thr | Ile | Gly | Ser |  |  |
|     |     |     | 50  |     | 55  |     |     |     | 60  |     |     |     |     |     |     |  |  |
| Ser | His | Cys | Ser | Xaa | Phe | Xaa | Gly | Arg | Leu | Ser | Gly | Ser | Ala | Thr | Thr |  |  |
|     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     | 80  |     |     |  |  |
| Xaa | Gly | Gly | Gln | Asp | Pro | Thr | Met | Asp | Pro | Ala | Tyr | Xaa | Ala | Xaa | Xaa |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Xaa | Xaa | Ala | Val | Pro | Ala | Gly | Xaa | Xaa | Pro | Ala | Arg | Ala | His | Gly | Leu |  |  |
|     |     |     | 100 |     |     | 105 |     |     |     |     |     | 110 |     |     |     |  |  |
| Arg | Leu | Pro | Gln | Arg | Leu | Arg | Arg | Gly | Leu | Leu | Gln | Gly | Arg | His | Gly |  |  |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |  |
| Gln | Pro | Gly | Pro | Ala | Val | Leu | Gly | Pro | Gly | Ala | Ala | Gln | Arg | Gln | Glu |  |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| His | Arg | Arg | Ala | Gly | Arg | His | Leu | Arg | Gln | Arg | Pro | Gly | His | Leu | Pro |  |  |
|     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |  |
| Gly | Arg | Leu | Arg | Arg | Arg | His | Gly | Gln | Asp | Gly | Leu | Arg | Arg | Arg | Ala |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |  |
| His | Arg | His | Gln | Arg | Gln | Gly | Gln | Gly | Gln | Leu | Gln | Ser | Arg | Leu | Ile |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |  |
| His | Arg | His | His | Ser | Cys | Gly | Val | Val | Asp | Ser | Leu | Tyr |     |     |     |  |  |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:3018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1575184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3018:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ile | Leu | Ser | Gly | Ala | His | Thr | Ile | Gly | Ser | Ser | His | Cys | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Xaa | Phe | Xaa | Gly | Arg | Leu | Ser | Gly | Ser | Ala | Thr | Thr | Xaa | Gly | Gly | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Pro | Thr | Met | Asp | Pro | Ala | Tyr | Xaa | Ala | Xaa | Xaa | Xaa | Xaa | Ala | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ala | Gly | Xaa | Xaa | Pro | Ala | Arg | Ala | His | Gly | Leu | Arg | Leu | Pro | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Arg | Arg | Gly | Leu | Leu | Gln | Gly | Arg | His | Gly | Gln | Pro | Gly | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Val | Leu | Gly | Pro | Gly | Ala | Ala | Gln | Arg | Gln | Glu | His | Arg | Arg | Ala |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Arg | His | Leu | Arg | Gln | Arg | Pro | Gly | His | Leu | Pro | Gly | Arg | Leu | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Arg | Arg | His | Gly | Gln | Asp | Gly | Leu | Arg | Arg | Arg | Ala | His | Arg | His | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Gln | Gly | Gln | Gly | Gln | Leu | Gln | Ser | Arg | Leu | Ile | His | Arg | His | His |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Cys | Gly | Val | Val | Asp | Ser | Leu | Tyr |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..424

(D) OTHER INFORMATION: / Ceres Seq. ID 1575191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3019:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atacatttcg  | actctcaacy | cccaaggtcc | cttttttttt | ctcgatctgg | aagcncgcga | 60  |
| gtagcagcca  | tggacgtgag | cggagcaggc | ggtaaggcga | agaagggcgc | ggcggggcgc | 120 |
| aaggccggcg  | ggccgacgaa | gaagtcggtg | tcgcggtcct | ccaggggccg | gcccgcctgc | 180 |
| tcctgggtccc | agcccgacgc | caccatctcc | gccaaattaa | gcccattgtg | catggatgct | 240 |
| cttggtacac  | atgcatgaag | tagtagagag | caacggtcaa | cttactcctt | atattcccat | 300 |
| aataataaaa  | tacttaggag | tacttacttc | aaaaaaagaa | ggatctcatg | actgtaaccg | 360 |
| aagtgcattt  | ttctcttgag | ttggggtgta | acataaacc  | agcaccaaag | ctatttgcca | 420 |
| tctc        |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1575192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3020:

Ile His Phe Asp Ser Gln Xaa Pro Arg Ser Leu Phe Phe Ser Arg Ser  
1 5 10 15  
Gly Ser Xaa Ala Val Ala Ala Met Asp Val Ser Gly Ala Gly Gly Lys  
20 25 30  
Ala Lys Lys Gly Ala Ala Gly Arg Lys Ala Gly Gly Pro Thr Lys Lys  
35 40 45  
Ser Val Ser Arg Ser Ser Arg Ala Gly Pro Ala Cys Ser Trp Ser Gln  
50 55 60  
Pro Asp Ala Thr Ile Ser Ala Lys Leu Ser Pro Cys Cys Met Asp Ala  
65 70 75 80  
Leu Gly Thr His Ala  
85

(2) INFORMATION FOR SEQ ID NO:3021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1575193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3021:

Met Asp Val Ser Gly Ala Gly Gly Lys Ala Lys Lys Gly Ala Ala Gly  
1 5 10 15  
Arg Lys Ala Gly Gly Pro Thr Lys Lys Ser Val Ser Arg Ser Ser Arg  
20 25 30  
Ala Gly Pro Ala Cys Ser Trp Ser Gln Pro Asp Ala Thr Ile Ser Ala  
35 40 45  
Lys Leu Ser Pro Cys Cys Met Asp Ala Leu Gly Thr His Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1575194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3022:

Met Leu Leu Val His Met His Glu Val Val Glu Ser Asn Gly Gln Leu  
1 5 10 15  
Thr Pro Tyr Ile Pro Ile Ile Ile Lys Tyr Leu Gly Val Leu Thr Ser  
20 25 30  
Lys Lys Glu Gly Ser His Asp Cys Asn Arg Ser Asp Ile Phe Ser  
35 40 45

(2) INFORMATION FOR SEQ ID NO:3023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..631

(D) OTHER INFORMATION: / Ceres Seq. ID 1575195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3023:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| tgcttaaggt  | tcttgacaag  | gagaaacgcc | aggcacattg | tgctgatgtt  | ggatctcact  | 60  |
| tggtggagcg  | tctaaaatcg  | cttcaggaca | agcacgaaat | tataggtgat  | gttagaggaa  | 120 |
| ggggactgat  | gcttgggggtg | gaactcgtta | cggacagaaa | ggagaagacc  | cctgccaaagt | 180 |
| cagaaacccat | tgaactgttt  | gagaagctca | gagatctcgg | ggtactagtt  | ggaaagggcg  | 240 |
| gtctgcatgg  | taacgtcttc  | agaataaaac | caccgatgtg | cttttcgaag  | gacgatgcag  | 300 |
| acttcttggg  | ggactccatg  | gactacgcaa | tgtcaaggct | ctgaaggaac  | atgctctgag  | 360 |
| ttgacaatgt  | gtctgcgtgg  | aaacaacact | tcttgcaacc | gcaagatgca  | tggcctgaaa  | 420 |
| tgaactgaa   | aggcagatga  | tttaatgggc | atgctccccg | ggtgggtatgt | tggtgttatg  | 480 |
| gtgaagttaa  | atagtccccc  | tccccgaat  | aaattgatga | aaggggacag  | aacgtcttgc  | 540 |
| ccagcttggtg | aactgtttgt  | agaagaactg | cagttaataa | atagaatagc  | gagcaagcaa  | 600 |
| gcgtgatatc  | aatctgcata  | cgtcCatttt | c          |             |             |     |

(2) INFORMATION FOR SEQ ID NO:3024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1575196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3024:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Lys | Val | Leu | Asp | Lys | Glu | Lys | Arg | Gln | Ala | His | Cys | Ala | Asp | Val |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Ser | His | Leu | Glu | Arg | Leu | Lys | Ser | Leu | Gln | Asp | Lys | His | Glu |     |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ile | Ile | Gly | Asp | Val | Arg | Gly | Arg | Gly | Leu | Met | Leu | Gly | Val | Glu | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Thr | Asp | Arg | Lys | Glu | Lys | Thr | Pro | Ala | Lys | Ser | Glu | Thr | Ile | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Leu | Phe | Glu | Lys | Leu | Arg | Asp | Leu | Gly | Val | Leu | Val | Gly | Lys | Gly | Gly |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |  |
| Leu | His | Gly | Asn | Val | Phe | Arg | Ile | Lys | Pro | Pro | Met | Cys | Phe | Ser | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Asp | Asp | Ala | Asp | Phe | Leu | Val | Asp | Ser | Met | Asp | Tyr | Ala | Met | Ser | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |  |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1575197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3025:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Gly | Val | Glu | Leu | Val | Thr | Asp | Arg | Lys | Glu | Lys | Thr | Pro | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Ser | Glu | Thr | Ile | Glu | Leu | Phe | Glu | Lys | Leu | Arg | Asp | Leu | Gly | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Leu | Val | Gly | Lys | Gly | Gly | Leu | His | Gly | Asn | Val | Phe | Arg | Ile | Lys | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Pro | Met | Cys | Phe | Ser | Lys | Asp | Asp | Ala | Asp | Phe | Leu | Val | Asp | Ser | Met |  |

50  
Asp Tyr Ala Met Ser Arg Leu  
65 70

55

60

(2) INFORMATION FOR SEQ ID NO:3026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3026:

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| atatatttcg  | cccatttggt | ggttttcgtg  | aagttcgtct  | tgtcaacaag  | gagtcagac   | 60  |
| atcctggtgg  | agatccacat | gtgttggtgt  | tcgtcgattt  | tgacaaccct  | gctcaggcta  | 120 |
| caattgctct  | ggaagcatta | caagggtata  | agtttgacga  | acacgagcgt  | gattcagccc  | 180 |
| atttgcgctc  | gcaattctca | cgctttcccg  | gtccaagggtc | agctgggtggg | cctcgcggta  | 240 |
| ggcgtaaaga  | cgtgcggacc | tcgtgggtgc  | cgaacctatc  | gtttatacga  | gcgatccaac  | 300 |
| tacgggGggc  | taacgcttcg | atatgcgctg  | aatttcgggg  | cgggtggcttt | ttaggggttcg | 360 |
| tcagctcatt  | tcgtgaatgc | gtgaaaggga  | caatgcaata  | agtgatattc  | tgccatatgt  | 420 |
| tattagatgc  | cgtataatgt | gttaggcgatg | gaaagttatt  | cgacatactg  | tatctgctgc  | 480 |
| cttagctatt  | gtggtctact | gtaacttcat  | tacottgctt  | cacatccgag  | acaatttgag  | 540 |
| tttggttatca | tgtggattat | ctgttttgaa  | aatgaaaact  | agatgatgtt  | agcct       |     |

(2) INFORMATION FOR SEQ ID NO:3027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3027:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Tyr Phe Ala His Leu Leu Val Phe Val Lys Phe Val Leu Ser Thr |  |
| 1 5 10 15                                                       |  |
| Arg Ser Pro Asp Ile Leu Val Glu Ile His Met Cys Cys Val Ser Ser |  |
| 20 25 30                                                        |  |
| Ile Leu Thr Thr Leu Leu Arg Leu Gln Leu Leu Trp Lys His Tyr Lys |  |
| 35 40 45                                                        |  |
| Val Ile Ser Leu Thr Asn Thr Ser Val Ile Gln Pro Ile Cys Val Cys |  |
| 50 55 60                                                        |  |
| Asn Ser His Ala Phe Pro Val Gln Gly Gln Leu Val Gly Leu Ala Val |  |
| 65 70 75 80                                                     |  |
| Gly Val Lys Thr Cys Gly Pro Arg Gly Cys Arg Thr Tyr Arg Leu Tyr |  |
| 85 90 95                                                        |  |
| Glu Arg Ser Asn Tyr Gly Gly Leu Thr Leu Arg Tyr Ala Leu Asn Phe |  |
| 100 105 110                                                     |  |
| Gly Ala Val Ala Phe                                             |  |
| 115                                                             |  |

(2) INFORMATION FOR SEQ ID NO:3028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



(A) NAME/KEY: peptide  
(B) LOCATION: 1..81  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3028:

Ile Phe Arg Pro Phe Val Gly Phe Arg Glu Val Arg Leu Val Asn Lys  
1 5 10 15  
Glu Ser Arg His Pro Gly Gly Asp Pro His Val Leu Cys Phe Val Asp  
20 25 30  
Phe Asp Asn Pro Ala Gln Ala Thr Ile Ala Leu Glu Ala Leu Gln Gly  
35 40 45  
Tyr Lys Phe Asp Glu His Glu Arg Asp Ser Ala His Leu Arg Leu Gln  
50 55 60  
Phe Ser Arg Phe Pro Gly Pro Arg Ser Ala Gly Gly Pro Arg Gly Arg  
65 70 75 80  
Arg

(2) INFORMATION FOR SEQ ID NO:3029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3029:

Met Cys Cys Val Ser Ser Ile Leu Thr Leu Leu Arg Leu Gln Leu  
1 5 10 15  
Leu Trp Lys His Tyr Lys Val Ile Ser Leu Thr Asn Thr Ser Val Ile  
20 25 30  
Gln Pro Ile Cys Val Cys Asn Ser His Ala Phe Pro Val Gln Gly Gln  
35 40 45  
Leu Val Gly Leu Ala Val Gly Val Lys Thr Cys Gly Pro Arg Gly Cys  
50 55 60  
Arg Thr Tyr Arg Leu Tyr Glu Arg Ser Asn Tyr Gly Gly Leu Thr Leu  
65 70 75 80  
Arg Tyr Ala Leu Asn Phe Gly Ala Val Ala Phe  
85 90

(2) INFORMATION FOR SEQ ID NO:3030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 688 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..688  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3030:

gaaccgatcc ggttttaaag atccgctact agtgtcaccg gcaacgtgtc gacgcggtcg 60  
tgtcgtgtgt gttcctggtg aggaagcgaa cctgcctgct ctgcttgctt gccgggcaag 120  
aagtgagaac agcgtgghgg tgcggaagcg accggaccga ggatggctac aagaaggacc 180  
gtrgcggcga gcgttactgc ccaccagcct gcgtrggcgg ccgtggcgag gaggatggag 240  
ggcgtgtcgc gctacttcag cgacaaggcc tccggcaggg tgctcagcga rgaggagcgc 300  
gccgccgaga acgtctacat acagaagatg gawcaggaba agctggagaa actnawgang 360  
aaggadgaca aggccaaggc cgadgcggcc aagadggccg cgccgccgcc agrvgSacac 420  
gaagaatggt gaggaggctc atccgagctg atcatcgcca aaatcggacc agtgctcccg 480  
tgaatcgtgt gatgctgtac tactgatgac acgtagatgc aaatagacgc cgtcgtacta 540

ctctgctttg caactctgct cgtcgtgctg tgtgtgatcc catccctgtc actgttgtga 600  
acttcgcttg tagctagcga cggttttgcc ttgtcccttg tgggtgcaaa tgtaatggag 660  
tggaggcgtc cttgagcctc tttcatgt

(2) INFORMATION FOR SEQ ID NO:3031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3031:

Asn Arg Ser Gly Leu Lys Asp Pro Leu Leu Val Ser Pro Ala Thr Cys  
1 5 10 15  
Arg Arg Gly Arg Val Val Cys Val Pro Gly Glu Glu Ala Asn Pro Ala  
20 25 30  
Cys Leu Leu Ala Cys Arg Ala Arg Ser Glu Asn Ser Val Xaa Val Arg  
35 40 45  
Lys Arg Pro Asp Arg Gly Trp Leu Gln Glu Gly Pro Xaa Arg Arg Ala  
50 55 60  
Leu Leu Pro Thr Ser Leu Arg Xaa Arg Pro Trp Arg Gly Gly Trp Arg  
65 70 75 80  
Ala Cys Arg Ala Thr Ser Ala Thr Arg Pro Pro Ala Gly Cys Ser Ala  
85 90 95  
Xaa Arg Ser Ala Pro Pro Arg Thr Ser Thr Tyr Arg Arg Trp Xaa Arg  
100 105 110  
Xaa Ser Trp Arg Asn Xaa Xaa Xaa Arg Xaa Thr Arg Pro Arg Pro Xaa  
115 120 125  
Arg Pro Arg Xaa Pro Arg Arg Arg Gln Xaa Xaa Thr Lys Asn Gly Glu  
130 135 140  
Glu Ala His Pro Ser  
145

(2) INFORMATION FOR SEQ ID NO:3032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1575212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3032:

Met Ala Thr Arg Arg Thr Xaa Ala Ala Ser Val Thr Ala His Gln Pro  
1 5 10 15  
Ala Xaa Ala Ala Val Ala Arg Arg Met Glu Gly Val Ser Arg Tyr Phe  
20 25 30  
Ser Asp Lys Ala Ser Gly Arg Val Leu Ser Xaa Glu Glu Arg Ala Ala  
35 40 45  
Glu Asn Val Tyr Ile Gln Lys Met Xaa Gln Xaa Lys Leu Glu Lys Xaa  
50 55 60  
Xaa Xaa Lys Xaa Asp Lys Ala Lys Ala Xaa Ala Ala Lys Xaa Ala Ala  
65 70 75 80  
Pro Pro Pro Xaa Xaa His Glu Glu Trp  
85

(2) INFORMATION FOR SEQ ID NO:3033:

(i) SEQUENCE CHARACTERISTICS:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aaccacctgc  | agaggaccgc  | cgtcgcgcgc | tatcattcgt | ttctggagac | cctctagacc | 60  |
| ccgcgcgcac  | cacaccacca  | ccaccaatgg | caggactcgg | atcaaaggcc | ctcgcgctgg | 120 |
| tgcgcgtcct  | ggcggccgtc  | gtcctctcag | tgkcctccgc | ggcogaggcg | ccgcgcacca | 180 |
| gccccgtctN  | ccgCgcgcgc  | csgsgctcgg | cgckkttcgc | cgcggccctc | gtcgctcctc | 240 |
| ccgcgcgctt  | cctcttcgcc  | gcgctccgcc | actgagccga | tggggccctt | ccaccgcgcg | 300 |
| cgcgcgcgcg  | tagatctatt  | tattggagtg | gtattcagta | gtactggtac | tagggagatt | 360 |
| tcttcgtttgg | tgtcgtgtcg  | tgcgcgcat  | ttggtcggat | ctggtgtcct | tgggtgggtg | 420 |
| agggtttgtta | cgcgcgtcgtg | gtgtcggttg | tgtgatctga | ttctgatccc | cttgtagata | 480 |
| ctgtgctatc  | tgcgcgtgat  | cgtgagtgat | gattccgtct | ggttgctact | gatacactat | 540 |
| tgttcttatt  | tggtt       |            |            |            |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3034:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1575219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3035:

Pro Pro Ala Glu Asp Pro Arg Ser Pro Leu Ser Phe Val Ser Gly Asp  
1 5 10 15  
Pro Ser Ser Pro Ala Ala Thr Thr Pro Pro Pro Pro Met Ala Gly Leu  
20 25 30  
Gly Ser Lys Ala Leu Ala Val Val Ala Val Leu Ala Ala Val Val Leu  
35 40 45  
Ser Val Xaa Ser Ala Ala Glu Ala Pro Ala Pro Ser Pro Val Xaa Arg  
50 55 60  
Arg Arg Xaa Ala Ser Ala Xaa Phe Ala Ala Ala Leu Val Ala Ser Ser  
65 70 75 80  
Ala Ala Phe Leu Phe Ala Ala Val Arg His  
85 90

(2) INFORMATION FOR SEQ ID NO:3036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 614 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..614

(D) OTHER INFORMATION: / Ceres Seq. ID 1575232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3036:

accaccactc atcaccacca gctgccattg ccatctactg acctgtgacc tccgcatttc 60  
caaacagccc gagcgagcga gctagcagag cggNcggcag gcacctccct cctcaaggaa 120  
catggcccg cagcagcagt tggcagtagt ggcggcggcc gtggtggcct tggtgccgcc 180  
ggcgtcagcg gctcaacgc cggtaacgcc gccagcatcc cctccaagtg cggcgtcagc 240  
atccctaca ccatcagcac ctccaccgac tgctccaggg tgaactgaac cctaaacgac 300  
gacgacggcg ccggcgggccg cctgaagacg atccatatct atcccgccgt cgtcggcgct 360  
gcggttcgga ccgtcatgac catatctacc tacgcatgat caccgacttgc atgtctacta 420  
ctactactga ataaaaaacc tctccgcgca cgtcgtcctt gtgtctgtgt gtgtgagaga 480  
gagaggagag ccggccatgt ccttttggct gtttggttta tttttgagtt catgcggctc 540  
ttatttattt ccatgtaccc agtaccacc ttgtaccatg catgttcctt atgatacact 600  
cacctctttt tggt

(2) INFORMATION FOR SEQ ID NO:3037:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1575233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3037:

Met Ala Arg Thr Gln Gln Leu Ala Val Val Ala Ala Val Val Ala  
1 5 10 15  
Leu Val Pro Pro Ala Ser Ala Ala Ser Thr Pro Val Thr Pro Pro Ala  
20 25 30  
Ser Pro Pro Ser Ala Ala Ser Ala Ser Pro Thr Pro Ser Ala Pro Pro  
35 40 45  
Pro Thr Ala Pro Gly  
50

(2) INFORMATION FOR SEQ ID NO:3038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..39
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575234
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3038:

Met Ser Phe Trp Leu Phe Gly Leu Phe Leu Ser Ser Cys Gly Leu Tyr  
1 5 10 15  
Leu Phe Pro Cys Thr Gln Tyr Pro Pro Cys Thr Met His Val Pro Tyr  
20 25 30  
Asp Thr Leu Thr Ser Phe Cys  
35

(2) INFORMATION FOR SEQ ID NO:3039:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 615 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..615
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575235
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3039:

gcaaaaccgcg tctcgcgcgga agaatccgca tttccccttc cccgcaccca acccccgtcg 60  
gagagagaga tggcatcggt ggGcgagat gcagcccctc gcgccggcgg ggtaccgcbG 120  
cgcgccggag atgaaggaga agtgaggagg gtcggtggtg gacctggagg ccggcacogg 180  
ggagacgctg taccggggga tctcgcgcgcg ggagagcgcc ctccgatggg gcttcgtccg 240  
caaggtctac ggcatectcg tgcgcagctg ctctcacca ccgcctctc cgccctcacc 300  
gttctccacc ccaccctcaa cgccacgctc tccgactccc cgggcctcgc gctcgtgctc 360  
gcgctoctgc ctttcctcct gatgatccca ttgtatcatt atcagcacia gcacccacac 420  
aatttcggtt tcttggtct gttcacgttg tgcctgagct tcagcatcgg tgtggcttgt 480  
gctaacaccc aagggaatat cgttctggag gcttttagtg tgacggctgg cgtggtggtt 540  
tctctgaygc gtatgccttc tggcgctcaa agaagggcaa ggaattcggg taactggggc 600  
ctatcctgtc ttccg

(2) INFORMATION FOR SEQ ID NO:3040:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 205 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..205
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575236
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3040:

Ala Asn Arg Val Ser Arg Glu Glu Ser Ala Phe Pro Leu Pro Arg Thr  
1 5 10 15  
Gln Pro Pro Ser Glu Arg Glu Met Ala Ser Val Gly Gly Asp Ala Ala  
20 25 30  
Pro Arg Ala Gly Gly Val Pro Xaa Arg Ala Gly Asp Glu Gly Glu Gly  
35 40 45  
Gly Gly Val Gly Gly Gly Pro Gly Gly Arg His Arg Gly Asp Ala Val  
50 55 60  
Pro Gly Asp Leu Ala Arg Gly Glu Arg Pro Pro Met Gly Leu Arg Pro  
65 70 75 80  
Gln Gly Leu Arg His Pro Arg Ala Gln Leu Leu Leu Thr Thr Ala Val

85 90 95  
Ser Ala Leu Thr Val Leu His Pro Thr Leu Asn Ala Thr Leu Ser Asp  
100 105 110  
Ser Pro Gly Leu Ala Leu Val Leu Ala Val Leu Pro Phe Ile Leu Met  
115 120 125  
Ile Pro Leu Tyr His Tyr Gln His Lys His Pro His Asn Phe Val Phe  
130 135 140  
Leu Gly Leu Phe Thr Leu Cys Leu Ser Phe Ser Ile Gly Val Ala Cys  
145 150 155 160  
Ala Asn Thr Gln Gly Lys Ile Val Leu Glu Ala Leu Val Leu Thr Ala  
165 170 175  
Gly Val Val Val Ser Leu Xaa Arg Met Pro Ser Gly Arg Gln Arg Arg  
180 185 190  
Ala Arg Asn Ser Gly Thr Trp Gly Leu Ser Cys Leu Pro  
195 200 205

(2) INFORMATION FOR SEQ ID NO:3041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1575237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3041:

Met Ala Ser Val Gly Gly Asp Ala Ala Pro Arg Ala Gly Gly Val Pro  
1 5 10 15  
Xaa Arg Ala Gly Asp Glu Gly Glu Gly Gly Val Gly Gly Pro  
20 25 30  
Gly Gly Arg His Arg Gly Asp Ala Val Pro Gly Asp Leu Ala Arg Gly  
35 40 45  
Glu Arg Pro Pro Met Gly Leu Arg Pro Gln Gly Leu Arg His Pro Arg  
50 55 60  
Ala Gln Leu Leu Leu Thr Thr Ala Val Ser Ala Leu Thr Val Leu His  
65 70 75 80  
Pro Thr Leu Asn Ala Thr Leu Ser Asp Ser Pro Gly Leu Ala Leu Val  
85 90 95  
Leu Ala Val Leu Pro Phe Ile Leu Met Ile Pro Leu Tyr His Tyr Gln  
100 105 110  
His Lys His Pro His Asn Phe Val Phe Leu Gly Leu Phe Thr Leu Cys  
115 120 125  
Leu Ser Phe Ser Ile Gly Val Ala Cys Ala Asn Thr Gln Gly Lys Ile  
130 135 140  
Val Leu Glu Ala Leu Val Leu Thr Ala Gly Val Val Val Ser Leu Xaa  
145 150 155 160  
Arg Met Pro Ser Gly Arg Gln Arg Arg Ala Arg Asn Ser Gly Thr Trp  
165 170 175  
Gly Leu Ser Cys Leu Pro  
180

(2) INFORMATION FOR SEQ ID NO:3042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1575238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3042:

Met Gly Leu Arg Pro Gln Gly Leu Arg His Pro Arg Ala Gln Leu Leu  
1 5 10 15  
Leu Thr Thr Ala Val Ser Ala Leu Thr Val Leu His Pro Thr Leu Asn  
20 25 30  
Ala Thr Leu Ser Asp Ser Pro Gly Leu Ala Leu Val Leu Ala Val Leu  
35 40 45  
Pro Phe Ile Leu Met Ile Pro Leu Tyr His Tyr Gln His Lys His Pro  
50 55 60  
His Asn Phe Val Phe Leu Gly Leu Phe Thr Leu Cys Leu Ser Phe Ser  
65 70 75 80  
Ile Gly Val Ala Cys Ala Asn Thr Gln Gly Lys Ile Val Leu Glu Ala  
85 90 95  
Leu Val Leu Thr Ala Gly Val Val Val Ser Leu Xaa Arg Met Pro Ser  
100 105 110  
Gly Arg Gln Arg Arg Ala Arg Asn Ser Gly Thr Trp Gly Leu Ser Cys  
115 120 125  
Leu Pro  
130

(2) INFORMATION FOR SEQ ID NO:3043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1575243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3043:

|            |            |             |             |            |            |     |
|------------|------------|-------------|-------------|------------|------------|-----|
| cagascagaa | ascagccgca | gccccagccc  | ccacaagacg  | aggcaacaat | ggcgctagaa | 60  |
| gcagccaccg | cccccgcg   | actcctcgcc  | gcggtgcctcg | tcctgctggt | cctcggcggc | 120 |
| ggcaccggcc | cgtcgctcgt | gCtgcgcggc  | gccggggcgc  | aggccggcag | gggagccgga | 180 |
| tccaggatac | gtcatgtatc | cggcattggg  | ccccgcgcgc  | cactaatcgt | cgtcgttcga | 240 |
| ggcgacgac  | gacgCtccgc | cgccaacgac  | ggcgagtgcc  | acatgcctat | gctctcgtgt | 300 |
| gggccccgta | cgttattgag | cgctactagt  | actagggaaa  | gtgtacgtgt | gatgtgtgtc | 360 |
| actcagtgtc | gattgatcaa | tgatgtctcat | tttcgagcag  | acccaggaat | gctgagtga  | 420 |
| gagagcagag | cgtNtgttct | acaagtgcac  | cgaggaataa  | agtggacaga | aatgttggct | 480 |
| ggttcacgtg | ccttctgagt | aataaaatgg  | acatcttcg   |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1575244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3044:

Gln Xaa Arg Xaa Gln Pro Gln Pro Gln Pro Gln Asp Glu Ala Thr  
1 5 10 15  
Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys  
20 25 30  
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu  
35 40 45  
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg  
50 55 60

His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg  
65 70 75 80  
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro  
85 90 95  
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg  
100 105 110  
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp  
115 120 125  
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala  
130 135 140  
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala  
145 150 155 160  
Gly Ser Arg Ala Phe  
165

(2) INFORMATION FOR SEQ ID NO:3045:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1575245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3045:

Xaa Gln Lys Xaa Ala Ala Ala Pro Ala Pro Thr Arg Arg Gly Asn Asn  
1 5 10 15  
Gly Ala Arg Ser Ser His Arg Pro Pro Arg Thr Pro Arg Arg Val Pro  
20 25 30  
Arg Pro Ala Gly Pro Arg Arg Arg His Arg Pro Val Val Gly Ala Ala  
35 40 45  
Arg Arg Arg Gly Ala Gly Arg Gln Gly Ser Arg Ile Gln Asp Thr Ser  
50 55 60  
Cys Ile Arg His Gly Ala Pro Pro Ser Thr Asn Arg Arg Arg Ser Arg  
65 70 75 80  
Ala Thr Thr Thr Leu Arg Arg Gln Arg Arg Arg Val Pro His Ala Tyr  
85 90 95  
Ala Leu Val Trp Ala Pro Tyr Val Ile Glu Arg Tyr  
100 105

(2) INFORMATION FOR SEQ ID NO:3046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3046:

Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys  
1 5 10 15  
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu  
20 25 30  
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg  
35 40 45  
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg  
50 55 60  
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro



65                      70                      75                      80  
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg  
                                 85                      90                      95  
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp  
                                 100                      105                      110  
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala  
                                 115                      120                      125  
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala  
                                 130                      135                      140  
Gly Ser Arg Ala Phe  
145

(2) INFORMATION FOR SEQ ID NO:3047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..945
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3047:

ataaaccttt tcaactgctcc agccgcgcgcc gccgcgcttt cttcgtcttc ctcgcagcgc                      60  
cgccgctcca tcttcgctg atccgctcgc tcccgcctct cgccacgcag gcggcggcgc                      120  
tcaggcccggt gatttcagcg acggcgctcas ggcttccct cccgtctctt cccagtcgcc                      180  
tcgcgccttc gcctccggtc ctccgcacac cggcgggtga ccctgcatcc accatgactg                      240  
gtgtcagcac tggattgttg acgggcttga ggagggtcat ggaacagcaa aggatttcaa                      300  
cgcgtttctg cagacaatca cgagtttcga gctctactgt ttctttctct gacctcgatg                      360  
agaaggggtga catggaatat gatgatAact ctccaaattc aaagagggag ttacgacccc                      420  
aagggtgtaga tcccaataag ggctgggaat tccgtgggtg gcacagggcc atcatctgtg                      480  
gcaaagttgg acaagtccct gtgcaaaaaa ttttaaggaa tgggcataca gtaaccgttt                      540  
ttactgttgg aactggtggc atgtttgacc agagggtaat tgggcctaag gatttgccaa                      600  
agccagctca gtggcaccgc atagctgtcc ataatgacta cttaagtgtc tatgtgttc                      660  
agaagctggt gaagaattcg caccagacct tcaacatcaa gaatgacttc acccctgagg                      720  
aggaagagga gatccgcagg gagaaccagt gggccttcga gtaaggaggt gctggatcta                      780  
ttgatgcta agtttcgttg tgtctactac tatgtctact ttatgttgc ctaatggttg                      840  
taagtatttt gggagtcact ttgcttgoga atgtctcgcg taagacttat gtggtcaatg                      900  
gtcggttatt aacttattac catgaaagcm ytcgtctgct gcccc

(2) INFORMATION FOR SEQ ID NO:3048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3048:

Lys Pro Phe His Cys Ser Ser Arg Arg Arg Arg Phe Phe Val Phe  
1                      5                      10                      15  
Leu Ala Ala Pro Pro Leu His Leu Pro Leu Ile Arg Ser Leu Pro Pro  
                                 20                      25                      30  
Leu Ala Thr Gln Ala Ala Ala Leu Arg Pro Val Ile Ser Ala Thr Ala  
                                 35                      40                      45  
Ser Xaa Leu Pro Leu Pro Ser Leu Pro Ser Arg Leu Ala Pro Ser Pro  
50                      55                      60  
Pro Val Leu Arg Thr Pro Ala Gly Asp Pro Ala Ser Thr Met Thr Gly  
65                      70                      75                      80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Thr | Gly | Leu | Leu | Thr | Gly | Leu | Arg | Arg | Val | Met | Glu | Gln | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Ile | Ser | Thr | Ala | Phe | Cys | Arg | Gln | Ser | Arg | Val | Ser | Ser | Ser | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ser | Phe | Ser | Asp | Leu | Asp | Glu | Lys | Gly | Asp | Met | Glu | Tyr | Asp | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ser | Pro | Asn | Ser | Lys | Arg | Glu | Leu | Arg | Pro | Gln | Gly | Val | Asp | Pro |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Lys | Gly | Trp | Glu | Phe | Arg | Gly | Val | His | Arg | Ala | Ile | Ile | Cys | Gly |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Lys | Val | Gly | Gln | Val | Pro | Val | Gln | Lys | Ile | Leu | Arg | Asn | Gly | His | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Thr | Val | Phe | Thr | Val | Gly | Thr | Gly | Gly | Met | Phe | Asp | Gln | Arg | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Gly | Pro | Lys | Asp | Leu | Pro | Lys | Pro | Ala | Gln | Trp | His | Arg | Ile | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | His | Asn | Asp | Tyr | Leu | Ser | Ala | Tyr | Ala | Val | Gln | Lys | Leu | Val | Lys |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Ser | His | Glu | Thr | Phe | Asn | Ile | Lys | Asn | Asp | Phe | Thr | Pro | Glu | Glu |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Glu | Glu | Glu | Ile | Arg | Glu | Asn | Gln | Trp | Ala | Phe | Glu |     |     |     |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1575338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3049:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Gly | Val | Ser | Thr | Gly | Leu | Leu | Thr | Gly | Leu | Arg | Arg | Val | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gln | Gln | Arg | Ile | Ser | Thr | Ala | Phe | Cys | Arg | Gln | Ser | Arg | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Thr | Val | Ser | Phe | Ser | Asp | Leu | Asp | Glu | Lys | Gly | Asp | Met | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Asp | Asp | Asn | Ser | Pro | Asn | Ser | Lys | Arg | Glu | Leu | Arg | Pro | Gln | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asp | Pro | Asn | Lys | Gly | Trp | Glu | Phe | Arg | Gly | Val | His | Arg | Ala | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Cys | Gly | Lys | Val | Gly | Gln | Val | Pro | Val | Gln | Lys | Ile | Leu | Arg | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | His | Thr | Val | Thr | Val | Phe | Thr | Val | Gly | Thr | Gly | Gly | Met | Phe | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Arg | Val | Ile | Gly | Pro | Lys | Asp | Leu | Pro | Lys | Pro | Ala | Gln | Trp | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ile | Ala | Val | His | Asn | Asp | Tyr | Leu | Ser | Ala | Tyr | Ala | Val | Gln | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Lys | Asn | Ser | His | Glu | Thr | Phe | Asn | Ile | Lys | Asn | Asp | Phe | Thr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Pro | Glu | Glu | Glu | Glu | Glu | Ile | Arg | Arg | Glu | Asn | Gln | Trp | Ala | Phe | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:3050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..161
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575339
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3050:

Met Glu Gln Gln Arg Ile Ser Thr Ala Phe Cys Arg Gln Ser Arg Val  
1 5 10 15  
Ser Ser Ser Thr Val Ser Phe Ser Asp Leu Asp Glu Lys Gly Asp Met  
20 25 30  
Glu Tyr Asp Asp Asn Ser Pro Asn Ser Lys Arg Glu Leu Arg Pro Gln  
35 40 45  
Gly Val Asp Pro Asn Lys Gly Trp Glu Phe Arg Gly Val His Arg Ala  
50 55 60  
Ile Ile Cys Gly Lys Val Gly Gln Val Pro Val Gln Lys Ile Leu Arg  
65 70 75 80  
Asn Gly His Thr Val Thr Val Phe Thr Val Gly Thr Gly Gly Met Phe  
85 90 95  
Asp Gln Arg Val Ile Gly Pro Lys Asp Leu Pro Lys Pro Ala Gln Trp  
100 105 110  
His Arg Ile Ala Val His Asn Asp Tyr Leu Ser Ala Tyr Ala Val Gln  
115 120 125  
Lys Leu Val Lys Asn Ser His Glu Thr Phe Asn Ile Lys Asn Asp Phe  
130 135 140  
Thr Pro Glu Glu Glu Glu Ile Arg Arg Glu Asn Gln Trp Ala Phe  
145 150 155 160  
Glu

(2) INFORMATION FOR SEQ ID NO:3051:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 762 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..762
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575343
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3051:

acaagtcccts agcgaacctc gccactcgcc cactccgctc ccaaagaaga agaagacgac 60  
gacgacagca argtgccgcc gtcacgagat ycgtecgagg tgaccatgtc tacgcctacg 120  
angaagcgctc ccaggaaaac caacggctcc acgtcgctcg cgtecgccgc gatgcgtcgg 180  
acgacgagcc tgtmggamct cgcgccgcmg ccggatctct ccgggaggcc caagamgcgg 240  
gcggcgaggg ggcattgcgtt ggcagggccca gggaccgagt ggggcgccga gataacgatg 300  
acgcactcgg cggacttctt ccccgccatg gagacggcag ccttctctcaa ggCctgcggg 360  
atctgcaacc gccgcctcgg ccccgccgtt gacaccttca tctacatggg tgaggtggcc 420  
ttctgcagcc aggagtktag gcagcagcag atgaacctcg acgagctcat ggagaagaag 480  
tgctccactc cggctggcgg cggcggttgt ggcgtcggcg gcggcgccgg tggtggctca 540  
gatcagcccc gcaagagcag caccgtagcg gccgcctagc atcgccagag gggtaataac 600  
aacgaagaaa aattttggag ccctgggtggc gtaggcccca aaaacgcagc agtttccatc 660  
agcctatgta tctctgtat ttctggagtc actgtgtgtg tatattggtg ggaaggggaa 720  
ggatgtaggg attccaactg ggggcatggt ttgcaatgca tc

(2) INFORMATION FOR SEQ ID NO:3052:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 192 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..192  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3052:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Pro | Xaa | Arg | Thr | Ser | Pro | Leu | Ala | His | Ser | Ala | Pro | Lys | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Glu | Asp | Asp | Asp | Asp | Ser | Xaa | Val | Pro | Pro | Ser | Arg | Asp | Xaa | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Val | Thr | Met | Ser | Thr | Pro | Thr | Xaa | Lys | Arg | Pro | Arg | Lys | Thr | Asn |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Ser | Thr | Ser | Ser | Ser | Ser | Ser | Ala | Met | Arg | Arg | Thr | Thr | Ser | Leu |
|     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |
| Xaa | Xaa | Leu | Ala | Pro | Xaa | Pro | Asp | Leu | Ser | Gly | Arg | Pro | Lys | Xaa | Arg |
| 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |     |
| Ala | Ala | Arg | Gly | His | Ala | Val | Ala | Gly | Pro | Gly | Thr | Ala | Trp | Gly | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Ile | Thr | Met | Thr | His | Ser | Ala | Asp | Phe | Leu | Pro | Ala | Met | Glu | Thr |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Ala | Phe | Leu | Lys | Ala | Cys | Gly | Ile | Cys | Asn | Arg | Arg | Leu | Gly | Pro |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Asp | Thr | Phe | Ile | Tyr | Met | Gly | Glu | Val | Ala | Phe | Cys | Ser | Gln |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Glu | Xaa | Arg | Gln | Gln | Gln | Met | Asn | Leu | Asp | Glu | Leu | Met | Glu | Lys | Lys |
| 145 |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Cys | Ser | Thr | Pro | Ala | Gly | Gly | Gly | Gly | Gly | Val | Gly | Gly | Gly | Gly | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Gly | Gly | Ser | Asp | Gln | Pro | Gly | Lys | Ser | Ser | Thr | Val | Ala | Ala | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:3053:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 157 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..157  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3053:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Pro | Thr | Xaa | Lys | Arg | Pro | Arg | Lys | Thr | Asn | Gly | Ser | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ser | Ser | Ser | Ser | Ala | Met | Arg | Arg | Thr | Thr | Ser | Leu | Xaa | Xaa | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Pro | Xaa | Pro | Asp | Leu | Ser | Gly | Arg | Pro | Lys | Xaa | Arg | Ala | Ala | Arg |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | His | Ala | Val | Ala | Gly | Pro | Gly | Thr | Ala | Trp | Gly | Ala | Glu | Ile | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Met | Thr | His | Ser | Ala | Asp | Phe | Leu | Pro | Ala | Met | Glu | Thr | Ala | Ala | Phe |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Leu | Lys | Ala | Cys | Gly | Ile | Cys | Asn | Arg | Arg | Leu | Gly | Pro | Gly | Arg | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Thr | Phe | Ile | Tyr | Met | Gly | Glu | Val | Ala | Phe | Cys | Ser | Gln | Glu | Xaa | Arg |
|     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| Gln | Gln | Gln | Met | Asn | Leu | Asp | Glu | Leu | Met | Glu | Lys | Lys | Cys | Ser | Thr |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |

Pro Ala Gly Gly Gly Gly Gly Gly Val Gly Gly Gly Gly Gly Gly Gly  
130 135 140  
Ser Asp Gln Pro Gly Lys Ser Ser Thr Val Ala Ala Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1575346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3054:

Met Arg Arg Thr Thr Ser Leu Xaa Xaa Leu Ala Pro Xaa Pro Asp Leu  
1 5 10 15  
Ser Gly Arg Pro Lys Xaa Arg Ala Ala Arg Gly His Ala Val Ala Gly  
20 25 30  
Pro Gly Thr Ala Trp Gly Ala Glu Ile Thr Met Thr His Ser Ala Asp  
35 40 45  
Phe Leu Pro Ala Met Glu Thr Ala Ala Phe Leu Lys Ala Cys Gly Ile  
50 55 60  
Cys Asn Arg Arg Leu Gly Pro Gly Arg Asp Thr Phe Ile Tyr Met Gly  
65 70 75 80  
Glu Val Ala Phe Cys Ser Gln Glu Xaa Arg Gln Gln Gln Met Asn Leu  
85 90 95  
Asp Glu Leu Met Glu Lys Lys Cys Ser Thr Pro Ala Gly Gly Gly Gly  
100 105 110  
Gly Gly Val Gly Gly Gly Gly Gly Gly Gly Ser Asp Gln Pro Gly Lys  
115 120 125  
Ser Ser Thr Val Ala Ala Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:3055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..699

(D) OTHER INFORMATION: / Ceres Seq. ID 1575351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3055:

accatcact gcagctcaaa cacagaagcg cccaagaag cagcagcgca ggagcgagcg 60  
atcgctatgg ctacgggaag aggcagtgcg acgcgggggc ttgccctcgg cgccctactc 120  
gccgcgcgtt tctcctcct cctcggcgtc gccgacgcgg ccaccacag ggtcgactgg 180  
tcttcaacg cggacagctg gtccaagggc aagagcttcC gtgccggcga cgtcctcgag 240  
ttcaactacg acccctccgt gcacaacgtg gtggccgtgg acgccggcgg ctacaacggc 300  
tgccggccct ccggcacgtc gtacgggtcc gggagcgacc gcatcacgt cggccccggc 360  
accagctact tcactctgcag cttcaacagg cactgcggga tggggatgaa gatggtcgtc 420  
aatgccagct gagcacgacg cttatatgtt agtactgcaa aaatatatgg gctagtgggtg 480  
gtccgataga tcgtgcaaga actcaatcgt gtggcatact cgtaccgtgt gttcgatgga 540  
cacggttcat gtgttgtgta tgcattgcgc tgcgtgtagg tcaggcatga tgtacgtgtg 600  
gctgatggcg tgtagtaaaa gcgtcctgca gctttgttgt tactttgttc gatcgaagca 660  
gcggcttctt ttgtttgttc atcaataaca tctttcatt

(2) INFORMATION FOR SEQ ID NO:3056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..143
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3056:

Thr His His Cys Ser Ser Asn Thr Glu Ala Pro Gln Glu Ala Ala Ala  
1 5 10 15  
Gln Glu Arg Ala Ile Ala Met Ala Gln Gly Arg Gly Ser Ala Thr Arg  
20 25 30  
Gly Leu Ala Leu Gly Ala Leu Leu Ala Ala Phe Leu Leu Leu Leu  
35 40 45  
Gly Val Ala Asp Ala Ala Thr His Arg Val Asp Trp Ser Phe Asn Ala  
50 55 60  
Asp Ser Trp Ser Lys Gly Lys Ser Phe Arg Ala Gly Asp Val Leu Glu  
65 70 75 80  
Phe Asn Tyr Asp Pro Ser Val His Asn Val Val Ala Val Asp Ala Gly  
85 90 95  
Gly Tyr Asn Gly Cys Arg Pro Ser Gly Thr Ser Tyr Gly Ser Gly Ser  
100 105 110  
Asp Arg Ile Thr Leu Gly Pro Gly Thr Ser Tyr Phe Ile Cys Ser Leu  
115 120 125  
Asn Arg His Cys Gly Met Gly Met Lys Met Val Val Asn Ala Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3057:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3057:

Pro Ile Thr Ala Ala Gln Thr Gln Lys Arg Pro Lys Lys Gln Gln Arg  
1 5 10 15  
Arg Ser Glu Arg Ser Leu Trp Leu Arg Glu Glu Ala Val Arg Arg Gly  
20 25 30  
Gly Leu Pro Ser Ala Pro Tyr Ser Pro Pro Leu Ser Ser Ser Ser  
35 40 45  
Ala Ser Pro Thr Arg Pro Pro Thr Gly Ser Thr Gly Pro Ser Thr Arg  
50 55 60  
Thr Ala Gly Pro Arg Ala Arg Ala Ser Val Pro Ala Thr Ser Ser Ser  
65 70 75 80  
Ser Thr Thr Thr Pro Cys Thr Thr Trp Trp Pro Trp Thr Pro Ala  
85 90 95  
Ala Thr Thr Ala Ala Gly Pro Pro Ala Arg Arg Thr Ala Pro Gly Ala  
100 105 110  
Thr Ala Ser Arg Ser Ala Pro Ala Pro Ala Thr Ser Ser Ala Ala Ser  
115 120 125  
Thr Gly Thr Ala Gly Trp Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:3058:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..149  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575354  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3058:

Pro Ser Leu Gln Leu Lys His Arg Ser Ala Pro Arg Ser Ser Ser Ala  
1 5 10 15  
Gly Ala Ser Asp Arg Tyr Gly Ser Gly Lys Arg Gln Cys Asp Ala Gly  
20 25 30  
Ala Cys Pro Arg Arg Pro Thr Arg Arg Phe Pro Pro Pro Arg  
35 40 45  
Arg Arg Arg Arg Gly His Pro Gln Gly Arg Leu Val Leu Gln Arg Gly  
50 55 60  
Gln Leu Val Gln Gly Gln Glu Leu Pro Cys Arg Arg Arg Pro Arg Val  
65 70 75 80  
Gln Leu Arg Pro Leu Arg Ala Gln Arg Gly Gly Arg Gly Arg Arg Arg  
85 90 95  
Leu Gln Arg Leu Pro Ala Leu Arg His Val Val Arg Leu Arg Glu Arg  
100 105 110  
Pro His His Ala Arg Pro Arg His Gln Leu Leu His Leu Gln Pro Gln  
115 120 125  
Gln Ala Leu Arg Asp Gly Asp Glu Asp Gly Arg Gln Cys Gln Leu Ser  
130 135 140  
Thr Thr Leu Ile Cys  
145

- (2) INFORMATION FOR SEQ ID NO:3059:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 685 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..685  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575361

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gacgatgtct cttgccgcgg cgtaacccct cgctccatt ccccgcgcca tcgccgtca   | 60  |
| ggctccttgc gcggcattcc tgtocatccg cttaggtrgc gcgacggcga cgcggttcgc | 120 |
| tggactggcg gtggcctcgc agccagcgga gckwcgcgcc gcggcgatgg tcacgatggc | 180 |
| gaagaggag caggagctgg aggagatccg ggccatgacg acggaacaga tggaagarga  | 240 |
| ggtgtagac ctcaaggggg agcttttctt gctcgcctt aaGcgctcgg cgcgccagga   | 300 |
| gttcaagaac agcgagttca gccgcagtcg caagaggatt gctcgtatgc taaccgtgaa | 360 |
| aagagagcgg gaaattgaac aaggaatcaa taaaagattg tctaggaagc ttgataggaa | 420 |
| atggaagcag agcattgtgg tcagaccacc accatctcta agggggaaca aagaggagta | 480 |
| gaaagccgca aaaagagggc aatgtgcaaa agtcgtttca tgcgagtgtt gcaggaaggt | 540 |
| cccttcatga tttcaacctt tattgcgttg ttatgtattc catgtttaca ttttgctaag | 600 |
| cattgctatc tgaatctgaa tttcagttgt tagtctcttc tgtaaatttc gacttattta | 660 |
| aatttacact tctatctgtg ttatc                                       |     |

- (2) INFORMATION FOR SEQ ID NO:3060:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1575362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3060:

Thr Met Ser Leu Ala Ala Ala Ser Pro Leu Ala Ser Ile Pro Arg Gly  
1 5 10 15  
Ile Ala Ala Gln Ala Pro Cys Ala Ala Phe Leu Ser Ile Arg Leu Gly  
20 25 30  
Xaa Ala Thr Ala Thr Arg Phe Ala Gly Leu Ala Val Ala Ser Gln Pro  
35 40 45  
Ala Glu Xaa Arg Ala Ala Ala Met Val Thr Met Ala Lys Arg Glu Gln  
50 55 60  
Glu Leu Glu Glu Ile Arg Ala Met Thr Thr Glu Gln Met Glu Xaa Glu  
65 70 75 80  
Val Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser  
85 90 95  
Ala Arg Gln Glu Phe Lys Asn Ser Glu Phe Ser Arg Met Arg Lys Arg  
100 105 110  
Ile Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Glu Gln Gly  
115 120 125  
Ile Asn Lys Arg Leu Ser Arg Lys Leu Asp Arg Lys Trp Lys Gln Ser  
130 135 140  
Ile Val Val Arg Pro Pro Pro Ser Leu Arg Gly Asn Lys Glu Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1575363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3061:

Met Ser Leu Ala Ala Ala Ser Pro Leu Ala Ser Ile Pro Arg Gly Ile  
1 5 10 15  
Ala Ala Gln Ala Pro Cys Ala Ala Phe Leu Ser Ile Arg Leu Gly Xaa  
20 25 30  
Ala Thr Ala Thr Arg Phe Ala Gly Leu Ala Val Ala Ser Gln Pro Ala  
35 40 45  
Glu Xaa Arg Ala Ala Ala Met Val Thr Met Ala Lys Arg Glu Gln Glu  
50 55 60  
Leu Glu Glu Ile Arg Ala Met Thr Thr Glu Gln Met Glu Xaa Glu Val  
65 70 75 80  
Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala  
85 90 95  
Arg Gln Glu Phe Lys Asn Ser Glu Phe Ser Arg Met Arg Lys Arg Ile  
100 105 110  
Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Glu Gln Gly Ile  
115 120 125  
Asn Lys Arg Leu Ser Arg Lys Leu Asp Arg Lys Trp Lys Gln Ser Ile  
130 135 140  
Val Val Arg Pro Pro Pro Ser Leu Arg Gly Asn Lys Glu Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:3062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..104  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3062:

Met Val Thr Met Ala Lys Arg Glu Gln Glu Leu Glu Glu Ile Arg Ala  
1                  5                  10                  15  
Met Thr Thr Glu Gln Met Glu Xaa Glu Val Val Asp Leu Lys Gly Glu  
                  20                  25                  30  
Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala Arg Gln Glu Phe Lys Asn  
                  35                  40                  45  
Ser Glu Phe Ser Arg Met Arg Lys Arg Ile Ala Arg Met Leu Thr Val  
                  50                  55                  60  
Lys Arg Glu Arg Glu Ile Glu Gln Gly Ile Asn Lys Arg Leu Ser Arg  
65                  70                  75                  80  
Lys Leu Asp Arg Lys Trp Lys Gln Ser Ile Val Val Arg Pro Pro Pro  
                  85                  90                  95  
Ser Leu Arg Gly Asn Lys Glu Glu  
                  100

(2) INFORMATION FOR SEQ ID NO:3063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..794  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3063:

cagaaggggg caaagctcgc ggcctcgcgt cgcgccgggtc gttccgggtcc aacgcgggcga 60  
cscaaaggct gccgtccccg ggcttcctcc tccccctcac cccttcccct cgmcaaacca 120  
caggaagaag cgagcagggc atcgagtttt ctogatcgat ggcacgcggc cctgccgatt 180  
cctacgggtg cgcggcgctgc ggcgcgcccc tgaacctgtc ggcggcgcac ctgtaccggg 240  
cggacttcta cttcgaggcc gggaacaagg gcacgctgtc cttctcgtgg gtggacgagt 300  
cgcgCctgcg gttcgcgccc gaggaccgca tccgccctt cttcgagacc ctcaactact 360  
ggggcatcca gcggaagcgc acgcgcatca gctgcgnacc tgcggccacc tgcttggcca 420  
skctacgacg acggtccgcc ggccatgcag ggcaccggcc agttcgggat ggggcccgagc 480  
caggtcatcc cgcgcgcgcc caggtaccgc ttcaagatca aggccatcgc cgccagctcc 540  
tcggcacctg ccgcgcgcgc ctatgaaaag tgatgctcca tagatttctt catctggttg 600  
cgtgtcctgt gtgctgtcgg tgctgtggtt cgtgacttcc tgtaaattac gtagcttctt 660  
gcaattcgcg tcttcgcttg ttttcttttag aaacagtgtg tttgaaatgg catgcgactg 720  
aaactatgat tgaaatggca tgcgacttct aatatacaca caagacagaa gatataaata 780  
aaaaactatg attg

(2) INFORMATION FOR SEQ ID NO:3064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..193  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3064:

Arg Arg Gly Gln Ser Ser Arg Pro Arg Val Ala Pro Val Val Pro Val  
1                  5                  10                  15  
Gln Arg Gly Asp Xaa Lys Ala Ala Val Pro Gly Leu Pro Pro Pro

20 25 30  
His Pro Phe Pro Ser Xaa Asn His Arg Lys Lys Arg Ala Gly His Arg  
35 40 45  
Val Phe Ser Ile Asp Gly Ile Gly Ala Cys Arg Phe Leu Arg Val Arg  
50 55 60  
Gly Val Arg Arg Ala Pro Glu Pro Val Gly Gly Ala Pro Val Pro Gly  
65 70 75 80  
Gly Leu Leu Leu Arg Gly Arg Glu Gln Gly His Ala Val Leu Leu Val  
85 90 95  
Gly Gly Arg Val Ala Pro Ala Val Arg Ala Arg Gly Pro His Pro Pro  
100 105 110  
Leu Leu Arg Asp Pro Gln Leu Leu Gly His Pro Ala Glu Ala His Ala  
115 120 125  
His Gln Leu Xaa Thr Cys Gly His Leu Leu Gly Xaa Xaa Thr Thr Thr  
130 135 140  
Val Arg Arg Pro Cys Arg Ala Pro Ala Ser Ser Gly Trp Gly Pro Ala  
145 150 155 160  
Arg Ser Ser Arg Ala Ala Pro Gly Thr Ala Ser Arg Ser Arg Pro Ser  
165 170 175  
Pro Pro Ala Pro Arg His Leu Pro Pro Pro Met Lys Ser Asp Ala  
180 185 190  
Pro

(2) INFORMATION FOR SEQ ID NO:3065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1575388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3065:

Glu Gly Gly Lys Ala Arg Gly Leu Ala Ser Arg Arg Ser Phe Arg Ser  
1 5 10 15  
Asn Ala Ala Xaa Gln Arg Leu Pro Ser Pro Gly Phe Leu Leu Pro Leu  
20 25 30  
Thr Pro Ser Pro Xaa Gln Thr Thr Gly Arg Ser Glu Gln Gly Ile Glu  
35 40 45  
Phe Ser Arg Ser Met Ala Ser Ala Pro Ala Asp Ser Tyr Gly Cys Ala  
50 55 60  
Ala Cys Gly Ala Pro Leu Asn Leu Ser Ala Ala His Leu Tyr Pro Ala  
65 70 75 80  
Asp Phe Tyr Phe Glu Ala Gly Asn Lys Gly Thr Leu Ser Phe Ser Trp  
85 90 95  
Val Asp Glu Ser Arg Leu Arg Phe Ala Pro Glu Asp Arg Ile Arg Pro  
100 105 110  
Phe Phe Glu Thr Leu Asn Tyr Trp Gly Ile Gln Arg Lys Arg Thr Arg  
115 120 125  
Ile Ser Cys Xaa Pro Ala Ala Thr Cys Leu Ala Xaa Leu Arg Arg Arg  
130 135 140  
Ser Ala Gly His Ala Gly His Arg Pro Val Arg Asp Gly Ala Gln Pro  
145 150 155 160  
Gly His Pro Ala Pro Pro Gln Val Pro Leu Gln Asp Gln Gly His Arg  
165 170 175  
Arg Gln Leu Leu Gly Thr Cys Arg Arg Arg Leu  
180 185

(2) INFORMATION FOR SEQ ID NO:3066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575389  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3066:

Met Ala Ser Ala Pro Ala Asp Ser Tyr Gly Cys Ala Ala Cys Gly Ala  
1 5 10 15  
Pro Leu Asn Leu Ser Ala Ala His Leu Tyr Pro Ala Asp Phe Tyr Phe  
20 25 30  
Glu Ala Gly Asn Lys Gly Thr Leu Ser Phe Ser Trp Val Asp Glu Ser  
35 40 45  
Arg Leu Arg Phe Ala Pro Glu Asp Arg Ile Arg Pro Phe Phe Glu Thr  
50 55 60  
Leu Asn Tyr Trp Gly Ile Gln Arg Lys Arg Thr Arg Ile Ser Cys Xaa  
65 70 75 80  
Pro Ala Ala Thr Cys Leu Ala Xaa Leu Arg Arg Arg Ser Ala Gly His  
85 90 95  
Ala Gly His Arg Pro Val Arg Asp Gly Ala Gln Pro Gly His Pro Ala  
100 105 110  
Pro Pro Gln Val Pro Leu Gln Asp Gln Gly His Arg Arg Gln Leu Leu  
115 120 125  
Gly Thr Cys Arg Arg Arg Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:3067:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 836 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..836  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575402  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3067:

atccgatccg agccatatta aacagacgca tgcacgcngc gccgggccgga gcgcacggcg 60  
gcggcgccct cctgcccacc cagcttcgcg ctattagcta gcttgctgca gcagcgtacg 120  
tgcttttcgt tcgtcccgcc ggtcgccatg accttcccgc tggtttgcta ctgctacgcg 180  
gtgccgcgcc ccgtggccgc gctgctcaag ctccctccacg ccgccgtgct cgtgttcgtg 240  
ctgctcctct ccttccctcg cctctacgag ttctcctacg accccgagga tcacgcgcca 300  
ccagccatca acggcgccgc ccccaggcca gaggcggtga agcggcgcc cccgctcgtc 360  
gagttcctgg agctgggtgga ttctgctgctg tcaccgtcgt cgggggtggg ggccgaGCcg 420  
acgtgccggg tgtgcctcga gtggcttgag gccaaaggacg aggtgcggcg gctgggcaac 480  
tgcacccaac cgttccacac gcgctgcatc gaccgctgga tcgacctggg cgaggtgacg 540  
tgcccgcctt gccgttccca cctgctgccc cggcgccgcg ccggcctact cagcatggca 600  
cggtcgggct agtcgcgcgt ccttggttcc cttcatccct taattgccag tacgatacgt 660  
gcccgtgcac agccgtgcct ggcttcaggc cagcgcgcg cggtcgttac gcgcacagat 720  
gccactgggc actggtgcgc gatgggggca gaccatgaga ccaaccgtga actaggacga 780  
ctgtctatgt aaagaatttt ttccggtcaa tggatggcg caagccaaat tactwg

(2) INFORMATION FOR SEQ ID NO:3068:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1575403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3068:

Met Thr Phe Pro Leu Val Cys Tyr Cys Tyr Ala Val Pro Arg Pro Val  
1 5 10 15  
Ala Ala Leu Leu Lys Leu Leu His Ala Ala Val Leu Val Phe Val Leu  
20 25 30  
Leu Leu Ser Phe Leu Gly Leu Tyr Glu Phe Ser Tyr Asp Pro Glu Asp  
35 40 45  
His Ala Pro Pro Ala Ile Asn Gly Gly Arg Pro Arg Pro Glu Ala Val  
50 55 60  
Lys Arg Arg Leu Pro Leu Val Glu Phe Leu Glu Leu Val Asp Ser Ser  
65 70 75 80  
Ser Ser Pro Ser Ser Gly Val Gly Ala Glu Pro Thr Cys Arg Val Cys  
85 90 95  
Leu Glu Trp Leu Glu Ala Lys Asp Glu Val Arg Arg Leu Gly Asn Cys  
100 105 110  
Thr His Ala Phe His Thr Arg Cys Ile Asp Arg Trp Ile Asp Leu Gly  
115 120 125  
Glu Val Thr Cys Pro Leu Cys Arg Ser His Leu Leu Pro Arg Arg Arg  
130 135 140  
Ala Gly Leu Leu Ser Met Ala Arg Leu Gly  
145 150

(2) INFORMATION FOR SEQ ID NO:3069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 674 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1575404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3069:

catcaacaat gatgcctcta aggtgaactc tcatgggtcca catcagagtt ctgggtccac 60  
tttgctatgg gagaaaaatg agcctccagt caatcctacc cgctacaact tgtccgcatt 120  
tgcaataaca ctaaatgagt taacaccaga gctcgaggag aagctgccac cgacggattc 180  
aaggctgaga ccagatcaac ggcacctgga gaatggggag tacgagaagg ccaatgctga 240  
aaaactgctc ctcgagacac agcaacggat ggcaaggaag atgcaggaga gtggctggaa 300  
accaagatgg ttccaaaggg acagcgagga tggaacgtac cgctacgtcg gaggttactg 360  
ggaggcaagg gagcagagaa catgggtcgg ctgcaatgac atatttggtg acttgtctag 420  
cagccagaag ctcccaccat ccgctctcta cactgagctga agtatatagg ggtgggtaag 480  
gcgggaagg catgttcagt agttgttgac atcgattaa ccagagggtt tttctctcgt 540  
ttctgWtttg tgtaagctg tgagctaaca tgtttttctt gtcaattgtc acattgaagc 600  
caaggacatc caagcataac ccaacctttt gtcgatacta ggatacttat gagagatctt 660  
gtggacatta ttgc

(2) INFORMATION FOR SEQ ID NO:3070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1575405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3070:

Ile Asn Asn Asp Ala Ser Lys Val Asn Ser His Gly Pro His Gln Ser  
1 5 10 15  
Ser Gly Ser Thr Leu Leu Trp Glu Lys Asn Glu Pro Pro Val Asn Pro  
20 25 30  
Thr Arg Tyr Asn Leu Ser Ala Phe Ala Ile Thr Leu Asn Glu Leu Thr  
35 40 45  
Pro Glu Leu Glu Glu Lys Leu Pro Pro Thr Asp Ser Arg Leu Arg Pro  
50 55 60  
Asp Gln Arg His Leu Glu Asn Gly Glu Tyr Glu Lys Ala Asn Ala Glu  
65 70 75 80  
Lys Leu Arg Leu Glu Thr Gln Gln Arg Met Ala Arg Lys Met Gln Glu  
85 90 95  
Ser Gly Trp Lys Pro Arg Trp Phe Gln Arg Asp Ser Glu Asp Gly Thr  
100 105 110  
Tyr Arg Tyr Val Gly Gly Tyr Trp Glu Ala Arg Glu Gln Arg Thr Trp  
115 120 125  
Val Gly Cys Asn Asp Ile Phe Gly Asn Leu Ser Ser Ser Gln Lys Leu  
130 135 140  
Pro Pro Ser Ala Leu Tyr Thr Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:3071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3071:

Met Gly Ser Thr Arg Arg Pro Met Leu Lys Asn Cys Ala Ser Arg His  
1 5 10 15  
Ser Asn Gly Trp Gln Gly Arg Cys Arg Arg Val Ala Gly Asn Gln Asp  
20 25 30  
Gly Ser Lys Gly Thr Ala Arg Met Glu Arg Thr Ala Thr Ser Glu Val  
35 40 45  
Thr Gly Arg Gln Gly Ser Arg Glu His Gly Ser Ala Ala Met Thr Tyr  
50 55 60  
Leu Val Thr Cys Leu Ala Ala Arg Ser Ser His His Pro Leu Ser Thr  
65 70 75 80  
Arg Ala Glu Val Tyr Arg Gly Gly  
85

(2) INFORMATION FOR SEQ ID NO:3072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3072:

Met Leu Lys Asn Cys Ala Ser Arg His Ser Asn Gly Trp Gln Gly Arg  
1 5 10 15  
Cys Arg Arg Val Ala Gly Asn Gln Asp Gly Ser Lys Gly Thr Ala Arg  
20 25 30  
Met Glu Arg Thr Ala Thr Ser Glu Val Thr Gly Arg Gln Gly Ser Arg

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 35  |     | 40  |     | 45  |     |     |     |     |     |     |     |     |     |     |
| Glu | His | Gly | Ser | Ala | Ala | Met | Thr | Tyr | Leu | Val | Thr | Cys | Leu | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ser | Ser | His | His | Pro | Leu | Ser | Thr | Arg | Ala | Glu | Val | Tyr | Arg | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..521

(D) OTHER INFORMATION: / Ceres Seq. ID 1575428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3073:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| cgtttatctc | ttcttccact | gcctcccaac | caCttcgtcc | tcgccggctc  | gcaactcctt | 60  |
| gatggcggcc | acggcgagtc | tcactaccac | tgctccctcc | cctccagctc  | tcctcaaagc | 120 |
| atcagctcct | ttgcttatct | cctttcgccc | cgtctcccgc | cactgcaaga  | acctgtgcat | 180 |
| caagaccaag | gccacagaaa | atgatcagtc | tgctaaaaag | catcagaagg  | tgaagagcat | 240 |
| tctttgccag | gactgcgaag | gaaatggggc | aatcacatgc | accaaattgtg | aaggaaatgg | 300 |
| ggtaaattct | gttgactatt | ttgaaggccg | atttaaagct | ggatctttat  | gctggttgtc | 360 |
| agaattgggt | cggcaggtgt | ctaataaagg | cttcctgttg | ggaaagaatt  | ggatccacgg | 420 |
| gcagctttta | gtcattttgt | tggaggcatt | ggattcattg | gagggtcgat  | ttgtgattgt | 480 |
| aatcacgatt | aatgtaatgg | attggaaatt | cgaaggggc  | c           |            |     |

(2) INFORMATION FOR SEQ ID NO:3074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1575429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3074:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Leu | Phe | Phe | His | Cys | Leu | Pro | Thr | Thr | Ser | Ser | Ser | Pro | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asn | Ser | Leu | Met | Ala | Ala | Thr | Ala | Ser | Leu | Thr | Thr | Thr | Ala | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Pro | Pro | Ala | Leu | Leu | Lys | Ala | Ser | Ala | Pro | Leu | Leu | Ile | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Pro | Val | Ser | Arg | His | Cys | Lys | Asn | Leu | Cys | Ile | Lys | Thr | Lys | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Glu | Asn | Asp | Gln | Ser | Ala | Lys | Lys | His | Gln | Lys | Val | Lys | Ser | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Cys | Gln | Asp | Cys | Glu | Gly | Asn | Gly | Ala | Ile | Thr | Cys | Thr | Lys | Cys |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Glu | Gly | Asn | Gly | Val | Asn | Ser | Val | Asp | Tyr | Phe | Glu | Gly | Arg | Phe | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Gly | Ser | Leu | Cys | Trp | Leu | Ser | Glu | Leu | Val | Arg | Gln | Val | Ser | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Gly | Phe | Leu | Leu | Gly | Lys | Asn | Trp | Ile | His | Gly | Gln | Leu | Leu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Cys | Leu | Glu | Ala | Leu | Asp | Ser | Leu | Glu | Gly | Arg | Phe | Val | Ile | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Thr | Ile | Asn | Val | Met | Asp | Trp | Lys | Phe | Gly | Arg | Gly |     |     |     |

165

170

(2) INFORMATION FOR SEQ ID NO:3075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3075:

Met Ala Ala Thr Ala Ser Leu Thr Thr Thr Ala Pro Ser Pro Pro Ala  
1 5 10 15  
Leu Leu Lys Ala Ser Ala Pro Leu Leu Ile Ser Phe Arg Pro Val Ser  
20 25 30  
Arg His Cys Lys Asn Leu Cys Ile Lys Thr Lys Ala Thr Glu Asn Asp  
35 40 45  
Gln Ser Ala Lys Lys His Gln Lys Val Lys Ser Ile Leu Cys Gln Asp  
50 55 60  
Cys Glu Gly Asn Gly Ala Ile Thr Cys Thr Lys Cys Glu Gly Asn Gly  
65 70 75 80  
Val Asn Ser Val Asp Tyr Phe Glu Gly Arg Phe Lys Ala Gly Ser Leu  
85 90 95  
Cys Trp Leu Ser Glu Leu Val Arg Gln Val Ser Asn Lys Gly Phe Leu  
100 105 110  
Leu Gly Lys Asn Trp Ile His Gly Gln Leu Leu Val Ile Cys Leu Glu  
115 120 125  
Ala Leu Asp Ser Leu Glu Gly Arg Phe Val Ile Val Ile Thr Ile Asn  
130 135 140  
Val Met Asp Trp Lys Phe Gly Arg Gly  
145 150

(2) INFORMATION FOR SEQ ID NO:3076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..854
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3076:

gtagaggtct tttactaaca gggaaagga agggatggcc acagcgcgcc tgctccgttg 60  
cgctcctcc accttccctt tcagcacctg caccaccaat ccgttgcgct cgtrctcccc 120  
tctcgccgc mgccagcacc cccgcgcgc catggccacg gactcctccg ccgcctcggt 180  
ccagaagatc cagatccagc gcgaggacac cacttttgat gcttatgttg ttggcaaaga 240  
aaatgctcct ggaattgtgg ttttgcaaga atagtgrrcg ccgttggtgac caagggccac 300  
gacgagggga tgaaggcrgc ggcggcgctg ctggaggagt tcgggctccc gccggggctg 360  
ctgccgctgg aggacgtkac ggaggtgggg ttctgtgcgg ccaccggcta cttctggctc 420  
gcgcaGCgca agaaggtgga gcaccgggtc cgcaagatcg gcaagcaggt gagctacgac 480  
gtcgagatcg ccggctaogt ccggcccagg ggcatacagg ggtcaaggcc ggtcaaggcc 540  
aaggagctcg tgctctggcc gcccgctccac gagatggccg tcgacgacga cccgcccacc 600  
ggcaagatcc acttcaagag cctgcgcggc gtcaccaaga ccttccccgt tgannbcttc 660  
gccgcccggc agtagccacc caccgctacc atcttatatt atcactataa taatacatca 720  
tacaccatta tatatggcgc atatatatag tattaattaa tctcttgtgt tactacctta 780  
tatatatgtt atgtgtgtac ttgctttgct aatcctgatg atgatgaaga acgtaacctc 840  
tagtTTTTTT cctg

(2) INFORMATION FOR SEQ ID NO:3077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1575436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3077:

Arg Gly Leu Leu Leu Thr Gly Lys Gly Lys Gly Trp Pro Gln Arg Ala  
1 5 10 15  
Cys Ser Val Ala Pro Pro Pro Pro Ser Phe Ser Ala Pro Ala Pro Pro  
20 25 30  
Ile Arg Cys Ala Arg Xaa Pro Leu Ser Ser Xaa Ala Ser Thr Pro Ala  
35 40 45  
Pro Pro Trp Pro Arg Thr Pro Pro Pro Arg Ser Arg Arg Ser Arg  
50 55 60  
Ser Ser Ala Arg Thr Pro Leu Leu Met Leu Met Leu Leu Ala Lys Lys  
65 70 75 80  
Met Leu Leu Glu Leu Trp Phe Cys Lys Asn Ser Xaa Arg Gly Gly Asp  
85 90 95  
Gln Gly Pro Arg Arg Gly Asp Glu Gly Xaa Gly Gly Ala Ala Gly Gly  
100 105 110  
Val Arg Ala Pro Ala Gly Ala Ala Ala Gly Gly Arg Xaa Gly Gly  
115 120 125  
Gly Val Arg Ala Gly His Arg Leu Leu Leu Ala Arg Ala Ala Gln Glu  
130 135 140  
Gly Gly Ala Pro Val Pro Gln Asp Arg Gln Ala Gly Glu Leu Arg Arg  
145 150 155 160  
Arg Asp Arg Arg Leu Arg Pro Ala Gln Gly His Gln Glu Ala Gln Gly  
165 170 175  
Gly Gln Gly Gln Gly Ala Arg Ala Leu Ala Ala Arg Pro Arg Asp Gly  
180 185 190  
Arg Arg Arg Arg Pro Ala His Arg Gln Asp Pro Leu Gln Glu Pro Arg  
195 200 205  
Arg Arg His Gln Asp Leu Pro Arg  
210 215

(2) INFORMATION FOR SEQ ID NO:3078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1575437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3078:

Met Leu Met Leu Leu Ala Lys Lys Met Leu Leu Glu Leu Trp Phe Cys  
1 5 10 15  
Lys Asn Ser Xaa Arg Gly Gly Asp Gln Gly Pro Arg Arg Gly Asp Glu  
20 25 30  
Gly Xaa Gly Gly Ala Ala Gly Gly Val Arg Ala Pro Ala Gly Ala Ala  
35 40 45  
Ala Ala Gly Gly Arg Xaa Gly Gly Val Arg Ala Gly His Arg Leu  
50 55 60  
Leu Leu Ala Arg Ala Ala Gln Glu Gly Gly Ala Pro Val Pro Gln Asp  
65 70 75 80



Arg Gln Ala Gly Glu Leu Arg Arg Arg Asp Arg Arg Leu Arg Pro Ala  
85 90 95  
Gln Gly His Gln Glu Ala Gln Gly Gly Gln Gly Gln Gly Ala Arg Ala  
100 105 110  
Leu Ala Ala Arg Pro Arg Asp Gly Arg Arg Arg Arg Pro Ala His Arg  
115 120 125  
Gln Asp Pro Leu Gln Glu Pro Arg Arg Arg His Gln Asp Leu Pro Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1575438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3079:

Met Leu Leu Ala Lys Lys Met Leu Leu Glu Leu Trp Phe Cys Lys Asn  
1 5 10 15  
Ser Xaa Arg Gly Gly Asp Gln Gly Pro Arg Arg Gly Asp Glu Gly Xaa  
20 25 30  
Gly Gly Ala Ala Gly Gly Val Arg Ala Pro Ala Gly Ala Ala Ala  
35 40 45  
Gly Gly Arg Xaa Gly Gly Gly Val Arg Ala Gly His Arg Leu Leu Leu  
50 55 60  
Ala Arg Ala Ala Gln Glu Gly Gly Ala Pro Val Pro Gln Asp Arg Gln  
65 70 75 80  
Ala Gly Glu Leu Arg Arg Arg Asp Arg Arg Leu Arg Pro Ala Gln Gly  
85 90 95  
His Gln Glu Ala Gln Gly Gly Gln Gly Gln Gly Ala Arg Ala Leu Ala  
100 105 110  
Ala Arg Pro Arg Asp Gly Arg Arg Arg Pro Ala His Arg Gln Asp  
115 120 125  
Pro Leu Gln Glu Pro Arg Arg Arg His Gln Asp Leu Pro Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..826

(D) OTHER INFORMATION: / Ceres Seq. ID 1575439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3080:

gcagataaca accagcaatg gtcacgactg ccgctcgccggc ggtcgccggc gccgtgccgc 60  
cagctcggaag agcccaagcg gtaactgtgg ccacaaccac agcactacct cccaccctca 120  
ctagaaggca gtcctcgcc gcggctgccca ccggtccac cctccccacg gccgccgcct 180  
cagctgcggc cccaggttc gccgagattc cgggctccgg cggcgtgaag gccctggacc 240  
tccgggaagg ttcgggagag atcccggccg ttggcgacca ggttgccggt cactattatg 300  
ggagattagc agcgaaGcaa ggatggcgct tcgattcgac gtatgatcac aaggacgaga 360  
ccggcgatcc catgccgttt gtcttcaccc ttgggtccgg caaggttata cctggcatgg 420  
aagcagcagt gaagtccatg agagtcggcg gtcttcgccg agtgatcatt ccaccatcgc 480  
agggatacca aaacacgtca caagaaccgg ttctctctaa tttctttgat cggcagaggc 540

tggttcaccac tatattcaac ccgacgcgcc tcgcaaatgg cgagggttcc actctcggca 600  
cacttatctt cgacatcgag ctaatcaaca ttaggcaacg ttcataactg ttctgctcca 660  
tactcttggtg tctaaaaagt tggtccgtgc aagaatctgg ttatgcttta agtaactgtc 720  
agcgctcttc ggtcaatccc caattacata ttgtaatgca tactgatcgc tgacagacga 780  
tatatgaaga aaaatcaatt gaatgcggat ttgattccgt tgttct

(2) INFORMATION FOR SEQ ID NO:3081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1575440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3081:

Met Val Thr Thr Ala Val Ala Ala Val Ala Gly Ala Val Pro Pro Ala  
1 5 10 15  
Arg Lys Ala Gln Ala Val Thr Val Ala Thr Thr Thr Ala Leu Pro Pro  
20 25 30  
Thr Leu Thr Arg Arg Gln Leu Leu Ala Ala Val Ala Thr Gly Ser Thr  
35 40 45  
Leu Pro Thr Ala Ala Ala Ser Ala Ala Ala Pro Arg Phe Ala Glu Ile  
50 55 60  
Pro Gly Ser Gly Gly Val Lys Ala Leu Asp Leu Arg Glu Gly Ser Gly  
65 70 75 80  
Glu Ile Pro Ala Val Gly Asp Gln Val Ala Val His Tyr Tyr Gly Arg  
85 90 95  
Leu Ala Ala Lys Gln Gly Trp Arg Phe Asp Ser Thr Tyr Asp His Lys  
100 105 110  
Asp Glu Thr Gly Asp Pro Met Pro Phe Val Phe Thr Leu Gly Ser Gly  
115 120 125  
Lys Val Ile Pro Gly Met Glu Ala Ala Val Lys Ser Met Arg Val Gly  
130 135 140  
Gly Leu Arg Arg Val Ile Ile Pro Pro Ser Gln Gly Tyr Gln Asn Thr  
145 150 155 160  
Ser Gln Glu Pro Val Pro Pro Asn Phe Phe Asp Arg Gln Arg Leu Phe  
165 170 175  
Thr Thr Ile Phe Asn Pro Thr Arg Leu Ala Asn Gly Glu Gly Ser Thr  
180 185 190  
Leu Gly Thr Leu Ile Phe Asp Ile Glu Leu Ile Asn Ile Arg Gln Arg  
195 200 205  
Ser

(2) INFORMATION FOR SEQ ID NO:3082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1575441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3082:

ctcgtctcca ctgctctgct gtcctcgc cgcgcgcgc cgcgcgcgc ggcacgtaat 60  
gGcttccgcc gcggtgctcc ggaacgcgc ctcccggcgc ctcttctcct accctactct 120  
ccgcgcgcgt gcgatatatg taccttctgc gctacccgat gcgcccgcgc cggcggcagc 180  
gccggNccca gccgccaccg acggccggga ccctctgggc gaggtctatg gccaccttca 240

cgcgacagaa gccccatgtg aatgtcggca ccattgggca cgtcgatcac ggcaaaacca 300  
ctctcactgc tgccattacc aaggtcctgg ccgaggcagg gaaggccaaa gccgttgctt 360  
tcgacgagat cgacaaggct ccggaggaga aagccagagg aatcaccatt gcgacagCtc 420  
acgtcgagta tgagacggct aaaaggcatt atgtcacgt tgattgtcca ggtcacgcag 480  
attatgtcaa gaacatgatc actggagctg ctcagcgttt cctgtgttc

(2) INFORMATION FOR SEQ ID NO:3083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1575442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3083:

Ser Ser Pro Leu Cys Cys Ser Ser His Arg Arg Arg Arg Arg Arg Arg  
1 5 10 15  
Ser Asp Val Met Ala Ser Ala Ala Val Leu Arg Asn Ala Gly Ser Arg  
20 25 30  
Arg Leu Phe Ser Tyr Pro Thr Leu Arg Ala Ala Ala Ile Tyr Val Pro  
35 40 45  
Ser Ala Leu Pro Asp Ala Pro Ala Ala Ala Ala Pro Xaa Pro Ala  
50 55 60  
Ala Thr Asp Gly Arg Asp Pro Leu Gly Glu Val Tyr Gly His Leu His  
65 70 75 80  
Ala His Glu Ala Pro Cys Glu Cys Arg His His Trp Ala Arg Arg Ser  
85 90 95  
Arg Gln Asn His Ser His Cys Cys His Tyr Gln Gly Pro Gly Arg Gly  
100 105 110  
Arg Glu Gly Gln Ser Arg Cys Phe Arg Arg Asp Arg Gln Gly Ser Gly  
115 120 125  
Gly Glu Ser Gln Arg Asn His His Cys Asp Ser Ser Arg Arg Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1575443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3084:

Met Ala Ser Ala Ala Val Leu Arg Asn Ala Gly Ser Arg Arg Leu Phe  
1 5 10 15  
Ser Tyr Pro Thr Leu Arg Ala Ala Ala Ile Tyr Val Pro Ser Ala Leu  
20 25 30  
Pro Asp Ala Pro Ala Ala Ala Ala Pro Xaa Pro Ala Ala Thr Asp  
35 40 45  
Gly Arg Asp Pro Leu Gly Glu Val Tyr Gly His Leu His Ala His Glu  
50 55 60  
Ala Pro Cys Glu Cys Arg His His Trp Ala Arg Arg Ser Arg Gln Asn  
65 70 75 80  
His Ser His Cys Cys His Tyr Gln Gly Pro Gly Arg Gly Arg Glu Gly  
85 90 95  
Gln Ser Arg Cys Phe Arg Arg Asp Arg Gln Gly Ser Gly Gly Glu Ser  
100 105 110

Gln Arg Asn His His Cys Asp Ser Ser Arg Arg Val  
115 120

(2) INFORMATION FOR SEQ ID NO:3085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3085:

Met Tyr Leu Leu Arg Tyr Pro Met Arg Pro Arg Arg Arg Gln Arg Arg  
1 5 10 15  
Xaa Gln Pro Pro Pro Thr Ala Gly Thr Leu Trp Ala Arg Ser Met Ala  
20 25 30  
Thr Phe Thr Arg Thr Lys Pro His Val Asn Val Gly Thr Ile Gly His  
35 40 45  
Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile Thr Lys Val Leu  
50 55 60  
Ala Glu Ala Gly Lys Ala Lys Ala Val Ala Phe Asp Glu Ile Asp Lys  
65 70 75 80  
Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Ala Thr Ala His Val  
85 90 95  
Glu Tyr Glu Thr Ala Lys Arg His Tyr Ala His Val Asp Cys Pro Gly  
100 105 110  
His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala Ala Gln Arg Phe  
115 120 125  
Leu Cys  
130

(2) INFORMATION FOR SEQ ID NO:3086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3086:

atttctcctc ccactcccaa ccaaaccgctc gctaactatc actagtcgcc gtgtggtggt 60  
cgctgctcata tccctcgccct ctgcctcgac cgcccgatcg cccatagcct gctggcctgc 120  
tctgctagcc atggaccggt ccaagtcgta cgcgggcggg cgcatgcaga tcgagccgta 180  
ctacggcggc ggcggcggcg gaggaggagg cgcgcgggcg gacttcgggt cctactccta 240  
cagcgccggc gggacggggc cgtcgtccta ctctacaac cagtacgagt acggaggccc 300  
gggggcgggt gaggaggagg tgaagcagag caagtcgaag cggcgggtgc tggcggaccc 360  
ggacatggac cgcaaGcgcc cgcgtggcgg cgtacaaggc gtacggcgtg gagggcaggg 420  
tgaagggtc cctccgcaag agcttcagggt gggtaagga ccgctacctc gacctcgtct 480  
acggttggtc ttgatcccta gagcacgcac accaccgctc tccatggttg ttgtttggct 540  
ctcgtagatg ttgttcattc ttcttggtga tgtgaaacca accagtacag tgtatgtatt 600  
catgagatgt gtgactcaag aggttggttc ag

(2) INFORMATION FOR SEQ ID NO:3087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1575461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3087:

Phe Leu Leu Pro Leu Pro Thr Lys Pro Ser Leu Thr Ile Thr Ser Arg  
1 5 10 15  
Arg Val Val Val Val Ile Ser Leu Ala Ser Ala Ser Thr Ala Arg  
20 25 30  
Ser Pro Ile Ala Cys Trp Pro Ala Leu Leu Ala Met Asp Arg Ser Lys  
35 40 45  
Ser Tyr Ala Gly Gly Arg Met Gln Ile Glu Pro Tyr Tyr Gly Gly Gly  
50 55 60  
Gly Gly Gly Gly Gly Gly Ala Arg Ala Asp Phe Arg Ser Tyr Ser Tyr  
65 70 75 80  
Ser Ala Gly Gly Thr Gly Pro Ser Ser Tyr Ser Tyr Asn Gln Tyr Glu  
85 90 95  
Tyr Gly Gly Pro Gly Ala Gly Glu Glu Val Lys Gln Ser Lys Ser  
100 105 110  
Lys Arg Arg Trp Leu Ala Asp Pro Asp Met Asp Arg Lys Arg Pro Arg  
115 120 125  
Gly Gly Val Gln Gly Val Arg Arg Gly Gly Gln Gly Glu Gly Leu Pro  
130 135 140  
Pro Gln Glu Leu Gln Val Gly Gln Gly Pro Leu Pro Arg Pro Arg Leu  
145 150 155 160  
Arg Leu Val Leu Ile Leu Arg Ala Arg Thr Pro Pro Leu Ser Met Val  
165 170 175  
Val Val Trp Leu Ser  
180

(2) INFORMATION FOR SEQ ID NO:3088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1575462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3088:

Met Asp Arg Ser Lys Ser Tyr Ala Gly Gly Arg Met Gln Ile Glu Pro  
1 5 10 15  
Tyr Tyr Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Arg Ala Asp Phe  
20 25 30  
Arg Ser Tyr Ser Tyr Ser Ala Gly Gly Thr Gly Pro Ser Ser Tyr Ser  
35 40 45  
Tyr Asn Gln Tyr Glu Tyr Gly Gly Pro Gly Ala Gly Glu Glu Glu Val  
50 55 60  
Lys Gln Ser Lys Ser Lys Arg Arg Trp Leu Ala Asp Pro Asp Met Asp  
65 70 75 80  
Arg Lys Arg Pro Arg Gly Gly Val Gln Gly Val Arg Arg Gly Gly Gln  
85 90 95  
Gly Glu Gly Leu Pro Pro Gln Glu Leu Gln Val Gly Gln Gly Pro Leu  
100 105 110  
Pro Arg Pro Arg Leu Arg Leu Val Leu Ile Leu Arg Ala Arg Thr Pro  
115 120 125  
Pro Leu Ser Met Val Val Val Trp Leu Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:3089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3089:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ile | Glu | Pro | Tyr | Tyr | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Gly |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Arg | Ala | Asp | Phe | Arg | Ser | Tyr | Ser | Tyr | Ser | Ala | Gly | Gly | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Ser | Tyr | Ser | Tyr | Asn | Gln | Tyr | Glu | Tyr | Gly | Gly | Pro | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gly | Glu | Glu | Glu | Val | Lys | Gln | Ser | Lys | Ser | Lys | Arg | Arg | Trp | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Asp | Pro | Asp | Met | Asp | Arg | Lys | Arg | Pro | Arg | Gly | Gly | Val | Gln | Gly |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Arg | Arg | Gly | Gly | Gln | Gly | Glu | Gly | Leu | Pro | Pro | Gln | Glu | Leu | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Gln | Gly | Pro | Leu | Pro | Arg | Pro | Arg | Leu | Arg | Leu | Val | Leu | Ile |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ala | Arg | Thr | Pro | Pro | Leu | Ser | Met | Val | Val | Val | Trp | Leu | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:3090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3090:

|            |             |             |             |             |            |     |
|------------|-------------|-------------|-------------|-------------|------------|-----|
| aaaaattcca | agagatgaac  | atcttgttga  | gtcacttggtg | ttgctgcatt  | cttattctag | 60  |
| gcatctacgc | tccgacatcc  | gccacatcag  | acaatcctcc  | tctgcaggat  | gtatgcccc  | 120 |
| tggctcccca | ggcgagcgg   | cgagagttgt  | ccatgaacgg  | gttcctctgc  | aagcatccga | 180 |
| gcaccatcct | ggcgctccgac | ttcaagactc  | tgatgctaaa  | ccacgccgga  | gacctggaca | 240 |
| gcatagCctc | ggtcgtcggg  | gagcatgggtg | accgctgccg  | agttcccagg  | cctgaacacc | 300 |
| ctgggcctgt | cgatggcgcg  | caccgacatc  | gCccctaocg  | gggtgggtgct | cccgcactoc | 360 |
| cacccgcggg | cgtcggagat  | gatgttcgta  | cacgggtggca | gcgtgggtggc | cggcttcctg | 420 |
| gacaccgagg | gcaggctggt  | ccagaagcgt  | ctcggtgagg  | gagaggtggt  | cgtcttcccc | 480 |
| cgcggcttgc | ttcactacgt  | catgaactac  | ggtttcggcc  | tcgcgacggc  | gttctccgtg | 540 |
| ctgaacagcc | agaaccccgg  | cgtgggtcgg  | gtcgcccaocg | ccatgttttt  | tcgagtgag  | 600 |
| tcggacgtag | tcgaaggtct  | aatggccagg  | atgctcaagt  | ttggagagat  | ggaggtgact | 660 |
| agtgacaaca | acatcactgc  | tggtttccca  | tgggcattct  | gatctgagta  | ggtgcaattc | 720 |
| aagatcgttg | gtggtttaag  | ttccc       |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:3091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1575489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3091:

Lys Phe Gln Glu Met Asn Ile Leu Leu Ser His Leu Cys Cys Cys Ile  
1 5 10 15  
Leu Ile Leu Gly Ile Tyr Ala Pro Thr Ser Ala Thr Ser Asp Asn Pro  
20 25 30  
Pro Leu Gln Asp Val Cys Pro Met Ala Pro Gln Gly Glu Arg Arg Glu  
35 40 45  
Leu Ser Met Asn Gly Phe Leu Cys Lys His Pro Ser Thr Ile Leu Ala  
50 55 60  
Ser Asp Phe Lys Thr Leu Met Leu Asn His Ala Gly Asp Leu Asp Ser  
65 70 75 80  
Ile Ala Ser Val Val Gly Glu His Gly Asp Arg Cys Arg Val Pro Arg  
85 90 95  
Pro Glu His Pro Gly Pro Val Asp Gly Ala His Arg His Arg Pro Leu  
100 105 110  
Arg Gly Gly Ala Pro Ala Leu Pro Pro Ala Gly Val Gly Asp Asp Val  
115 120 125  
Arg Thr Arg Trp Gln Arg Gly Gly Arg Leu Pro Gly His Arg Gly Gln  
130 135 140  
Ala Val Pro Glu Ala Ser Arg  
145 150

(2) INFORMATION FOR SEQ ID NO:3092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1575490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3092:

Met Asn Ile Leu Leu Ser His Leu Cys Cys Cys Ile Leu Ile Leu Gly  
1 5 10 15  
Ile Tyr Ala Pro Thr Ser Ala Thr Ser Asp Asn Pro Pro Leu Gln Asp  
20 25 30  
Val Cys Pro Met Ala Pro Gln Gly Glu Arg Arg Glu Leu Ser Met Asn  
35 40 45  
Gly Phe Leu Cys Lys His Pro Ser Thr Ile Leu Ala Ser Asp Phe Lys  
50 55 60  
Thr Leu Met Leu Asn His Ala Gly Asp Leu Asp Ser Ile Ala Ser Val  
65 70 75 80  
Val Gly Glu His Gly Asp Arg Cys Arg Val Pro Arg Pro Glu His Pro  
85 90 95  
Gly Pro Val Asp Gly Ala His Arg His Arg Pro Leu Arg Gly Gly Ala  
100 105 110  
Pro Ala Leu Pro Pro Ala Gly Val Gly Asp Asp Val Arg Thr Arg Trp  
115 120 125  
Gln Arg Gly Gly Arg Leu Pro Gly His Arg Gly Gln Ala Val Pro Glu  
130 135 140  
Ala Ser Arg  
145

(2) INFORMATION FOR SEQ ID NO:3093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..145  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3093:

Met Val Thr Ala Ala Glu Phe Pro Gly Leu Asn Thr Leu Gly Leu Ser  
1                  5                  10                  15  
Met Ala Arg Thr Asp Ile Ala Pro Tyr Gly Val Val Leu Pro His Ser  
                  20                  25                  30  
His Pro Arg Ala Ser Glu Met Met Phe Val His Gly Gly Ser Val Val  
                  35                  40                  45  
Ala Gly Phe Leu Asp Thr Glu Gly Arg Leu Phe Gln Lys Arg Leu Gly  
50                  55                  60  
Glu Gly Glu Val Phe Val Phe Pro Arg Gly Leu Leu His Tyr Val Met  
65                  70                  75                  80  
Asn Tyr Gly Phe Gly Leu Ala Thr Ala Phe Ser Val Leu Asn Ser Gln  
                  85                  90                  95  
Asn Pro Gly Val Val Gly Val Ala His Ala Met Phe Phe Ala Ser Glu  
                  100                  105                  110  
Ser Asp Val Val Glu Gly Leu Met Ala Arg Met Leu Lys Phe Gly Glu  
                  115                  120                  125  
Met Glu Val Thr Ser Asp Asn Asn Ile Thr Ala Gly Phe Pro Trp Ala  
130                  135                  140  
Phe  
145

(2) INFORMATION FOR SEQ ID NO:3094:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1105 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1105  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3094:

agaaggaaga ggctgaccgc ctgcaagagg agaggcacca tttggaagag agtactcgga          60  
aaaagcttct ggagatggag tctgcaattt ctagggcaaa tgctcagctg gagaaagcag          120  
aagcttctgc tcgcagacgt gaggttgaga atgcacaact cacgttacag atggaagctg          180  
caaagcganc atgcagcaga gtcagcaaca aatatttcag agctttttaa gaaagacgag          240  
aacagccgta aaaggtctca gcgttgggaa tctgatagag ccctattaca agaggaactt          300  
gcagcacaaa agagcagggt atttcggggt caagaacaac tccagcatgc taaagaacta          360  
aaggatcaag tgcaggcaag gtggaacaaa gaggaggctg caaagactga ggcaattgcc          420  
cttgtaacct cagtgaggaa agagagaggg caaattgaga cctccatgag gtcagaagag          480  
aatttgctgc atctcaaagc agcgaatgac gcacaaagat acaagagtga gatccgtgtc          540  
cttgagcagc gtattgcgca Gctgaaggtg tcattggact cttcaagggt tgctgcccc          600  
aagtggggag ccgacaataa atcctatgca ttgcatcttt ctgaaggagg aaagaacaac          660  
aatgcccgaag ttttgtccaa cacagcagta ccccaaggtc tcgattttga cgatatacag          720  
cgcgaccggg agtgcgctcat gtgcttgagc gaggagatgt ccgtggtgtt cctcccctgc          780  
gcccaccagg tcgtctgtgc caaatgcagc gacctccatg agaagcaagg gatgaaggaa          840  
tgcccttcgt gccgggcccc catccagcgc aggggtgcgc cccgccctgc cggttgctag          900  
atttcacata tactatttgg attttacttt tcttcttttt ttcaacttga ttgctcagct          960  
taagttgatg gaagattgga gagaataatc aggtggtgtg agtggttgaa actgtgacaa         1020  
taatacatcg ttaaacacca aacaagcccc agcagacagt ggggtactggt ttggtttggt         1080  
atatggctat accggttgct tctgt

(2) INFORMATION FOR SEQ ID NO:3095:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 299 amino acids  
    (B) TYPE: amino acid



- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..299  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3095:

Arg Arg Lys Arg Leu Thr Ala Cys Lys Arg Arg Gly Thr Ile Trp Lys  
1                  5                  10                  15  
Arg Val Leu Gly Lys Ser Phe Trp Arg Trp Ser Leu Gln Phe Leu Gly  
                  20                  25                  30  
Gln Met Leu Ser Trp Arg Lys Gln Lys Leu Leu Leu Ala Asp Val Arg  
                  35                  40                  45  
Leu Arg Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His  
                  50                  55                  60  
Ala Ala Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu  
65                  70                  75                  80  
Asn Ser Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu  
                  85                  90                  95  
Gln Glu Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu  
                  100                 105                 110  
Gln Leu Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp  
                 115                 120                 125  
Lys Gln Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser  
130                 135                 140  
Val Arg Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu  
145                 150                 155                 160  
Asn Leu Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser  
                 165                 170                 175  
Glu Ile Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu  
                 180                 185                 190  
Asp Ser Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser  
195                 200                 205  
Tyr Ala Leu His Leu Ser Glu Gly Arg Lys Asn Asn Asn Ala Gln Val  
210                 215                 220  
Leu Ser Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln  
225                 230                 235                 240  
Arg Asp Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val  
                 245                 250                 255  
Phe Leu Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu  
260                 265                 270  
His Glu Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile  
275                 280                 285  
Gln Arg Arg Val Arg Ala Arg Pro Ala Gly Cys  
290                 295

(2) INFORMATION FOR SEQ ID NO:3096:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 266 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..266  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3096:

Met Leu Ser Trp Arg Lys Gln Lys Leu Leu Leu Ala Asp Val Arg Leu  
1                  5                  10                  15  
Arg Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His Ala

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |
| Ala | Glu | Ser | Ala | Thr | Asn |
|     | 35  |     | 40  |     | 45  |
| Ser | Arg | Lys | Arg | Ser | Gln |
|     | 50  |     | 55  |     | 60  |
| Glu | Glu | Leu | Ala | Ala | Gln |
|     | 65  |     | 70  |     | 75  |
| Leu | Gln | His | Ala | Lys | Glu |
|     |     |     | 85  |     | 90  |
| Gln | Glu | Glu | Ala | Lys | Thr |
|     |     |     | 100 |     | 105 |
| Arg | Lys | Glu | Arg | Gly | Gln |
|     |     |     | 115 |     | 120 |
| Leu | Leu | His | Leu | Lys | Ala |
|     |     |     | 130 |     | 135 |
| Ile | Arg | Val | Leu | Glu | Gln |
|     |     |     | 145 |     | 150 |
| Ser | Ser | Arg | Val | Ala | Pro |
|     |     |     | 165 |     | 170 |
| Ala | Leu | His | Leu | Ser | Glu |
|     |     |     | 180 |     | 185 |
| Ser | Asn | Thr | Ala | Val | Pro |
|     |     |     | 195 |     | 200 |
| Asp | Arg | Glu | Cys | Val | Met |
|     |     |     | 210 |     | 215 |
| Leu | Pro | Cys | Ala | His | Gln |
|     |     |     | 225 |     | 230 |
| Glu | Lys | Gln | Gly | Met | Lys |
|     |     |     | 245 |     | 250 |
| Arg | Arg | Val | Arg | Ala | Arg |
|     |     |     | 260 |     | 265 |

(2) INFORMATION FOR SEQ ID NO:3097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1575495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3097:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Asn | Ser | Arg | Tyr | Arg | Trp | Lys | Leu | Gln | Ser | Xaa | His | Ala | Ala |
|     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | Ala | Thr | Asn | Ile | Ser | Glu | Leu | Leu | Lys | Lys | Asp | Glu | Asn | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Lys | Arg | Ser | Gln | Arg | Trp | Glu | Ser | Asp | Arg | Ala | Leu | Leu | Gln | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Leu | Ala | Ala | Gln | Lys | Ser | Arg | Leu | Phe | Arg | Val | Gln | Glu | Gln | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | His | Ala | Lys | Glu | Leu | Lys | Asp | Gln | Val | Gln | Ala | Arg | Trp | Lys | Gln |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Glu | Ala | Ala | Lys | Thr | Glu | Ala | Ile | Ala | Leu | Val | Thr | Ser | Val | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Glu | Arg | Gly | Gln | Ile | Glu | Thr | Ser | Met | Arg | Ser | Glu | Glu | Asn | Leu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | His | Leu | Lys | Ala | Ala | Asn | Asp | Ala | Gln | Arg | Tyr | Lys | Ser | Glu | Ile |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Val | Leu | Glu | Gln | Arg | Ile | Ala | Gln | Leu | Lys | Val | Ser | Leu | Asp | Ser |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser Tyr Ala  
145 150 155 160  
Leu His Leu Ser Glu Gly Arg Lys Asn Asn Asn Ala Gln Val Leu Ser  
165 170 175  
Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln Arg Asp  
180 185 190  
Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val Phe Leu  
195 200 205  
Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu His Glu  
210 215 220  
Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile Gln Arg  
225 230 235 240  
Arg Val Arg Ala Arg Pro Ala Gly Cys  
245

(2) INFORMATION FOR SEQ ID NO:3098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3098:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agcgagagta gcggtcgtgg atgattctgc ctttwtctct ccttcctca cctgctctct   | 60  |
| ctctctctcc ctttctttcc cgcgcgacg gtgacgacga ccgcgcgass ccgccgactc   | 120 |
| cctactgcat caggtgcctc ggccttcgtc gtgctctccg ccggcaacga gtatagacgg  | 180 |
| gcgcgcatgg ccaccttcga gctgtaccgg aggtccacca tcggcatgtg cctcaccgag  | 240 |
| acgctcgacg agatgggtctc caacggcacc ytcagcccg agctcgctat ccaggctctc  | 300 |
| gtccagttcg acaagtccat gacggatgct ctggagaacc aagtgaagag caaggttact  | 360 |
| gtcaagggtc acctgcacac ctacaggttc tgtgacaacg tgtggacctt catcttgaca  | 420 |
| gacgcaagct tcaagaatga ggaggccacg gagcaggtgg gcaaggtgaa gattgtggca  | 480 |
| tgtgattcca aattgctcgg acaataggcc tgtgtaCctt cgagggtcaag gaaggaagct | 540 |
| ttnaagtgcg gcgaggcggg gtctgtctgc gcgtcaGctg tacacgccta ggctaccgag  | 600 |
| aggcggggtc tgtctgcgtc agctgtacac gcctaggtac cgcccgaacg gcatttcatt  | 660 |
| tgccttcttc gtactgtatg tgtatcttct tttttccct tgtatacaat ctgctgcagc   | 720 |
| tataccggcc aagagtatgg catggtatgg cggcaggcag ccgcaaactt gtttttacct  | 780 |

(2) INFORMATION FOR SEQ ID NO:3099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3099:

Met Ala Thr Phe Glu Leu Tyr Arg Arg Ser Thr Ile Gly Met Cys Leu  
1 5 10 15  
Thr Glu Thr Leu Asp Glu Met Val Ser Asn Gly Thr Xaa Ser Pro Glu  
20 25 30  
Leu Ala Ile Gln Val Leu Val Gln Phe Asp Lys Ser Met Thr Asp Ala  
35 40 45  
Leu Glu Asn Gln Val Lys Ser Lys Val Thr Val Lys Gly His Leu His  
50 55 60  
Thr Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Ile Leu Thr Asp Ala

(2) INFORMATION FOR SEO ID NO:3100:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1575498

(xi) SEQUENCE DESCRIPTION: SEO ID NO:3100:

(2) INFORMATION FOR SEQ ID NO:3101:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1575499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3101:

(2) INFORMATION FOR SEQ ID NO:3102:

(A) LENGTH: 728 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..728  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3102:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| aaagtgactg  | aaaagtcccg | catgttctcc | tgcctccgct | cgcgcgccgc  | aacaaccatt  | 60  |
| tccttctcta  | gcgcgcgcct | ccgatccctt | cccagggcta | cagaaccagt  | tcattccaggc | 120 |
| gcgaatggcg  | gcggcgagga | gcctgcttct | gaggcacctc | cgcttgccgg  | cggccccgtc  | 180 |
| agcggcgctc  | gtgaggccga | cggcgctcgt | gcattgagcc | ctgtgggggc  | agcgggtgat  | 240 |
| gtcttcggag  | gatgccaagg | gctctttcct | ggacaagagc | gagggtcactg | aacgcattcat | 300 |
| caaggtcgtc  | aagagcttcc | cgaagatcga | tgacccctcc | aaggtgacac  | cagatgccca  | 360 |
| tttcaagaat  | gatcttggcc | tagacagttt | ggatgcagtg | gaggttggtca | tggccctgga  | 420 |
| agaggaattc  | agattcgaga | tacctgacaa | tgaaGgctga | caagattgac  | tccgtcaaaag | 480 |
| ttgcagttga  | cttcattgcc | tcacaccgcg | aagcgaaatg | ataaagatgc  | gttgccctggt | 540 |
| atagcaaaagc | tatatcgta  | ttaatctctg | tttatgaaga | aagttcagtt  | tgaagatgta  | 600 |
| cactaccgtg  | cccatttgga | tacttctgct | gatgctactg | tccttttttg  | aacgaatttt  | 660 |
| gctactgtgg  | attgtctgca | ctaaataaaa | tgtttgaacc | tgagaaggaa  | cttggtatgcc | 720 |
| gtttggtt    |            |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:3103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1575557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3103:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Thr | Glu | Lys | Ser | Arg | Met | Phe | Ser | Cys | Leu | Arg | Ser | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Thr | Thr | Ile | Ser | Phe | Ser | Ser | Arg | Arg | Leu | Arg | Ser | Pro | Pro | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Glu | Pro | Val | His | Pro | Gly | Ala | Asn | Gly | Gly | Gly | Glu | Glu | Pro |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ser | Glu | Ala | Pro | Pro | Leu | Gly | Gly | Gly | Pro | Val | Ser | Gly | Val | Arg |
|     |     |     |     | 50  |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ala | Asp | Gly | Val | Val | Ala |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1575558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3104:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Arg | Ser | Leu | Leu | Leu | Arg | His | Leu | Arg | Leu | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Ser | Ala | Ala | Ser | Val | Arg | Pro | Thr | Ala | Ser | Leu | His | Glu | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Trp | Gly | Gln | Arg | Trp | Met | Ser | Ser | Glu | Asp | Ala | Lys | Gly | Ser | Phe |
|     |     |     |     | 35  |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Asp | Lys | Ser | Glu | Val | Thr | Glu | Arg | Ile | Ile | Lys | Val | Val | Lys | Ser |
|     |     |     |     | 50  |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Pro | Lys | Ile | Asp | Asp | Pro | Ser | Lys | Val | Thr | Pro | Asp | Ala | His | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

Lys Asn Asp Leu Gly Leu Asp Ser Leu Asp Ala Val Glu Val Val Met  
85 90 95  
Ala Leu Glu Glu Glu Phe Arg Phe Glu Ile Pro Asp Asn Glu Gly  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1575559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3105:

Met Ser Ser Glu Asp Ala Lys Gly Ser Phe Leu Asp Lys Ser Glu Val  
1 5 10 15  
Thr Glu Arg Ile Ile Lys Val Val Lys Ser Phe Pro Lys Ile Asp Asp  
20 25 30  
Pro Ser Lys Val Thr Pro Asp Ala His Phe Lys Asn Asp Leu Gly Leu  
35 40 45  
Asp Ser Leu Asp Ala Val Glu Val Val Met Ala Leu Glu Glu Glu Phe  
50 55 60  
Arg Phe Glu Ile Pro Asp Asn Glu Gly  
65 70

(2) INFORMATION FOR SEQ ID NO:3106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1575573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3106:

tacatcgacg acgacggcga cgtgttcac gtggaccgca tcaaggagct catcaagtac 60  
aagggttcc aggtcgcccc tgccgagctg gaggccatcc tgctgtctca cccgtccgtc 120  
gaggaGccg ccgtcttcgg gctgccggac gaggaggccg gcgagggtccc ggcgtcgtgc 180  
gtggtgcggc gacgtggcgc gccggagagc gaggcggaca tgatggcgta cgtggcgggg 240  
cgcggtgcgt cgtacaagaa gctccggctG ctgcgcttcg tggacgccat cccaagtcg 300  
gtgtccggca agatcctgcg gaggcagctc agggacgagt tcRgtcaaga agacggcagc 360  
agcgtataaa tgcacatcat cctgtgggtg gctgcttgat tataccagtg caagatcctg 420  
cattcgccac ttgatgaaga caataatata attagggtag agtcagatgt tccaggctac 480  
tgatacaatt gttgtttctg caaaaggtag tccaactag tgcatatata ttggcattgt 540  
ggacct

(2) INFORMATION FOR SEQ ID NO:3107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3107:

Tyr Ile Asp Asp Asp Gly Asp Val Phe Ile Val Asp Arg Ile Lys Glu

1 5 10 15  
Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala  
20 25 30  
Ile Leu Leu Ser His Pro Ser Val Glu Asp Ala Ala Val Phe Gly Leu  
35 40 45  
Pro Asp Glu Glu Ala Gly Glu Val Pro Ala Ser Cys Val Val Arg Arg  
50 55 60  
Arg Gly Ala Pro Glu Ser Glu Ala Asp Met Met Ala Tyr Val Ala Gly  
65 70 75 80  
Arg Val Ala Ser Tyr Lys Lys Leu Arg Leu Leu Arg Phe Val Asp Ala  
85 90 95  
Ile Pro Lys Ser Val Ser Gly Lys Ile Leu Arg Arg Gln Leu Arg Asp  
100 105 110  
Glu Phe Xaa Gln Glu Asp Gly Ser Val Ile Met His Ile Ile Leu  
115 120 125  
Trp Val Ala Ala  
130

(2) INFORMATION FOR SEQ ID NO:3108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1575575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3108:

Thr Ser Thr Thr Ala Thr Cys Ser Ser Trp Thr Ala Ser Arg Ser  
1 5 10 15  
Ser Ser Ser Thr Arg Ala Ser Arg Ser Pro Leu Pro Ser Trp Arg Pro  
20 25 30  
Ser Cys Cys Leu Thr Arg Pro Ser Arg Thr Pro Pro Ser Ser Gly Cys  
35 40 45  
Arg Thr Arg Arg Pro Ala Arg Ser Arg Arg Arg Ala Trp Cys Gly Asp  
50 55 60  
Val Ala Arg Arg Arg Ala Arg Arg Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:3109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1575576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3109:

His Arg Arg Arg Arg Arg Arg Val His Arg Gly Pro His Gln Gly Ala  
1 5 10 15  
His Gln Val Gln Gly Leu Pro Gly Arg Pro Cys Arg Ala Gly Gly His  
20 25 30  
Pro Ala Val Ser Pro Val Arg Arg Gly Arg Arg Arg Leu Arg Ala Ala  
35 40 45  
Gly Arg Gly Gly Arg Arg Gly Pro Gly Val Val Arg Gly Ala Ala Thr  
50 55 60  
Trp Arg Ala Gly Glu Arg Gly Gly His Asp Gly Val Arg Gly Gly Ala  
65 70 75 80

Arg Cys Val Val Gln Glu Ala Pro Ala Ala Ala Leu Arg Gly Arg His  
85 90 95  
Pro Gln Val Gly Val Arg Gln Asp Pro Ala Glu Ala Ala Gln Gly Arg  
100 105 110  
Val Xaa Ser Arg Arg Arg Gln Gln Arg Asn Asn Ala His His Pro Val  
115 120 125  
Gly Gly Cys Leu Ile Ile Pro Val Gln Asp Pro Ala Phe Ala Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3110:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| gtccaccttt | cggggtcacc  | ggcttctgct | ttcttgetac | gccaccgcgc  | ctctcgtcta | 60  |
| tttatggagt | ccccgatcc   | atgaagccgg | ggcaggccga | gagttgtcaa  | ggacgacgtc | 120 |
| tgcggcag   | gtcctgctc   | ctcctcctcc | ttcctggccg | cgcgcgcgagc | ttgggttagt | 180 |
| tagtgtctct | tcttcgcgga  | gacctgtgag | aggagccatc | atcatggccg  | ctggtgagac | 240 |
| tgttgctctc | aagggttgcta | tgtcatgcga | gggctgcgcc | ggggcgggtca | gaagagtgtc | 300 |
| ctccaagatg | gaaggagttg  | aaaccttcga | catagacctc | aaggagcaga  | aggtgacagt | 360 |
| caaaggcaat | gtcaagcctg  | aggacgtctt | ccagacgggt | tccaagtcgg  | ggaagaggac | 420 |
| ctcgtactgg | gaGggcgaaG  | Ccacggcccc | ggacgtgcg  | gcggctccag  | aagccgaagc | 480 |
| agctcccagc | accgcggcag  | aagcgctctc | tgctgctgct | ccggcgggcgc | cagagatcac | 540 |
| cccagcaaaa | stgacgcctg  | atcgtaacgc | tattattcac | tcacatgtga  | tgctgcggct | 600 |
| gcgactccta | aaccttaaat  | ctagaaatag | ctggggattg | agtttgcat   | gcatcgtgtt | 660 |
| cttgccggtc | tagcaagtga  | ctataagaat | aatggaataa | acgatgacca  | actggcgtat | 720 |
| gtttataata | aagcaaatgg  | tgatgtgggt | gagatgcata | acgttagggg  | agaaagtgac | 780 |
| gatgtgtatg | ctgggtgggt  | tggtgagctt | cagatttttc | aaatgaatgc  | tttcgtcgcg | 840 |
| gagtcacgtc | cacacgcata  | cgtgcaaagc | cgtgggactt | att         |            |     |

(2) INFORMATION FOR SEQ ID NO:3111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3111:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Thr Phe Arg Gly His Arg Leu Leu Leu Ser Cys Tyr Ala Thr Ala |  |
| 1 5 10 15                                                       |  |
| Pro Leu Val Tyr Leu Trp Ser Pro Pro Ile His Glu Ala Gly Ala Gly |  |
| 20 25 30                                                        |  |
| Arg Glu Leu Ser Arg Thr Thr Ser Ala Gly Ser Ala Pro Ala Pro Pro |  |
| 35 40 45                                                        |  |
| Pro Pro Ser Trp Pro Pro Arg Glu Leu Gly Leu Val Ser Val Ser Ser |  |
| 50 55 60                                                        |  |
| Ser Arg Arg Pro Val Arg Gly Ala Ile Ile Met Ala Ala Val Glu Thr |  |
| 65 70 75 80                                                     |  |
| Val Val Leu Lys Val Ala Met Ser Cys Glu Gly Cys Ala Gly Ala Val |  |
| 85 90 95                                                        |  |
| Arg Arg Val Leu Ser Lys Met Glu Gly Val Glu Thr Phe Asp Ile Asp |  |
| 100 105 110                                                     |  |



Leu Lys Glu Gln Lys Val Thr Val Lys Gly Asn Val Lys Pro Glu Asp  
115 120 125  
Val Phe Gln Thr Val Ser Lys Ser Gly Lys Arg Thr Ser Tyr Trp Glu  
130 135 140  
Gly Glu Ala Thr Ala Pro Asp Ala Ala Ala Ala Pro Glu Ala Glu Ala  
145 150 155 160  
Ala Pro Ser Thr Ala Ala Glu Ala Pro Pro Ala Ala Ala Pro Ala Ala  
165 170 175  
Pro Glu Ile Thr Pro Ala Lys Xaa Thr Pro Asp Arg His Ala Ile Ile  
180 185 190  
His Ser His Val Met Leu Arg Leu Arg Leu Leu Asn Leu Lys Ser Arg  
195 200 205  
Asn Ser Trp Gly Leu Ser Leu His Cys Ile Val Phe Leu Pro Val  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3112:

Met Ala Ala Val Glu Thr Val Val Leu Lys Val Ala Met Ser Cys Glu  
1 5 10 15  
Gly Cys Ala Gly Ala Val Arg Arg Val Leu Ser Lys Met Glu Gly Val  
20 25 30  
Glu Thr Phe Asp Ile Asp Leu Lys Glu Gln Lys Val Thr Val Lys Gly  
35 40 45  
Asn Val Lys Pro Glu Asp Val Phe Gln Thr Val Ser Lys Ser Gly Lys  
50 55 60  
Arg Thr Ser Tyr Trp Glu Gly Glu Ala Thr Ala Pro Asp Ala Ala Ala  
65 70 75 80  
Ala Pro Glu Ala Glu Ala Ala Pro Ser Thr Ala Ala Glu Ala Pro Pro  
85 90 95  
Ala Ala Ala Pro Ala Ala Pro Glu Ile Thr Pro Ala Lys Xaa Thr Pro  
100 105 110  
Asp Arg His Ala Ile Ile His Ser His Val Met Leu Arg Leu Arg Leu  
115 120 125  
Leu Asn Leu Lys Ser Arg Asn Ser Trp Gly Leu Ser Leu His Cys Ile  
130 135 140  
Val Phe Leu Pro Val  
145

(2) INFORMATION FOR SEQ ID NO:3113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1575591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3113:

Met Ser Cys Glu Gly Cys Ala Gly Ala Val Arg Arg Val Leu Ser Lys  
1 5 10 15  
Met Glu Gly Val Glu Thr Phe Asp Ile Asp Leu Lys Glu Gln Lys Val

20 25 30  
Thr Val Lys Gly Asn Val Lys Pro Glu Asp Val Phe Gln Thr Val Ser  
35 40 45  
Lys Ser Gly Lys Arg Thr Ser Tyr Trp Glu Gly Glu Ala Thr Ala Pro  
50 55 60  
Asp Ala Ala Ala Ala Pro Glu Ala Glu Ala Ala Pro Ser Thr Ala Ala  
65 70 75 80  
Glu Ala Pro Pro Ala Ala Ala Pro Ala Ala Pro Glu Ile Thr Pro Ala  
85 90 95  
Lys Xaa Thr Pro Asp Arg His Ala Ile Ile His Ser His Val Met Leu  
100 105 110  
Arg Leu Arg Leu Leu Asn Leu Lys Ser Arg Asn Ser Trp Gly Leu Ser  
115 120 125  
Leu His Cys Ile Val Phe Leu Pro Val  
130 135

(2) INFORMATION FOR SEQ ID NO:3114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..698  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3114:

acacatatc cctacgcctc gctatcgctt tccgcgaact gaggactccc gagaggccga 60  
gaccaccccg atgtccgccg tggagaccga catcaacgcg ccgccgcccg cccagcccg 120  
cgaggatcc tccgtcggtc cgtcctcctc atcctccgc aagcccaaca agcgcttcga 180  
gatcaagaag tggaaacgcg tcgcgctctg ggcatgggat atcgctgctg acaactgcgc 240  
catctgccgc aaccacatca tggatctatg catcgagtgc caggcgaacc aaGctagcgc 300  
gaccagcgag gagtgcactg tcgcttgggg tgtctgtaat catgcttttc acttccactg 360  
catcagcagg tggcttaaga ctgcaccaagt gtgccatta gataacagtg agtgggagtt 420  
ccagaaatat ggccactagt tcctgggcac cgtcatgtga tgttggggct ttgctgccac 480  
tcaagtgttt ttgtctgcc aacagctcca tctcttactg ctttcgatgc ttgcatctat 540  
caccgctcaa ttataactag ctacgagtac gtacacctgg gactgtattt ggacgatcca 600  
ttgagaggat agtaggcca ttttatcaat ggtatgtgga tcttcataag tgagcttgta 660  
ttgtgctgtg gtaccatttt ctgaagtcac gttttttt

(2) INFORMATION FOR SEQ ID NO:3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3115:

His Ile Phe Pro Thr Pro Arg Tyr Arg Leu Pro Arg Thr Glu Asp Ser  
1 5 10 15  
Arg Glu Ala Glu Thr Thr Pro Met Ser Ala Met Glu Thr Asp Ile Asn  
20 25 30  
Ala Pro Pro Pro Ala Pro Ala Gly Glu Gly Ser Ser Val Gly Pro Ser  
35 40 45  
Ser Ser Ser Ser Arg Lys Pro Asn Lys Arg Phe Glu Ile Lys Lys Trp  
50 55 60  
Asn Ala Val Ala Leu Trp Ala Trp Asp Ile Val Val Asp Asn Cys Ala  
65 70 75 80

Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn  
85 90 95  
Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys  
100 105 110  
Asn His Ala Phe His Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg  
115 120 125  
Gln Val Cys Pro Leu Asp Asn Ser Glu Trp Glu Phe Gln Lys Tyr Gly  
130 135 140  
His  
145

(2) INFORMATION FOR SEQ ID NO:3116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3116:

Thr Tyr Ser Leu Arg Leu Ala Ile Ala Phe Arg Glu Leu Arg Thr Pro  
1 5 10 15  
Glu Arg Pro Arg Pro Pro Arg Cys Pro Pro Trp Arg Pro Thr Ser Thr  
20 25 30  
Arg Arg Arg Pro Pro Gln Pro Ala Arg Asp Pro Pro Ser Val Arg Pro  
35 40 45  
Pro His Pro Pro Ala Ser Pro Thr Ser Ala Ser Arg Ser Arg Ser Gly  
50 55 60  
Thr Pro Ser Arg Ser Gly His Gly Ile Ser Ser Ser Thr Thr Ala Pro  
65 70 75 80  
Ser Ala Ala Thr Thr Ser Trp Ile Tyr Ala Ser Ser Ala Arg Arg Thr  
85 90 95  
Lys Leu Ala Arg Pro Ala Arg Ser Ala Leu Ser Leu Gly Val Ser Val  
100 105 110  
Ile Met Leu Phe Thr Ser Thr Ala Ser Ala Gly Gly Leu Arg Leu Ala  
115 120 125  
Lys Cys Ala His  
130

(2) INFORMATION FOR SEQ ID NO:3117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1575595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3117:

Met Ser Ala Met Glu Thr Asp Ile Asn Ala Pro Pro Pro Ala Pro Ala  
1 5 10 15  
Gly Glu Gly Ser Ser Val Gly Pro Ser Ser Ser Ser Arg Lys Pro  
20 25 30  
Asn Lys Arg Phe Glu Ile Lys Lys Trp Asn Ala Val Ala Leu Trp Ala  
35 40 45  
Trp Asp Ile Val Val Asp Asn Cys Ala Ile Cys Arg Asn His Ile Met  
50 55 60  
Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu

65                      70                      75                      80  
Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His Phe His  
                         85                      90                      95  
Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn  
                         100                      105                      110  
Ser Glu Trp Glu Phe Gln Lys Tyr Gly His  
                         115                      120

(2) INFORMATION FOR SEQ ID NO:3118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..708
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3118:

ahtcgaaaaa agacatcaga aaccaagtac cagcaccact gaccaccaag ccaccaatca 60  
tggccgccac tttgcatctc cacctcctcg tgacccttct tttcgtcgcc actctcaccg 120  
tggcctctgt tgccgacgac tcgcccgcgg caccacacc accggcaccg ccgcagccga 180  
ccgcgtacca gatgctggag cggtaacaact tcacgcaggg catcctgccc cagggcgtga 240  
cggggtacgt cctcaNacgc cgacgggtcc ttcgaggtgt acctcccggc ggactgcagc 300  
ttccgcgccg gcagcatgcg ggtccagtac agcagccgcg tcgcccggcca cattcagccg 360  
ctgtccatca catccctgga gggagtgaag gtgaagggtc tgttctcgtg ggtcggcgctc 420  
aagcaggtcg accgcgacgg cgaccagctc cgtttctccg ccggccctat gtcgaaatcg 480  
ttccccatcg acacatttgc caacagcccc caatgcagct gaggcccttt ggtcgattgc 540  
ggaagaaaag Cctgttagtt tcatttttct tgtgtgcytt tagtttgtaa tgtcattttg 600  
caaggatgga tcggttacac agagagtgtc aggaatccct aggacgtggt tcgagatcat 660  
tcttacttgt aaccaatttg attgtttttg ctttgatgcc cattcacc

(2) INFORMATION FOR SEQ ID NO:3119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3119:

Ser Lys Lys Asp Ile Arg Asn Gln Val Pro Ala Pro Leu Thr Thr Lys  
1                      5                      10                      15  
Pro Pro Ile Met Ala Ala Thr Leu His Leu His Leu Leu Val Thr Leu  
                         20                      25                      30  
Leu Phe Val Ala Thr Leu Thr Val Ala Ser Val Ala Asp Asp Ser Pro  
                         35                      40                      45  
Pro Ala Pro Thr Pro Pro Ala Pro Pro Gln Pro Thr Ala Tyr Gln Met  
50                      55                      60  
Leu Glu Arg Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val Thr  
65                      70                      75                      80  
Gly Tyr Val Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Pro Gly  
                         85                      90                      95  
Gly Leu Gln Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln Pro  
                         100                      105                      110  
Arg Arg Arg Pro His Ser Ala Ala Val His His Ile Pro Gly Gly Ser  
115                      120                      125  
Glu Gly Glu Gly Ala Val Leu Val Gly Arg Arg Gln Ala Gly Arg Pro  
130                      135                      140

Arg Arg Arg Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile Val  
145 150 155 160  
Pro His Arg His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro Phe  
165 170 175  
Gly Arg Leu Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys Xaa  
180 185 190  
Phe Ser Leu  
195

(2) INFORMATION FOR SEQ ID NO:3120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1575598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3120:

Met Ala Ala Thr Leu His Leu His Leu Leu Val Thr Leu Leu Phe Val  
1 5 10 15  
Ala Thr Leu Thr Val Ala Ser Val Ala Asp Asp Ser Pro Pro Ala Pro  
20 25 30  
Thr Pro Pro Ala Pro Pro Gln Pro Thr Ala Tyr Gln Met Leu Glu Arg  
35 40 45  
Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val Thr Gly Tyr Val  
50 55 60  
Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Gly Gly Leu Gln  
65 70 75 80  
Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln Pro Arg Arg Arg  
85 90 95  
Pro His Ser Ala Ala Val His His Ile Pro Gly Gly Ser Glu Gly Glu  
100 105 110  
Gly Ala Val Leu Val Gly Arg Arg Gln Ala Gly Arg Pro Arg Arg Arg  
115 120 125  
Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile Val Pro His Arg  
130 135 140  
His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro Phe Gly Arg Leu  
145 150 155 160  
Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys Xaa Phe Ser Leu  
165 170 175

(2) INFORMATION FOR SEQ ID NO:3121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3121:

Met Leu Glu Arg Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val  
1 5 10 15  
Thr Gly Tyr Val Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Pro  
20 25 30  
Gly Gly Leu Gln Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln

35 40 45  
Pro Arg Arg Arg Pro His Ser Ala Ala Val His His Ile Pro Gly Gly  
50 55 60  
Ser Glu Gly Glu Gly Ala Val Leu Val Gly Arg Arg Gln Ala Gly Arg  
65 70 75 80  
Pro Arg Arg Arg Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile  
85 90 95  
Val Pro His Arg His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro  
100 105 110  
Phe Gly Arg Leu Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys  
115 120 125  
Xaa Phe Ser Leu  
130

(2) INFORMATION FOR SEQ ID NO:3122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..588
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3122:

gtccgcccgc tccgtgttca ttgccccact cctcacgcc tctcgcgccc gccgctccac 60  
cacccccata cagctcagg gaaagggggt ctgggttgca tacaggcgaa aggcacgcgc 120  
cgccgCtgcc gcgcgagcct ctccgtcccc atcgccgcgc agatggatcc gtcgtcggag 180  
cccctgtacg cgcaggtcga gccgtacgac tccgggttcc tcaaggtctc cgatgtccac 240  
accatctact acgagcagtc cgggaacccg caggscatg cggcgggtgtt tctccacggc 300  
ggccccggag ccggcacgtc gcccggaac aggaggttct ttgaccgcga gttctacagg 360  
atcgttctgt ttgaccagag ggggtgcaggc agaagcactc cccatgcttg tttagagcag 420  
aacactactt gggacttggt agctgacatt gagaagctca gggagcatct tggcatccct 480  
gaatggcagg tgtttggtgg ttcattggga agcaccttgg cacttgccca cagccaggag 540  
caccctgata aggtcactgg ccttggtctg agaggaattt tcttgctt

(2) INFORMATION FOR SEQ ID NO:3123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3123:

Val Arg Pro Leu Arg Val His Cys Pro Thr Pro Ser Arg Leu Ser Arg  
1 5 10 15  
Pro Pro Leu His His Pro His Pro Arg Ser Gly Lys Gly Gly Leu Gly  
20 25 30  
Cys Ile Gln Ala Lys Gly Thr Arg Arg Cys Arg Ala Ser Leu Ser  
35 40 45  
Val Pro Ile Ala Ala Gln Met Asp Pro Ser Ser Glu Pro Leu Tyr Ala  
50 55 60  
Gln Val Glu Pro Tyr Asp Ser Gly Phe Leu Lys Val Ser Asp Val His  
65 70 75 80  
Thr Ile Tyr Tyr Glu Gln Ser Gly Asn Pro Gln Xaa His Ala Ala Val  
85 90 95  
Phe Leu His Gly Gly Pro Gly Ala Gly Thr Ser Pro Gly Asn Arg Arg  
100 105 110

Phe Phe Asp Pro Gln Phe Tyr Arg Ile Val Leu Phe Asp Gln Arg Gly  
115 120 125  
Ala Gly Arg Ser Thr Pro His Ala Cys Leu Glu Gln Asn Thr Thr Trp  
130 135 140  
Asp Leu Val Ala Asp Ile Glu Lys Leu Arg Glu His Leu Gly Ile Pro  
145 150 155 160  
Glu Trp Gln Val Phe Gly Gly Ser Trp Gly Ser Thr Leu Ala Leu Ala  
165 170 175  
Tyr Ser Gln Glu His Pro Asp Lys Val Thr Gly Leu Val Leu Arg Gly  
180 185 190  
Ile Phe Leu Leu  
195

(2) INFORMATION FOR SEQ ID NO:3124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3124:

Ser Ala Arg Ser Val Phe Ile Ala Pro Leu Pro His Ala Ser Arg Ala  
1 5 10 15  
Arg Arg Ser Thr Thr Pro Ile His Ala Gln Gly Lys Gly Val Trp Val  
20 25 30  
Ala Tyr Arg Arg Lys Ala Arg Ala Ala Ala Arg Ala Ser Pro  
35 40 45  
Ser Pro Ser Pro Arg Arg Trp Ile Arg Arg Arg Ser Pro Cys Thr Arg  
50 55 60  
Arg Ser Ser Arg Thr Thr Pro Gly Ser Ser Arg Ser Pro Met Ser Thr  
65 70 75 80  
Pro Ser Thr Thr Ser Ser Pro Gly Thr Arg Arg Xaa Met Arg Arg Cys  
85 90 95  
Phe Ser Thr Ala Val Pro Glu Pro Ala Arg Arg Pro Ala Thr Gly Gly  
100 105 110  
Ser Leu Thr Arg Ser Ser Thr Gly Ser Phe Cys Leu Thr Arg Gly Val  
115 120 125  
Gln Ala Glu Ala Leu Pro Met Leu Val  
130 135

(2) INFORMATION FOR SEQ ID NO:3125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3125:

Met Asp Pro Ser Ser Glu Pro Leu Tyr Ala Gln Val Glu Pro Tyr Asp  
1 5 10 15  
Ser Gly Phe Leu Lys Val Ser Asp Val His Thr Ile Tyr Tyr Glu Gln  
20 25 30  
Ser Gly Asn Pro Gln Xaa His Ala Val Phe Leu His Gly Gly Pro  
35 40 45  
Gly Ala Gly Thr Ser Pro Gly Asn Arg Arg Phe Phe Asp Pro Gln Phe

50 55 60  
Tyr Arg Ile Val Leu Phe Asp Gln Arg Gly Ala Gly Arg Ser Thr Pro  
65 70 75 80  
His Ala Cys Leu Glu Gln Asn Thr Thr Trp Asp Leu Val Ala Asp Ile  
85 90 95  
Glu Lys Leu Arg Glu His Leu Gly Ile Pro Glu Trp Gln Val Phe Gly  
100 105 110  
Gly Ser Trp Gly Ser Thr Leu Ala Leu Ala Tyr Ser Gln Glu His Pro  
115 120 125  
Asp Lys Val Thr Gly Leu Val Leu Arg Gly Ile Phe Leu Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3126:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gacacacctc | ccaaacccta | cactcccggc | ggcggcggcg | gcggcgagC  | agcggcagca | 60  |
| gcacccgaag | atggtgaagt | tcctcaagcc | cgrcaaggcc | gttatcctcc | tccagggccg | 120 |
| Cttcgccggc | aggaagcgag | ttatcctgcg | cgtgttcgag | gagggcaccc | gcgaccgccc | 180 |
| ctatggccac | tgcctcgctg | caggcctcgc | caagtaccca | aagaaggtga | tccgcaagga | 240 |
| ctcctcttac | ctgtaaatag | ataaataggt | cttggccaga | ttttctgtgt | tttgagctg  | 300 |
| caggattcgt | cctaagacga | gtcatgagtg | taatgtgaag | caacttctcc | agggatagat | 360 |
| ctcaaccaag | tttggtagsc | atacgaaGtt | attgactgga | atttag     |            |     |

(2) INFORMATION FOR SEQ ID NO:3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3127:

Asp Thr Pro Pro Lys Pro Tyr Thr Pro Gly Gly Gly Gly Gly Gly Ala  
1 5 10 15  
Ala Ala Ala Ala Ala Ser Glu Asp Gly Glu Val Pro Gln Ala Xaa Gln  
20 25 30  
Gly Arg Tyr Pro Pro Pro Gly Pro Leu Arg Arg Gln Glu Gly Ser Tyr  
35 40 45  
Pro Ala Arg Val Arg Gly Gly His Pro Arg Pro Pro Leu Trp Pro Leu  
50 55 60  
Pro Arg Arg Arg Pro Arg Gln Val Pro Lys Glu Gly Asp Pro Gln Gly  
65 70 75 80  
Leu Leu Leu Pro Val Asn Arg  
85

(2) INFORMATION FOR SEQ ID NO:3128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..84  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3128:

Thr His Leu Pro Asn Pro Thr Leu Pro Ala Ala Ala Ala Gln  
1 5 10 15  
Gln Arg Gln Gln His Pro Lys Met Val Lys Phe Leu Lys Pro Xaa Lys  
20 25 30  
Ala Val Ile Leu Leu Gln Gly Arg Phe Ala Gly Arg Lys Ala Val Ile  
35 40 45  
Leu Arg Val Phe Glu Glu Gly Thr Arg Asp Arg Pro Tyr Gly His Cys  
50 55 60  
Leu Val Ala Gly Leu Ala Lys Tyr Pro Lys Lys Val Ile Arg Lys Asp  
65 70 75 80  
Ser Ser Tyr Leu

(2) INFORMATION FOR SEQ ID NO:3129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..61  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3129:

Met Val Lys Phe Leu Lys Pro Xaa Lys Ala Val Ile Leu Leu Gln Gly  
1 5 10 15  
Arg Phe Ala Gly Arg Lys Ala Val Ile Leu Arg Val Phe Glu Glu Gly  
20 25 30  
Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys  
35 40 45  
Tyr Pro Lys Lys Val Ile Arg Lys Asp Ser Ser Tyr Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..880  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3130:

caatgtaagt tcgaacaaca agaagggggt gtacagcttg atcggtggggt caaatgccga 60  
cgtaaaatttt tcttacggcc atacatcggt caattcggtt ttgactctgg gaaaagctct 120  
cctcctacaa gagcaatcag cctctccatc taacggaagt tctagatggt ttgaccgcaa 180  
tccactcgag aagggttgta ccggggattc tgtttctcct gccagcaca ggcgccgtat 240  
agacgggtccg gacgattatg ttgaagggtt atctttgctc catctagcat gccgcgtcgc 300  
gacctgggca tggttgagct gctcttgagc tacggcgcca atgtaaacc caccagattca 360  
agagggcgga cgccgcttca tcacagcatc atgaaagggc gacatgtgta cgccaagcta 420  
ctgctttcca ggggcgctga ttctcaagcc gcgtagag atggtagaac agcgttacag 480  
tatgcaatcg acagcggaac catagaggac gaagagatcc ttgttttgct agaggacccA 540  
agtagataaa tcacgtaGgt gtagtagtcc aagtctcgag ttctgcgggtg gtgcattgtg 600  
gctgcctttt gcagtcacct ggcacacaca ggggccgagg atgccttgct agtattcagt 660  
ctctgccttt gtggcaagag gaagttatag tttttctagg tctgtctgcg gttttggtcg 720

cgcttagggt aaaagtggcc tgtttgtcgt ggatgcagtt tgcaagttgt tggtttgcc 780  
ttgtttgcag atgtgcaggt gtacacttgg gaagtggctg ccattgttgc gactgatgta 840  
catatagcga tgtctgatac aggttatttta tgcaagggtc

(2) INFORMATION FOR SEQ ID NO:3131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1575646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3131:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Val | Ser | Ser | Asn | Asn | Lys | Lys | Gly | Val | Tyr | Ser | Leu | Ile | Val | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Asn | Ala | Asp | Val | Asn | Phe | Ser | Tyr | Gly | His | Thr | Ser | Phe | Asn | Ser |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Leu | Thr | Leu | Gly | Lys | Ala | Leu | Leu | Leu | Gln | Glu | Gln | Ser | Ala | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Pro | Ser | Asn | Gly | Ser | Ser | Arg | Cys | Phe | Asp | Arg | Asn | Pro | Leu | Glu | Lys |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Cys | Thr | Gly | Asp | Ser | Val | Ser | Pro | Ala | Ser | Thr | Ser | Ala | Arg | Ile |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asp | Gly | Pro | Asp | Asp | Tyr | Val | Glu | Gly | Leu | Ser | Leu | Leu | His | Leu | Ala |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Cys | Arg | Val | Ala | Thr | Trp | Ala | Trp | Leu | Ser | Cys | Ser | Cys | Ser | Thr | Ala |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Met |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1575647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3132:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Arg | Arg | Asp | Leu | Gly | Met | Val | Glu | Leu | Leu | Leu | Gln | Tyr | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala | Asn | Val | Asn | Pro | Thr | Asp | Ser | Arg | Gly | Arg | Thr | Pro | Leu | His | His |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ile | Met | Lys | Gly | Arg | His | Val | Tyr | Ala | Lys | Leu | Leu | Leu | Ser | Arg |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Gly | Ala | Asp | Ser | Gln | Ala | Ala | Asp | Arg | Asp | Gly | Arg | Thr | Ala | Leu | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Tyr | Ala | Ile | Asp | Ser | Gly | Thr | Ile | Glu | Asp | Glu | Glu | Ile | Leu | Val | Leu |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Leu | Glu | Asp | Pro | Ser | Arg |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..79  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3133:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Leu | Leu | Leu | Gln | Tyr | Gly | Ala | Asn | Val | Asn | Pro | Thr | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Arg | Gly | Arg | Thr | Pro | Leu | His | His | Ser | Ile | Met | Lys | Gly | Arg | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Tyr | Ala | Lys | Leu | Leu | Leu | Ser | Arg | Gly | Ala | Asp | Ser | Gln | Ala | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Arg | Asp | Gly | Arg | Thr | Ala | Leu | Gln | Tyr | Ala | Ile | Asp | Ser | Gly | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Asp | Glu | Glu | Ile | Leu | Val | Leu | Leu | Glu | Asp | Pro | Ser | Arg |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3134:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 762 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..762  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3134:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| accgtgccgc | cgccggcctc | tccaccgttc | attctcctat | ggcatctact  | cacgcaagca | 60  |
| gtctattcc  | tgattccttg | ctcggcttgc | gtggcccatg | gattcgatgt  | catatcatgt | 120 |
| gttgtttgc  | caccgcctg  | gtcgcagttc | gtgtcgatg  | gcgtgttctt  | cgcggaatga | 180 |
| atgagatgt  | cgcgaggac  | ggctactccg | gcgtcgaggt | ccgcgtcacc  | cccatgtgca | 240 |
| tcgagatcat | catccgtgcc | acccgcgccc | agaacatact | cgcgagaagg  | gccggaggat | 300 |
| cagagagctg | gcttctgtga | ttcagaagcg | ctttaactta | tcagagggtg  | gcgttgagct | 360 |
| ctacgcagag | aagctgaaca | accgcgggct | ctgcgacatt | gcccaggccg  | agwgcGtccg | 420 |
| ctacaagctt | ctcggtgaa  | tcgccgtgag | aaGgggcatg | ttatggtgtt  | ctcttatttg | 480 |
| tcacgcagag | tggtactaag | ggctgcgaga | tcagtttcaa | ttggaacatg  | ccaagctgaa | 540 |
| gcgatactca | cctgcaagga | gcgtcttctc | tgtgtactgc | gtcgaagctt  | tacottttta | 600 |
| tgtaaattac | gctgtaaatg | tacagtctct | ctggacactg | aattttctaag | ggcttttttt | 660 |
| atctttctga | cgcaccattc | actgatagct | ttatcggtgc | atagtatttt  | cttgaaatta | 720 |
| tatgccattc | taacgaacaa | taatattgta | gtatcattct | tt          |            |     |

(2) INFORMATION FOR SEQ ID NO:3135:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 105 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..105  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3135:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Ala | Ala | Gly | Leu | Ser | Thr | Val | His | Ser | Pro | Met | Ala | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| His | Ala | Ser | Ser | Pro | Ile | Pro | Asp | Ser | Leu | Leu | Gly | Leu | Arg | Gly | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Ile | Arg | Cys | His | Ile | Met | Cys | Cys | Leu | Leu | Thr | Arg | Leu | Val | Ala |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Val | Gly | Trp | Arg | Val | Leu | Arg | Gly | Xaa | Asn | Glu | Met | Leu | Ala |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |

Glu Asp Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Cys Ile  
65 70 75 80  
Glu Ile Ile Ile Arg Ala Thr Arg Ala Gln Asn Ile Leu Ala Arg Arg  
85 90 95  
Ala Gly Gly Ser Glu Ser Trp Leu Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:3136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3136:

Met Ala Ser Thr His Ala Ser Ser Pro Ile Pro Asp Ser Leu Leu Gly  
1 5 10 15  
Leu Arg Gly Pro Trp Ile Arg Cys His Ile Met Cys Cys Leu Leu Thr  
20 25 30  
Arg Leu Val Ala Val Arg Val Gly Trp Arg Val Leu Arg Gly Xaa Asn  
35 40 45  
Glu Met Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val Arg Val Thr  
50 55 60  
Pro Met Cys Ile Glu Ile Ile Ile Arg Ala Thr Arg Ala Gln Asn Ile  
65 70 75 80  
Leu Ala Arg Arg Ala Gly Gly Ser Glu Ser Trp Leu Leu  
85 90

(2) INFORMATION FOR SEQ ID NO:3137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3137:

Met Val Phe Ser Tyr Leu Ser Ser Arg Val Val Leu Arg Ala Ala Arg  
1 5 10 15  
Ser Val Ser Ile Gly Thr Cys Gln Ala Glu Ala Ile Leu Thr Cys Lys  
20 25 30  
Glu Arg Leu Leu Cys Val Leu Arg Arg Ser Phe Thr Phe Leu Cys Lys  
35 40 45  
Leu Arg Cys Lys Cys Thr Val Pro Leu Asp Thr Glu Phe Leu Arg Ala  
50 55 60  
Phe Phe Ile Phe Leu Thr His His Ser Leu Ile Ala Leu Ser Leu His  
65 70 75 80  
Ser Ile Phe Leu Lys Leu Tyr Ala Ile Leu Thr Asn Asn Asn Ile Val  
85 90 95  
Val Ser Phe Phe  
100

(2) INFORMATION FOR SEQ ID NO:3138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..689  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3138:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tattgaagtc | cattctgttg | gcacgtccc  | atctcccttg | aaccctttcg | cccacaccac | 60  |
| agcaccgctg | ccgaagtggg | aaagaaggcg | gcggcggagg | caccggcacc | ggcaccgcct | 120 |
| aggaaaggaa | accgaggaaa | ctacagccat | ggtggtacgg | atccgtctgg | cgcggttcgg | 180 |
| gtgccggaat | cgcccttct  | accgggtgat | ggccgccgat | agccgctccc | ctcgagacgg | 240 |
| caagcacctc | gaggtcctcg | gctactataa | cccgtctcca | gggaaggatg | gaggcaagag | 300 |
| gatgggcctg | aaattcgacc | gggtgaagta | ttggtgtca  | gttGGGgggc | acagccatca | 360 |
| gatcctgtgc | agagtattct | ctttcgtgcc | ggacttctgc | caccacctcc | attgctagct | 420 |
| atggcacgga | aggggtggcc | acgtgatagg | cgccccattc | atccaatgac | tggcgccct  | 480 |
| ctggatctcg | aggggtgtgc | aattattgat | aattccaatg | ctcctgaagg | cgatactgaa | 540 |
| gtgcctacag | atgaggtggc | tcaataagcc | ttttgtatta | gcatagcata | tgtagcggtg | 600 |
| ctgcaaaaga | aaacttgttt | gatgtgcttg | tggcaagact | ttgggtactc | gtacaatgtg | 660 |
| gcaaactttt | aaacaggtaa | ctttcatcc  |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3139:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 138 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..138  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3139:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Glu | Val | His | Ser | Val | Gly | Ile | Val | Pro | Ser | Pro | Leu | Asn | Pro | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Ala | His | Thr | Thr | Ala | Pro | Leu | Pro | Lys | Trp | Glu | Arg | Arg | Arg | Arg | Arg |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | His | Arg | His | Arg | His | Arg | Leu | Gly | Lys | Glu | Thr | Glu | Glu | Thr | Thr |  |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Met | Val | Val | Arg | Ile | Arg | Leu | Ala | Arg | Phe | Gly | Cys | Arg | Asn | Arg |  |
|     |     |     |     | 50  |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Phe | Tyr | Arg | Val | Met | Ala | Ala | Asp | Ser | Arg | Ser | Pro | Arg | Asp | Gly |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Lys | His | Leu | Glu | Val | Leu | Gly | Tyr | Tyr | Asn | Pro | Leu | Pro | Gly | Lys | Asp |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gly | Gly | Lys | Arg | Met | Gly | Leu | Lys | Phe | Asp | Arg | Val | Lys | Tyr | Trp | Leu |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Val | Gly | Gly | His | Ser | His | Gln | Ile | Leu | Cys | Arg | Val | Phe | Ser | Phe |  |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Pro | Asp | Phe | Cys | His | His | Leu | His | Cys |     |     |     |     |     |     |  |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:3140:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 89 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..89  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3140:

U.S. Pat. No. 7,326,560

Met Val Val Arg Ile Arg Leu Ala Arg Phe Gly Cys Arg Asn Arg Pro  
1 5 10 15  
Phe Tyr Arg Val Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys  
20 25 30  
His Leu Glu Val Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp Gly  
35 40 45  
Gly Lys Arg Met Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu Ser  
50 55 60  
Val Gly Gly His Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe Val  
65 70 75 80  
Pro Asp Phe Cys His His Leu His Cys  
85

(2) INFORMATION FOR SEQ ID NO:3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3141:

Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys His Leu Glu Val  
1 5 10 15  
Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp Gly Gly Lys Arg Met  
20 25 30  
Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu Ser Val Gly Gly His  
35 40 45  
Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe Val Pro Asp Phe Cys  
50 55 60  
His His Leu His Cys  
65

(2) INFORMATION FOR SEQ ID NO:3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3142:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gtggtgctag aagcaactga aaacagccga gcatctcct ctccctctcc ctctccgata   | 60  |
| cattctccag cgcasanang taaacatgtc tgaccgggca aagatgtcgt ggcaggcgta  | 120 |
| cgtggacgag cacctgatgt gcgagatcga rgccaccac ctgcgcggcg cgccatcgt    | 180 |
| cggccacgas gntgcgcct gggcgagag cacggcggtc cccgagttca agaccgagga    | 240 |
| catggccaac atcatgaagg acttcgacga gccagggcac ctgcgcgcga caggCctgtt  | 300 |
| cctcggacct accaagtaca tggatcatca aggcgagcct ggtgccgtca tccgtggcaa  | 360 |
| gaagggatca ggaggcatca ccgtgaagaa gacagggcag gcactcgtcg ttggcatcta  | 420 |
| cgacgagccg atgacgcctg gccagtgcga catggtggtg gaaaggctgg gcgactacct  | 480 |
| gcttgaacag ggcattgtaac tactacgtac cagctggaat gcatgtcgac gacgatgggt | 540 |
| tcgagtttcg acttccaata atagtaacaa caaagcaaag gccttctctc cggcgtatatt | 600 |
| gctttgtctc ttctctctca cgccataaga tatctagcaa ttggtgactc gccttaatta  | 660 |
| gttcgctttg cttttgaggt tgactcgacc attttgctgt agcgtgaatt gcatgcatgg  | 720 |
| acatgcaacg ctccaatgkc ytttgmmmtg tggaattttt tttttcc                |     |

(2) INFORMATION FOR SEQ ID NO:3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..137
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575721
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3143:

Met Ser Asp Arg Ala Lys Met Ser Trp Gln Ala Tyr Val Asp Glu His  
1 5 10 15  
Leu Met Cys Glu Ile Xaa Gly His His Leu Ala Ala Ala Ala Ile Val  
20 25 30  
Gly His Xaa Xaa Ala Ala Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe  
35 40 45  
Lys Thr Glu Asp Met Ala Asn Ile Met Lys Asp Phe Asp Glu Pro Gly  
50 55 60  
His Leu Ala Pro Thr Gly Leu Phe Leu Gly Pro Thr Lys Tyr Met Val  
65 70 75 80  
Ile Gln Gly Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly Ser Gly  
85 90 95  
Gly Ile Thr Val Lys Lys Thr Gly Gln Ala Leu Val Val Gly Ile Tyr  
100 105 110  
Asp Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu  
115 120 125  
Gly Asp Tyr Leu Leu Glu Gln Gly Met  
130 135

(2) INFORMATION FOR SEQ ID NO:3144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..131
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575722
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3144:

Met Ser Trp Gln Ala Tyr Val Asp Glu His Leu Met Cys Glu Ile Xaa  
1 5 10 15  
Gly His His Leu Ala Ala Ala Ala Ile Val Gly His Xaa Xaa Ala Ala  
20 25 30  
Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe Lys Thr Glu Asp Met Ala  
35 40 45  
Asn Ile Met Lys Asp Phe Asp Glu Pro Gly His Leu Ala Pro Thr Gly  
50 55 60  
Leu Phe Leu Gly Pro Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly  
65 70 75 80  
Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly Ile Thr Val Lys Lys  
85 90 95  
Thr Gly Gln Ala Leu Val Val Gly Ile Tyr Asp Glu Pro Met Thr Pro  
100 105 110  
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Leu Glu  
115 120 125  
Gln Gly Met  
130

(2) INFORMATION FOR SEQ ID NO:3145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..120
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3145:

Met Cys Glu Ile Xaa Gly His His Leu Ala Ala Ala Ala Ile Val Gly  
1 5 10 15  
His Xaa Xaa Ala Ala Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe Lys  
20 25 30  
Thr Glu Asp Met Ala Asn Ile Met Lys Asp Phe Asp Glu Pro Gly His  
35 40 45  
Leu Ala Pro Thr Gly Leu Phe Leu Gly Pro Thr Lys Tyr Met Val Ile  
50 55 60  
Gln Gly Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly  
65 70 75 80  
Ile Thr Val Lys Lys Thr Gly Gln Ala Leu Val Val Gly Ile Tyr Asp  
85 90 95  
Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly  
100 105 110  
Asp Tyr Leu Leu Glu Gln Gly Met  
115 120

(2) INFORMATION FOR SEQ ID NO:3146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 645 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..645
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575729
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3146:

gaggaagaat caggcagggg gctctaccat tcgcatccca ggccaacctc aaccccaatc 60  
caatccgttg caggctcgag gatggcttcg cgtgagcacc accagcccca ggaggaggag 120  
gacaccgcaG gcgtcgtcaa gctcatcagc gccgagggct tcgaattcgt cgtcgacaag 180  
aaggccgcca tgggtctcaa caccctacgc aacatgctca catcgccagg cggcttctcc 240  
gagacgcgcc agggcgaggt tcgcttcccg gagatcccca ccaatatcct cgagaagatc 300  
tgccagtact tctattggtc gctccattat tccagctctt ggttcaacac tttggatggc 360  
ctgcctattg aagagttatc tgggtccagaa ttttgatgtg atggagtctg acaaggccaa 420  
taagactgtc acatgtaatg ttatttgatt accaaaacat gaagagcagt caagataggt 480  
tgagatcgat cgtatatatt gttggttcct aggactcttg gtggaagata tgagggttgct 540  
cccaacactg aatttatgta tggctgaagt aaattcactg ttctgatttt ggtgtccaca 600  
ttcttatttg tttccagtc agcaaaactga agttcagttt gtgtt

(2) INFORMATION FOR SEQ ID NO:3147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..131
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575730
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3147:

Glu Glu Glu Ser Gly Arg Glu Leu Tyr His Ser His Pro Arg Pro Thr



|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser Thr Pro Ile Gln Ser Val Ala Gly Arg Arg Met Ala Ser Arg Glu |     |     |     |
|                                                                 | 20  | 25  | 30  |
| His His Gln Pro Gln Glu Glu Asp Thr Ala Gly Val Val Lys Leu     |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Ile Ser Ala Glu Gly Phe Glu Phe Val Val Asp Lys Lys Ala Ala Met |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Val Ser Asn Thr Leu Arg Asn Met Leu Thr Ser Pro Gly Gly Phe Ser |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Glu Thr Arg Gln Gly Glu Val Arg Phe Pro Glu Ile Pro Thr Asn Ile |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Leu Glu Lys Ile Cys Gln Tyr Phe Tyr Trp Ser Leu His Tyr Ser Ser |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Ser Trp Phe Asn Thr Leu Asp Gly Leu Pro Ile Glu Glu Leu Ser Gly |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Pro Glu Phe                                                     |     |     |     |
| 130                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3148:

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| Arg Lys Asn Gln Ala Gly Ser Ser Thr Ile Arg Ile Pro Gly Gln Pro |     |     |     |
| 1                                                               | 5   | 10  | 15  |
| Gln Pro Gln Ser Asn Pro Leu Gln Val Ala Gly Trp Leu Arg Val Ser |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Thr Thr Ser Pro Arg Arg Arg Arg Thr Pro Gln Ala Ser Ser Ser Ser |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Ser Ala Pro Arg Ala Ser Asn Ser Ser Ser Thr Arg Arg Pro Pro Trp |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Ser Pro Thr Pro Tyr Ala Thr Cys Ser His Arg Gln Ala Ala Ser Pro |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Arg Arg Ala Arg Ala Arg Phe Ala Ser Arg Arg Ser Pro Pro Ile Ser |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Ser Arg Arg Ser Ala Ser Thr Ser Ile Gly Arg Ser Ile Ile Pro Ala |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Leu Gly Ser Thr Leu Trp Met Ala Cys Leu Leu Lys Ser Tyr Leu Val |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Gln Asn Phe Asp Val Met Glu Ser Asp Lys Ala Asn Lys Thr Val Thr |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Cys Asn Val Ile                                                 |     |     |     |
| 145                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1575732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3149:

Met Ala Ser Arg Glu His His Gln Pro Gln Glu Glu Glu Asp Thr Ala  
1 5 10 15  
Gly Val Val Lys Leu Ile Ser Ala Glu Gly Phe Glu Phe Val Val Asp  
20 25 30  
Lys Lys Ala Ala Met Val Ser Asn Thr Leu Arg Asn Met Leu Thr Ser  
35 40 45  
Pro Gly Glu Phe Ser Glu Thr Arg Gln Gly Glu Val Arg Phe Pro Glu  
50 55 60  
Ile Pro Thr Asn Ile Leu Glu Lys Ile Cys Gln Tyr Phe Tyr Trp Ser  
65 70 75 80  
Leu His Tyr Ser Ser Ser Trp Phe Asn Thr Leu Asp Gly Leu Pro Ile  
85 90 95  
Glu Glu Leu Ser Gly Pro Glu Phe  
100

(2) INFORMATION FOR SEQ ID NO:3150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3150:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atatccgcat ccgctgcctc cgcctctcga gtctcgcca cccgtcgtec tcctagctcc  | 60  |
| tctactcgcc agtcgccatg ggcaagatta agatcggaat caacggcttc ggaaggatcg | 120 |
| gcaggctcgt agaggagctg gtgtctgagg aggacgacga ggaccacgac gattctccgc | 180 |
| caaggaagca gccggctgtt tcgcatcgta gaaaggctgt cgtgtttgat gacagcgacg | 240 |
| aggactaaaa tttgtaaaac cgtatgacga cctgacatgC tacgcttgct tttctcccc  | 300 |
| atttgtttaa gagaatgatt agttattttt                                  |     |

(2) INFORMATION FOR SEQ ID NO:3151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3151:

Ile Ser Ala Ser Ala Ala Ser Ala Ser Arg Val Ser Ser Thr Arg Arg  
1 5 10 15  
Pro Pro Ser Ser Ser Thr Arg Gln Ser Pro Trp Ala Arg Leu Arg Ser  
20 25 30  
Glu Ser Thr Ala Ser Glu Gly Ser Ala Gly Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:3152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3152:

Met Gly Lys Ile Lys Ile Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg  
1 5 10 15  
Leu Val Glu Glu Leu Val Ser Glu Glu Asp Asp Glu Asp His Asp Asp  
20 25 30  
Ser Pro Pro Arg Lys Gln Pro Ala Val Ser His Arg Arg Lys Ala Val  
35 40 45  
Val Phe Asp Asp Ser Asp Glu Asp  
50 55

(2) INFORMATION FOR SEQ ID NO:3153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..710
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3153:

atccacaaat taaactcacg cacacacaca attaggtcac atacacactt cccggctgcc 60  
tccctaggta gcagcttcta caatggaggc atccaacaag ctgcagttct tgctcctgtg 120  
gctggtcatg gcagctgccca ctgccgtgca cccttcctac tctgagaatt cgccctcaaga 180  
ctacctact ccccaaaaaca gcgcccgtgc cgccgtcggg gttggcccggt tgacctggag 240  
cacgaagctg cagcagttcg cagagaagta cgccgcacag agggccggcg actgccgtct 300  
ccagcactcg ggcggggccCt acggggagaa catcttctgg gggtcggccg gcttcgattg 360  
gaaggcggtg gacgcagtg gatcgtgggt agacgagaaa cagtgggtaca actacgccac 420  
caacagCtgc gccgcgggca aggtgtgttg cactacacgc aggtgggtgtg gcgcgccact 480  
acaagcatcg gCtgcgcgcg cgctgtgtgc cgcgacaacc gtggcgtctt tatcatctgc 540  
aactacgagc ccgcgggcaa cattgccggg atgaagccct actgatatat tgtgcctgcg 600  
aacgatggca actgatatta tatctagaca cgggcttggt gcagcgcatt actttccacg 660  
tgatatatga ataataatatt ataaataaat caaagagggt tgttattttgc

(2) INFORMATION FOR SEQ ID NO:3154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3154:

Met Glu Ala Ser Asn Lys Leu Ala Val Leu Leu Leu Trp Leu Val Met  
1 5 10 15  
Ala Ala Ala Thr Ala Val His Pro Ser Tyr Ser Glu Asn Ser Pro Gln  
20 25 30  
Asp Tyr Leu Thr Pro Gln Asn Ser Ala Arg Ala Ala Val Gly Val Gly  
35 40 45  
Pro Val Thr Trp Ser Thr Lys Leu Gln Gln Phe Ala Glu Lys Tyr Ala  
50 55 60  
Ala Gln Arg Ala Gly Asp Cys Arg Leu Gln His Ser Gly Gly Pro Tyr  
65 70 75 80  
Gly Glu Asn Ile Phe Trp Gly Ser Ala Gly Phe Asp Trp Lys Ala Val  
85 90 95  
Asp Ala Val Arg Ser Trp Val Asp Glu Lys Gln Trp Tyr Asn Tyr Ala  
100 105 110  
Thr Asn Ser Cys Ala Ala Gly Lys Val Cys Gly Thr Thr Arg Arg Trp  
115 120 125

Cys Gly Ala Pro Leu Gln Ala Ser Ala Ala Arg Ala Ser Cys Ala Ala  
130 135 140  
Thr Thr Val Ala Ser Leu Ser Ser Ala Thr Thr Ser Pro Ala Ala Thr  
145 150 155 160  
Leu Pro Gly

(2) INFORMATION FOR SEQ ID NO:3155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3155:

Met Ala Ala Ala Thr Ala Val His Pro Ser Tyr Ser Glu Asn Ser Pro  
1 5 10 15  
Gln Asp Tyr Leu Thr Pro Gln Asn Ser Ala Arg Ala Ala Val Gly Val  
20 25 30  
Gly Pro Val Thr Trp Ser Thr Lys Leu Gln Gln Phe Ala Glu Lys Tyr  
35 40 45  
Ala Ala Gln Arg Ala Gly Asp Cys Arg Leu Gln His Ser Gly Gly Pro  
50 55 60  
Tyr Gly Glu Asn Ile Phe Trp Gly Ser Ala Gly Phe Asp Trp Lys Ala  
65 70 75 80  
Val Asp Ala Val Arg Ser Trp Val Asp Glu Lys Gln Trp Tyr Asn Tyr  
85 90 95  
Ala Thr Asn Ser Cys Ala Ala Gly Lys Val Cys Gly Thr Thr Arg Arg  
100 105 110  
Trp Cys Gly Ala Pro Leu Gln Ala Ser Ala Ala Arg Ala Ser Cys Ala  
115 120 125  
Ala Thr Thr Val Ala Ser Leu Ser Ser Ala Thr Thr Ser Pro Ala Ala  
130 135 140  
Thr Leu Pro Gly  
145

(2) INFORMATION FOR SEQ ID NO:3156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3156:

actttttctct cctcggttccc aatttcaagg ctgcccaacc cttgcgcgcg taggtggtgg 60  
cgggtgaggat agagggttac ctgaggaggc agtgatggcg gccacgattc agtacaaccg 120  
gagcaacccg gcggtgaagc ggatcctgca ggaggtcaag gagatgcagt ccaaccctc 180  
acccgacttc atgtccctcc ccctcgagga ggacatcttc gagtggcaat ttgctatcct 240  
tggtccgaga gacagcgagt ttgagggtgg aatttatcat ggcaggatcc agctaCcttc 300  
ggattatcca ttcaagccac cgtccttcat gctacttaac ccaagtggac gctttgagat 360  
tcagaagaag atttgcttga gcatatccaa ttaccaccct gagcactggc agccttcattg 420  
gagtgtccgc acagcttttg tagccttgat tgccttcattg ccgacgaacc caRggtgggg 480  
cattgggctc actggattac aaaccagaag acagacgagc acttgctata aaatcacgtg 540  
agggtgccsc gaaatttggc tccccacaac gtcagaaact aattgatgag atccatgagc 600  
aaatgctcgt cggtgtgtag tggttcgctct tctgatccat tgtctgtgct ctgtactgta 660

gtgatcagcg tcaaaataaaa gaaatgcctg yccttggtt

(2) INFORMATION FOR SEQ ID NO:3157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3157:

Leu Phe Ser Pro Arg Ser Gln Phe Gln Gly Cys Pro Thr Leu Ala Pro  
1 5 10 15  
Val Gly Gly Gly Gly Glu Asp Arg Gly Leu Pro Glu Glu Ala Val Met  
20 25 30  
Ala Ala Thr Ile Gln Tyr Asn Arg Ser Asn Pro Ala Val Lys Arg Ile  
35 40 45  
Leu Gln Glu Val Lys Glu Met Gln Ser Asn Pro Ser Pro Asp Phe Met  
50 55 60  
Ser Leu Pro Leu Glu Glu Asp Ile Phe Glu Trp Gln Phe Ala Ile Leu  
65 70 75 80  
Gly Pro Arg Asp Ser Glu Phe Glu Gly Gly Ile Tyr His Gly Arg Ile  
85 90 95  
Gln Leu Pro Ser Asp Tyr Pro Phe Lys Pro Pro Ser Phe Met Leu Leu  
100 105 110  
Thr Pro Ser Gly Arg Phe Glu Ile Gln Lys Lys Ile Cys Leu Ser Ile  
115 120 125  
Ser Asn Tyr His Pro Glu His Trp Gln Pro Ser Trp Ser Val Arg Thr  
130 135 140  
Ala Leu Val Ala Leu Ile Ala Phe Met Pro Thr Asn Pro Xaa Trp Gly  
145 150 155 160  
Ile Gly Leu Thr Gly Leu Gln Thr Arg Arg Gln Thr Ser Thr Cys Tyr  
165 170 175  
Lys Ile Thr

(2) INFORMATION FOR SEQ ID NO:3158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3158:

Met Ala Ala Thr Ile Gln Tyr Asn Arg Ser Asn Pro Ala Val Lys Arg  
1 5 10 15  
Ile Leu Gln Glu Val Lys Glu Met Gln Ser Asn Pro Ser Pro Asp Phe  
20 25 30  
Met Ser Leu Pro Leu Glu Glu Asp Ile Phe Glu Trp Gln Phe Ala Ile  
35 40 45  
Leu Gly Pro Arg Asp Ser Glu Phe Glu Gly Gly Ile Tyr His Gly Arg  
50 55 60  
Ile Gln Leu Pro Ser Asp Tyr Pro Phe Lys Pro Pro Ser Phe Met Leu  
65 70 75 80  
Leu Thr Pro Ser Gly Arg Phe Glu Ile Gln Lys Lys Ile Cys Leu Ser  
85 90 95

Ile Ser Asn Tyr His Pro Glu His Trp Gln Pro Ser Trp Ser Val Arg  
100 105 110  
Thr Ala Leu Val Ala Leu Ile Ala Phe Met Pro Thr Asn Pro Xaa Trp  
115 120 125  
Gly Ile Gly Leu Thr Gly Leu Gln Thr Arg Arg Gln Thr Ser Thr Cys  
130 135 140  
Tyr Lys Ile Thr  
145

(2) INFORMATION FOR SEQ ID NO:3159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1575797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3159:

Met Gln Ser Asn Pro Ser Pro Asp Phe Met Ser Leu Pro Leu Glu Glu  
1 5 10 15  
Asp Ile Phe Glu Trp Gln Phe Ala Ile Leu Gly Pro Arg Asp Ser Glu  
20 25 30  
Phe Glu Gly Gly Ile Tyr His Gly Arg Ile Gln Leu Pro Ser Asp Tyr  
35 40 45  
Pro Phe Lys Pro Pro Ser Phe Met Leu Leu Thr Pro Ser Gly Arg Phe  
50 55 60  
Glu Ile Gln Lys Lys Ile Cys Leu Ser Ile Ser Asn Tyr His Pro Glu  
65 70 75 80  
His Trp Gln Pro Ser Trp Ser Val Arg Thr Ala Leu Val Ala Leu Ile  
85 90 95  
Ala Phe Met Pro Thr Asn Pro Xaa Trp Gly Ile Gly Leu Thr Gly Leu  
100 105 110  
Gln Thr Arg Arg Gln Thr Ser Thr Cys Tyr Lys Ile Thr  
115 120 125

(2) INFORMATION FOR SEQ ID NO:3160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..707

(D) OTHER INFORMATION: / Ceres Seq. ID 1575798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3160:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaagaatac | ggtttaacaa | acaccctacc | caaaggggcg | gaaaccaagc | cgccgtgacc | 60  |
| gccagaccca | agccaacaag | caagagcatt | actacttctg | cttccgaccg | aaacctttct | 120 |
| tggaacgcaa | gaagaatccc | aaccccgacc | gacctaccct | aatcgggcat | ggcgacggtg | 180 |
| gcgatggaca | tctcgaagcc | cactccagtg | gcgtccggcg | acgaggccgc | cggcggccaa | 240 |
| ggggaggagc | ggcggagggg | gcgaggggct | gcggcagtac | tacctgcagc | acatccacga | 300 |
| cctgcagctc | cagatccggc | agaagaccca | caacctcaac | cgtctcgagg | cccagcgcaa | 360 |
| tgacctcaac | tcccgagtta | gaatgctcag | ggaagagttg | cagttgcttc | aagagcctgg | 420 |
| ctcatatgtt | ggtgaggtgg | tgaaggtcat | ggggaaatca | aagggttctg | tgaaggtaca | 480 |
| ccccgaagGc | aaatatgttg | ttgatataga | taagagcatt | gatatcacia | agatcacacc | 540 |
| ttcaacaaga | gtcgtctctc | gtaatgacag | ctatatgctc | catctgatcc | taccaagcaa | 600 |
| agttgatcca | ttggtcaatc | tcatgaaagt | tgagaaggtt | cctgattcta | catatgatat | 660 |
| gattggaggc | cttgaccagc | aaattaaaga | gatcaaagag | gtcatttg   |            |     |

(2) INFORMATION FOR SEQ ID NO:3161:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..64  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1575799  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3161:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Val Ala Ser  
1                  5                  10                  15  
Gly Asp Glu Ala Ala Gly Gly Gln Gly Glu Glu Arg Arg Arg Gly Arg  
                  20                  25                  30  
Gly Ala Ala Ala Val Leu Pro Ala Ala His Pro Arg Pro Ala Ala Pro  
                  35                  40                  45  
Asp Pro Ala Glu Asp Pro Gln Pro Gln Pro Ser Arg Gly Pro Ala Gln  
50                  55                  60

- (2) INFORMATION FOR SEQ ID NO:3162:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 108 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..108  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1575800  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3162:

Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro Gly Ser Tyr Val  
1                  5                  10                  15  
Gly Glu Val Val Lys Val Met Gly Lys Ser Lys Val Leu Val Lys Val  
                  20                  25                  30  
His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp Ile  
                  35                  40                  45  
Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr  
50                  55                  60  
Met Leu His Leu Ile Leu Pro Ser Lys Val Asp Pro Leu Val Asn Leu  
65                  70                  75                  80  
Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly  
                  85                  90                  95  
Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile  
100                  105

- (2) INFORMATION FOR SEQ ID NO:3163:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 86 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..86  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1575801  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3163:

Met Gly Lys Ser Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr  
1                  5                  10                  15

Val Val Asp Ile Asp Lys Ser Ile Asp Ile Thr Lys Ile Thr Pro Ser  
20 25 30  
Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr Met Leu His Leu Ile Leu  
35 40 45  
Pro Ser Lys Val Asp Pro Leu Val Asn Leu Met Lys Val Glu Lys Val  
50 55 60  
Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly Leu Asp Gln Gln Ile Lys  
65 70 75 80  
Glu Ile Lys Glu Val Ile  
85

(2) INFORMATION FOR SEQ ID NO:3164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..737
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3164:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| atctctctctc | tggtcatagc | ctccaagaa  | acaagagcca  | accagcgctt | gcgaactcaa | 60  |
| gcgcgcgcgc  | aatgtctctg | gccccgtcca | tcccttccat  | caaggagaag | gtggggggcg | 120 |
| tctcggtcgc  | tcctccacac | cgtgcatgcc | ggtccttcgc  | ggtgatcagg | agctccaagg | 180 |
| cagagggccc  | catccggaga | cCtgcgcgcg | ctccgCtgtc  | gccaccgcca | ccgatgccac | 240 |
| ccaagacgcc  | ggctctgtcc | actctcccca | ccctgtcgca  | gcctccgacg | cccgtgaagc | 300 |
| ccgctgctcc  | acccacgtcg | tcgcagccga | tgccaccttc  | tcctgagccg | aagccagttg | 360 |
| acgccacagc  | ccagatgcgg | aagccgggtg | ctgggggccat | gacgctggag | taccagagga | 420 |
| aggtggccaa  | ggacctgcag | gagtacttca | agaagaagaa  | gctggaggag | gccgaccagg | 480 |
| gtccgttctt  | cgggttcttg | ccaagaatg  | agatttccaa  | cggaagggtg | gccatgtttg | 540 |
| ggtttgcagt  | agggatgcta | acagagtatg | caacaggctc  | ggattttgtt | cagcaaata  | 600 |
| agatccttct  | ctccaatttt | ggaattgtgg | acttggatta  | atggtggact | tttgggtgtt | 660 |
| tcgttatgta  | caagtctttt | aatgtaatg  | tacttacttg  | atatggtata | tagaaaattt | 720 |
| catattgcac  | gttgttc    |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:3165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3165:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Leu | Ser | Val | His | Ser | Leu | Pro | Arg | Asn | Lys | Ser | Gln | Pro | Ala | Leu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Asn | Ser | Ser | Ala | Ala | Ala | Met | Ser | Leu | Ala | Pro | Ser | Ile | Pro | Ser |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Lys | Val | Lys | Val | Gly | Ala | Val | Ser | Val | Ala | Pro | Pro | His | Arg | Ala |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Cys | Arg | Ser | Phe | Ala | Val | Ile | Arg | Ser | Ser | Lys | Ala | Glu | Gly | Pro | Ile |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Arg | Pro | Ala | Ala | Pro | Pro | Leu | Ser | Pro | Pro | Pro | Pro | Met | Pro | Pro |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | Thr | Pro | Ala | Leu | Ser | Thr | Pro | Pro | Thr | Leu | Ser | Gln | Pro | Pro | Thr |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Pro | Val | Lys | Pro | Ala | Ala | Pro | Pro | Thr | Ser | Ser | Gln | Pro | Met | Pro | Pro |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |



Ser Pro Glu Pro Lys Pro Val Asp Ala Thr Ala Gln Met Arg Lys Pro  
115 120 125  
Val Ala Gly Ala Met Thr Leu Glu Tyr Gln Arg Lys Val Ala Lys Asp  
130 135 140  
Leu Gln Glu Tyr Phe Lys Lys Lys Leu Glu Ala Asp Gln Gly  
145 150 155 160  
Pro Phe Phe Gly Phe Leu Pro Lys Asn Glu Ile Ser Asn Gly Arg Trp  
165 170 175  
Ala Met Phe Gly Phe Ala Val Gly Met Leu Thr Glu Tyr Ala Thr Gly  
180 185 190  
Ser Asp Phe Val Gln Gln Met Lys Ile Leu Leu Ser Asn Phe Gly Ile  
195 200 205  
Val Asp Leu Asp  
210

(2) INFORMATION FOR SEQ ID NO:3166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3166:

Met Ser Leu Ala Pro Ser Ile Pro Ser Ile Lys Val Lys Val Gly Ala  
1 5 10 15  
Val Ser Val Ala Pro Pro His Arg Ala Cys Arg Ser Phe Ala Val Ile  
20 25 30  
Arg Ser Ser Lys Ala Glu Gly Pro Ile Arg Arg Pro Ala Ala Pro Pro  
35 40 45  
Leu Ser Pro Pro Pro Pro Met Pro Pro Lys Thr Pro Ala Leu Ser Thr  
50 55 60  
Pro Pro Thr Leu Ser Gln Pro Pro Thr Pro Val Lys Pro Ala Ala Pro  
65 70 75 80  
Pro Thr Ser Ser Gln Pro Met Pro Pro Ser Pro Glu Pro Lys Pro Val  
85 90 95  
Asp Ala Thr Ala Gln Met Arg Lys Pro Val Ala Gly Ala Met Thr Leu  
100 105 110  
Glu Tyr Gln Arg Lys Val Ala Lys Asp Leu Gln Glu Tyr Phe Lys Lys  
115 120 125  
Lys Lys Leu Glu Glu Ala Asp Gln Gly Pro Phe Phe Gly Phe Leu Pro  
130 135 140  
Lys Asn Glu Ile Ser Asn Gly Arg Trp Ala Met Phe Gly Phe Ala Val  
145 150 155 160  
Gly Met Leu Thr Glu Tyr Ala Thr Gly Ser Asp Phe Val Gln Gln Met  
165 170 175  
Lys Ile Leu Leu Ser Asn Phe Gly Ile Val Asp Leu Asp  
180 185

(2) INFORMATION FOR SEQ ID NO:3167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3167:

Met Pro Pro Lys Thr Pro Ala Leu Ser Thr Pro Pro Thr Leu Ser Gln  
1 5 10 15  
Pro Pro Thr Pro Val Lys Pro Ala Ala Pro Pro Thr Ser Ser Gln Pro  
20 25 30  
Met Pro Pro Ser Pro Glu Pro Lys Pro Val Asp Ala Thr Ala Gln Met  
35 40 45  
Arg Lys Pro Val Ala Gly Ala Met Thr Leu Glu Tyr Gln Arg Lys Val  
50 55 60  
Ala Lys Asp Leu Gln Glu Tyr Phe Lys Lys Lys Lys Leu Glu Glu Ala  
65 70 75 80  
Asp Gln Gly Pro Phe Phe Gly Phe Leu Pro Lys Asn Glu Ile Ser Asn  
85 90 95  
Gly Arg Trp Ala Met Phe Gly Phe Ala Val Gly Met Leu Thr Glu Tyr  
100 105 110  
Ala Thr Gly Ser Asp Phe Val Gln Gln Met Lys Ile Leu Leu Ser Asn  
115 120 125  
Phe Gly Ile Val Asp Leu Asp  
130 135

(2) INFORMATION FOR SEQ ID NO:3168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3168:

atcaaaatag agttcacacg cacaacccgc cgccgcacgc cgggatctcg atagactctg 60  
gctgccgcgg aaagcggaaa gaaggcaggg atcgtggcca agatgcagat cttcgtgaag 120  
acgctgtcgt cgacaaggac gatcacgctg gaggttgagc cttcggacac ggtggcggac 180  
gtgaaggcca aggtgtacga gtcggagggc gtcccgcgg ccgagcagcg cctcatcttc 240  
gcggggaagc agCtgcgcgca cggtgcacg ctggctgact acaacatccc caaggagacg 300  
atgctgtcct tgtgtgcCg cctcctcgga ggcgGcccc agaagcgcaa taggaagacg 360  
ttcaccactc ctaagaaggg cacgcacgag cacaagaacc ccgggctcga cgccgtgctt 420  
gggcgggtaca ggategatga ggccacgggg aaggtggaga ggCtgcgcat gcagtgccct 480  
aaccgcggagt gcggcccaRg gcgtgctcat ggcgggcgac gccgaccggc acgtctgcgg 540  
cagctgcggc ctcaccttcg tcattccagaa ctagagcgcg gcagatagct aggtcgcttc 600  
gtactcccc catttgcaat gacaaagcgt ttttaccttt ctatgatatgc acttatgtct 660  
agatacatag attatcttat acttttttcg ttctttttta tttatcgtgt tttagttaaa 720  
aataaattaa ttgagtgaat atgtt

(2) INFORMATION FOR SEQ ID NO:3169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3169:

Met Gln Ile Phe Val Lys Thr Leu Ser Ser Thr Arg Thr Ile Thr Leu  
1 5 10 15  
Glu Val Glu Pro Ser Asp Thr Val Ala Asp Val Lys Ala Lys Val Tyr  
20 25 30  
Glu Ser Glu Gly Val Pro Pro Ala Glu Gln Arg Leu Ile Phe Ala Gly

(2) INFORMATION FOR SEO ID NO:3170:

(A) LENGTH: 95 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1575824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3170:

(2) INFORMATION FOR SEQ ID NO:3171:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..724

(D) OTHER INFORMATION: / Ceres Seq. ID 1575825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3171:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| gttttgaaaa  | aggaacggcc | catgttcagg | gagaaggctc | cgactgggct  | aggaggcgct | 60  |
| aggctatcgc  | cgcggccgcc | gttctctcac | ctgctgcac  | gctgcttcg   | cctccgccct | 120 |
| acaagGctac  | accagatgcc | cagattttcg | tccggttctt | Tctccggcaa  | cgagcagcca | 180 |
| ccagggtgtct | tggtatttgc | aaacagtgac | aaaaggttct | gCtctcgctgt | agagtcatgt | 240 |
| ctgcaaagat  | acgcgtagt  | atgaagtctt | ttatgagcca | aagcaaccag  | gtctcagggc | 300 |
| ttatgccatt  | cacaaagaag | attgactac  | ctgaatcacg | agccctgtac  | accgtgttgc | 360 |
| ggtcacctca  | tatcgataag | aagtccaggg | aacaattctc | gattgatgtc  | aagaaacagt | 420 |
| ttgtggaaca  | gacagccaaa | ccacacqaac | ttcacaggaa | gttcttctgq  | ttaaaacgcc | 480 |

tgccgataacc tggggctcag tatgaaatcc aaatttcttt caAgacacgt ctcgatatgg 540  
cgagcctaag gtcccaagct ccttgctgac tctcagatct tccttaccgt cctgaatggt 600  
tgaagtgact tgtatccatc gacatttcat atgttatgaa gacatgctta ttttgatggc 660  
ttttgaaaaa aaatgtacct gctaagtctt cattaccttg acagatcact agtcaagaaa 720  
atgc

(2) INFORMATION FOR SEQ ID NO:3172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1575826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3172:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Lys | Ile | Arg | Val | Val | Met | Lys | Ser | Phe | Met | Ser | Gln | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Gln | Val | Ser | Gly | Leu | Met | Pro | Phe | Thr | Lys | Lys | Ile | Gly | Leu | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Ser | Arg | Ala | Leu | Tyr | Thr | Val | Leu | Arg | Ser | Pro | His | Ile | Asp | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Ser | Arg | Glu | Gln | Phe | Ser | Met | His | Val | Lys | Lys | Gln | Phe | Val | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Thr | Ala | Lys | Pro | His | Glu | Leu | His | Arg | Lys | Phe | Phe | Trp | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Leu | Arg | Ile | Pro | Gly | Ala | Gln | Tyr | Glu | Ile | Gln | Ile | Ser | Phe | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Arg | Leu | Asp | Met | Ala | Ser | Leu | Arg | Ser | Gln | Ala | Pro | Cys |     |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:3173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1575827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3173:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Phe | Met | Ser | Gln | Ser | Asn | Gln | Val | Ser | Gly | Leu | Met | Pro |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Thr | Lys | Lys | Ile | Gly | Leu | Pro | Glu | Ser | Arg | Ala | Leu | Tyr | Thr | Val |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Arg | Ser | Pro | His | Ile | Asp | Lys | Lys | Ser | Arg | Glu | Gln | Phe | Ser | Met |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| His | Val | Lys | Lys | Gln | Phe | Val | Glu | Gln | Thr | Ala | Lys | Pro | His | Glu | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Arg | Lys | Phe | Phe | Trp | Leu | Lys | Arg | Leu | Arg | Ile | Pro | Gly | Ala | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Glu | Ile | Gln | Ile | Ser | Phe | Lys | Thr | Arg | Leu | Asp | Met | Ala | Ser | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Ser | Gln | Ala | Pro | Cys |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..815

(D) OTHER INFORMATION: / Ceres Seq. ID 1575844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3175:

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| catagaactg  | atgggtggcg  | cagaacatgg  | gataacacta | cacctgtaaa  | caatgtggat | 60  |
| tctgccaatg  | ttgtcctgca  | gggtggtgaa  | gctccccgca | cagctgcaaA  | tactactagt | 120 |
| gagGatTgca  | tccaaAcagG  | tacaccaaAg  | tccaggtagt | cctcagggtTg | ttTggcaaga | 180 |
| caacatTgac  | cctgacaata  | tgacatatga  | ggaactcttg | gattttgggtg | aggcagttgg | 240 |
| aaccocagagc | cgtggctctct | cccaagaatg  | catttcgttg | cttcccatca  | ctaagtataa | 300 |
| gtgtggattc  | ttttcaagga  | agaaaacacg  | ccgtgaaagg | tgtgtgattt  | gccaaatgga | 360 |
| gtacaggaga  | ggaaattttgc | agattacgct  | tccatgcaag | catgtatacc  | atgccagctg | 420 |
| cgtgacaaga  | tggtcttagca | taaacaagggt | atgcctgtt  | tgtttgtctg  | aagttcctgg | 480 |
| cgaggattct  | cagaggcaat  | gattcatcag  | ttgtgatgcc | actatgaagt  | tgctgctctg | 540 |
| ggtactgcgc  | ccccaatgga  | cgcatgattt  | ctttgaaggc | agcttgttgt  | cccacttta  | 600 |
| gaatttgtga  | ttagcgccat  | attaccaaat  | aggttattac | ttatcagatg  | tatttaggta | 660 |
| gtgtttgggt  | tcggaatatg  | gtaggatgga  | gtcactttgc | tcctaattta  | ttgttgtttg | 720 |
| aattgatttt  | atgtaggaca  | tagtaactct  | aaaattggaa | aaactatgct  | taaatactga | 780 |
| atcatctgac  | tccccaaat   | cttttggaag  | gagac      |             |            |     |

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3176:

Met Trp Ile Leu Pro Met Leu Ser Cys Arg Val Val Lys Leu Pro Ala

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Gln Leu Gln Ile Leu Leu Val Arg Ile Ala Ser Lys Gln Val His Gln |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Ser Pro Gly Ser Pro Gln Val Val Trp Gln Asp Asn Ile Asp Pro Asp |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Asn Met Thr Tyr Glu Glu Leu Leu Asp Leu Gly Glu Ala Val Gly Thr |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Gln Ser Arg Gly Leu Ser Gln Glu Cys Ile Ser Leu Leu Pro Ile Thr |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Lys Tyr Lys Cys Gly Phe Phe Ser Arg Lys Lys Thr Arg Arg Glu Arg |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Cys Val Ile Cys Gln Met Glu Tyr Arg Arg Gly Asn Leu Gln Ile Thr |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Leu Pro Cys Lys His Val Tyr His Ala Ser Cys Val Thr Arg Trp Leu |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Ser Ile Asn Lys Val Cys Pro Val Cys Phe Ala Glu Val Pro Gly Glu |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Asp Ser Gln Arg Gln                                             |     |     |     |
| 145                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1575846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3177:

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| Met Leu Ser Cys Arg Val Val Lys Leu Pro Ala Gln Leu Gln Ile Leu |     |     |     |
| 1                                                               | 5   | 10  | 15  |
| Leu Val Arg Ile Ala Ser Lys Gln Val His Gln Ser Pro Gly Ser Pro |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Gln Val Val Trp Gln Asp Asn Ile Asp Pro Asp Asn Met Thr Tyr Glu |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Glu Leu Leu Asp Leu Gly Glu Ala Val Gly Thr Gln Ser Arg Gly Leu |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Ser Gln Glu Cys Ile Ser Leu Leu Pro Ile Thr Lys Tyr Lys Cys Gly |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Phe Phe Ser Arg Lys Lys Thr Arg Arg Glu Arg Cys Val Ile Cys Gln |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Met Glu Tyr Arg Arg Gly Asn Leu Gln Ile Thr Leu Pro Cys Lys His |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Val Tyr His Ala Ser Cys Val Thr Arg Trp Leu Ser Ile Asn Lys Val |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Cys Pro Val Cys Phe Ala Glu Val Pro Gly Glu Asp Ser Gln Arg Gln |     |     |     |
|                                                                 | 130 | 135 | 140 |

(2) INFORMATION FOR SEQ ID NO:3178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3178:

Met Thr Tyr Glu Glu Leu Leu Asp Leu Gly Glu Ala Val Gly Thr Gln  
1 5 10 15  
Ser Arg Gly Leu Ser Gln Glu Cys Ile Ser Leu Leu Pro Ile Thr Lys  
20 25 30  
Tyr Lys Cys Gly Phe Phe Ser Arg Lys Lys Thr Arg Arg Glu Arg Cys  
35 40 45  
Val Ile Cys Gln Met Glu Tyr Arg Arg Gly Asn Leu Gln Ile Thr Leu  
50 55 60  
Pro Cys Lys His Val Tyr His Ala Ser Cys Val Thr Arg Trp Leu Ser  
65 70 75 80  
Ile Asn Lys Val Cys Pro Val Cys Phe Ala Glu Val Pro Gly Glu Asp  
85 90 95  
Ser Gln Arg Gln  
100

(2) INFORMATION FOR SEQ ID NO:3179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923

(D) OTHER INFORMATION: / Ceres Seq. ID 1575856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3179:

gtcctcgtct cgttcctctg ctcccttttg caacctccct tcatataggc cactgtgacc 60  
tgcttccctt tcgcagttgc tcatctccat agccacctcg gaagctcgag gccgaggatc 120  
cacatatata gcatctgtct tttatactaa taggttttag tttttgggag aatctacaca 180  
gcgagagaag taggtagctt tcttcaataa tctgggtcca gtccagcaag cttcaccttg 240  
ccctccatcg acggatcgac ctgctgcggg ccagagaca tccatccatc catccttcct 300  
tcctggctgt aagaagagga gatggtctca tggccgtgat ctacatcGc ggagcGctcg 360  
tcgcggccgt gtccctctgc ctccctctcg Gcgccgccac cagcatccCg caccgcgacg 420  
ttttccctt ctgaggagaa cctggcggag gacaagtgc ggctggggtc gacgcgcgcg 480  
atctgcgcga accggtgcag cgctgcaac cctgcatgc ccgtgcaggt gacgaccgcg 540  
cccgcggggc tcgggcgcgc ggccgcgcgc accgacgcgc cgacgcggtg 600  
gcccgttct cccgctactc cgactacaag ccgctggggt ggaaatgcgg ctgcgacggc 660  
cgctgtacg acccctagcc gagcgtgcaa cgccagtgc ctctgctccg gtccggtagg 720  
gtgggggaga ctggaggcca tccaggttct tcgtgtcatc tgttcttggg ttttgcccat 780  
gggcatggc ggcttgcttg cattgcagct tgtaccgcc gtagccgtag ccattttttt 840  
ttgctctctg ctgaacaat ttattactcg cgtgtaaaga gtaaccgtga ccgtgagcag 900  
taaaaattgt agtggttacc ggc

(2) INFORMATION FOR SEQ ID NO:3180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1575857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3180:

Met Ala Val Ile Ser His Arg Gly Ala Leu Val Ala Ala Val Ser Leu  
1 5 10 15  
Cys Leu Leu Leu Gly Ala Ala Thr Ser Ile Pro His Arg Asp Val Phe  
20 25 30  
Pro Phe Ser Gly Glu Pro Gly Gly Gln Val Ala Ala Gly Val Asp

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Ala Ala Asp Leu Pro Gln Pro Val Gln Arg Leu Gln Pro Leu His Ala |     |     |
| 50                                                              | 55  | 60  |
| Arg Ala Gly Asp Asp Arg Ala Arg Gly Ala Arg Ala Arg Gly Pro Arg |     |     |
| 65                                                              | 70  | 75  |
| His Arg Arg Arg Arg Arg Arg Arg Arg Gly Gly Arg Leu Leu Pro Leu |     |     |
| 85                                                              | 90  | 95  |
| Leu Arg Leu Gln Ala Ala Gly Val Glu Met Arg Leu Arg Arg Pro Pro |     |     |
| 100                                                             | 105 | 110 |
| Val Arg Pro Leu Ala Glu Arg Ala Thr Pro Val His Ser Ala Pro Val |     |     |
| 115                                                             | 120 | 125 |
| Arg                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:3181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3181:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gaaggagttc aaggtggag tgaagcaat cggtcgtgtt cggcacaaaa atctcgtcag   | 60  |
| gttgctcggc tactgcgtag aggtgctta caggatgctt gtgtatgagt atgtggacaa  | 120 |
| tggtaatctt gaccagtggc ttcatggtga tgttggcgaa gtgagcccac tgacatggga | 180 |
| catcaggatg aacatcatgc ttgcgaccgc taaagggctg gcctacctcc acgaggggct | 240 |
| ggaaccgaag ttgntccacc gcgacatcaa ggctagcaac atccttcttg accagcagt  | 300 |
| gaacgcaaaa gtatcggatt tcgggctcgc gaaGctgtt tgctcggaga gaagctacgt  | 360 |
| tacgaccggt gtcattggaa mcttcggtta cgtggcgccg gagtacgcca gcacgggcat | 420 |
| gctgaacgag aggagcgtg tgtatagctt cggcgtgctg ataatggaga tcatcaccgg  | 480 |
| cagatctcct gtggattaca caaggcggc tggagaggtg cacctggtgg agtggctcaa  | 540 |
| gaacatggtg gccgagagga aagcggagga ggtagtggac agtaagatgg ccgagaggcc | 600 |
| tcctcccaag acgctgaagc gggcgctcct ggtgngsstc cgctgcgtgg accctgacgc | 660 |
| gaacaagcgg cctaagatgg ggcattgtat ccacatgctc gaaatggacg acctccagtt | 720 |
| ccgagatagg tacagctcca agctaggtgg aggaagggag cctcagcaag cgcgagcacc | 780 |
| agcgtcggta cagatgagat gattgtcatt agagagtagc gatattaacc atgttatttt | 840 |
| tttcccgctc gtaaatacat tctttcccaa ctcgttccat cgattctcaa tggtytccga | 900 |
| ttkt                                                              |     |

(2) INFORMATION FOR SEQ ID NO:3182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3182:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Lys Glu Phe Lys Val Glu Val Glu Ala Ile Gly Arg Val Arg His Lys |    |
| 1                                                               | 5  |
| Asn Leu Val Arg Leu Leu Gly Tyr Cys Val Glu Gly Ala Tyr Arg Met | 10 |
| 20                                                              | 25 |
| Leu Val Tyr Glu Tyr Val Asp Asn Gly Asn Leu Asp Gln Trp Leu His | 30 |
| 35                                                              | 40 |
| Gly Asp Val Gly Glu Val Ser Pro Leu Thr Trp Asp Ile Arg Met Asn | 45 |
| 50                                                              | 55 |
|                                                                 | 60 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Met | Leu | Ala | Thr | Ala | Lys | Gly | Leu | Ala | Tyr | Leu | His | Glu | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Pro | Lys | Leu | Xaa | His | Arg | Asp | Ile | Lys | Ala | Ser | Asn | Ile | Leu | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Gln | Gln | Trp | Asn | Ala | Lys | Val | Ser | Asp | Phe | Gly | Leu | Ala | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Cys | Ser | Glu | Arg | Ser | Tyr | Val | Thr | Thr | Arg | Val | Met | Gly | Xaa | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Tyr | Val | Ala | Pro | Glu | Tyr | Ala | Ser | Thr | Gly | Met | Leu | Asn | Glu | Arg |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Asp | Val | Tyr | Ser | Phe | Gly | Val | Leu | Ile | Met | Glu | Ile | Ile | Thr | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg | Ser | Pro | Val | Asp | Tyr | Thr | Arg | Ala | Ala | Gly | Glu | Val | His | Leu | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Trp | Leu | Lys | Asn | Met | Val | Ala | Glu | Arg | Lys | Ala | Glu | Glu | Val | Val |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Ser | Lys | Met | Ala | Glu | Arg | Pro | Pro | Pro | Lys | Thr | Leu | Lys | Arg | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Val | Xaa | Xaa | Arg | Cys | Val | Asp | Pro | Asp | Ala | Asn | Lys | Arg | Pro |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Met | Gly | His | Val | Ile | His | Met | Leu | Glu | Met | Asp | Asp | Leu | Gln | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Asp | Arg | Tyr | Ser | Lys | Leu | Gly | Gly | Gly | Arg | Glu | Pro | Gln | Gln |     |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |     |
| Ala | Arg | Ala | Pro | Ala | Ser | Val | Gln | Met | Arg |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1575937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3183:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Tyr | Glu | Tyr | Val | Asp | Asn | Gly | Asn | Leu | Asp | Gln | Trp | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Gly | Asp | Val | Gly | Glu | Val | Ser | Pro | Leu | Thr | Trp | Asp | Ile | Arg | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ile | Met | Leu | Ala | Thr | Ala | Lys | Gly | Leu | Ala | Tyr | Leu | His | Glu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | Pro | Lys | Leu | Xaa | His | Arg | Asp | Ile | Lys | Ala | Ser | Asn | Ile | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asp | Gln | Gln | Trp | Asn | Ala | Lys | Val | Ser | Asp | Phe | Gly | Leu | Ala | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Leu | Cys | Ser | Glu | Arg | Ser | Tyr | Val | Thr | Thr | Arg | Val | Met | Gly | Xaa |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Gly | Tyr | Val | Ala | Pro | Glu | Tyr | Ala | Ser | Thr | Gly | Met | Leu | Asn | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Arg | Ser | Asp | Val | Tyr | Ser | Phe | Gly | Val | Leu | Ile | Met | Glu | Ile | Ile | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Arg | Ser | Pro | Val | Asp | Tyr | Thr | Arg | Ala | Ala | Gly | Glu | Val | His | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Glu | Trp | Leu | Lys | Asn | Met | Val | Ala | Glu | Arg | Lys | Ala | Glu | Glu | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Asp | Ser | Lys | Met | Ala | Glu | Arg | Pro | Pro | Pro | Lys | Thr | Leu | Lys | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Leu | Leu | Val | Xaa | Xaa | Arg | Cys | Val | Asp | Pro | Asp | Ala | Asn | Lys | Arg |

180 185 190  
Pro Lys Met Gly His Val Ile His Met Leu Glu Met Asp Asp Leu Gln  
195 200 205  
Phe Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly Gly Arg Glu Pro Gln  
210 215 220  
Gln Ala Arg Ala Pro Ala Ser Val Gln Met Arg  
225 230 235

(2) INFORMATION FOR SEQ ID NO:3184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1575938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3184:

Met Asn Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu  
1 5 10 15  
Gly Leu Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile  
20 25 30  
Leu Leu Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala  
35 40 45  
Lys Leu Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly  
50 55 60  
Xaa Phe Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn  
65 70 75 80  
Glu Arg Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile  
85 90 95  
Thr Gly Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His  
100 105 110  
Leu Val Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu  
115 120 125  
Val Val Asp Ser Lys Met Ala Glu Arg Pro Pro Pro Lys Thr Leu Lys  
130 135 140  
Arg Ala Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys  
145 150 155 160  
Arg Pro Lys Met Gly His Val Ile His Met Leu Glu Met Asp Asp Leu  
165 170 175  
Gln Phe Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly Gly Arg Glu Pro  
180 185 190  
Gln Gln Ala Arg Ala Pro Ala Ser Val Gln Met Arg  
195 200

(2) INFORMATION FOR SEQ ID NO:3185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..841

(D) OTHER INFORMATION: / Ceres Seq. ID 1575954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3185:

acaagcaaag cagcagcaac agccaacacc taaactaaag aacagtagta gtccctgtgt 60  
acgtctagca acgatccgca ccgagctcgc cagttttgct cgtagtttg grgacrgcga 120  
tggcgtccgg tcaggaaagc agggaggagc tggcgcgcat ggccgaggag gggcagaccg 180  
tcgtccccgg cggcaccggc ggcaagaccc tcgaggcgca ggagcacctc gccgaarggc 240

```
gcagtcacgg cgggcagacc cggagtgcgc agctgggcca tgaggggtac agcgagatgg 300
gcagcaaggg cgggcagacc cgcaaagagc agctgggcca cgaagggtac agcgagatgg 360
ggaggaaggg cggcctgagc accatgcagg agtccGgcgg cgagcgcgcc gCccgggagg 420
gcatcgagat cgacgagtc aagttcagga ccaagtccta gatctgatgc gtgccccgcg 480
ttagcatgta gtacgtagct gcaggaatgt agtgtcgtcg tagtagtagg gtagtcgtac 540
gacgtgccgc tcctcgtttg gcacgtgtgc cctgaataat gtagtgctgt cagtcgtcgt 600
cctagcacgc gtgtaggaga ccatacgtgc gcgtatgac atgcgtgttc gcttcagtta 660
ggttctgatg ttggtcgtcg tcaccgtgtt tgaagcaggc aggtctcttc aggctttgtc 720
gtcgtagcag cctgtgttct agctctacga cccatactc atagcgtgtg gtggtgggtc 780
gtgatgcctt aaggtctccg agtttgtatc cgtgcttgtt tcgttaaggt agtttggttc 840
t
```

(2) INFORMATION FOR SEQ ID NO:3186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1575955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3186:

```
Met Ala Ser Gly Gln Glu Ser Arg Glu Glu Leu Ala Arg Met Ala Glu
1 5 10 15
Glu Gly Gln Thr Val Val Pro Gly Gly Thr Gly Gly Lys Thr Leu Glu
20 25 30
Ala Gln Glu His Leu Ala Glu Xaa Arg Ser His Gly Gly Gln Thr Arg
35 40 45
Ser Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met Gly Ser Lys Gly
50 55 60
Gly Gln Thr Arg Lys Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met
65 70 75 80
Gly Arg Lys Gly Gly Leu Ser Thr Met Gln Glu Ser Gly Gly Glu Arg
85 90 95
Ala Ala Arg Glu Gly Ile Glu Ile Asp Glu Ser Lys Phe Arg Thr Lys
100 105 110
Ser
```

(2) INFORMATION FOR SEQ ID NO:3187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3187:

```
Met Ala Glu Glu Gly Gln Thr Val Val Pro Gly Gly Thr Gly Lys
1 5 10 15
Thr Leu Glu Ala Gln Glu His Leu Ala Glu Xaa Arg Ser His Gly Gly
20 25 30
Gln Thr Arg Ser Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met Gly
35 40 45
Ser Lys Gly Gly Gln Thr Arg Lys Glu Gln Leu Gly His Glu Gly Tyr
50 55 60
Ser Glu Met Gly Arg Lys Gly Gly Leu Ser Thr Met Gln Glu Ser Gly
65 70 75 80
```

Gly Glu Arg Ala Ala Arg Glu Gly Ile Glu Ile Asp Glu Ser Lys Phe  
85 90 95  
Arg Thr Lys Ser  
100

(2) INFORMATION FOR SEQ ID NO:3188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3188:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atttttcgag atgaacgaac agtcacgaac ccactgctcg aaaccgcagc cactggccag  | 60  |
| tcgatgccca tgactgcrgt gcccaggacc ggccccgggt gcctgggggc gccgccggct  | 120 |
| caggctctgt cgagctcact agccgggggt caaggcgccc cgaagcgact gggcgcatcg  | 180 |
| aagccgctgt ggatcggttc cactgagtca aacgtgagga gggagagagc aaaacgacct  | 240 |
| gacccctcct gcaccatctg caagggcaca gggagaatag actgccgcaa ctgctttggc  | 300 |
| cgaggaagaa caaaccatgc cgatgtggcc atgcttccga acggcgaatg gccacaatgg  | 360 |
| tgtcgaattt gtgggtgtag tggactgat tactgcctcc ggtgccatgg aactggtgag   | 420 |
| tatogtgaac ccattgggctt ccacttcact gtccaaagaa aatgagttag gtgggatggc | 480 |
| cttgtatgct acgatgcagc gcaGcTgvgN gggacatcgt agCccactca gcatgtttct  | 540 |
| ccactgtctc tcagaactca gatgatttat gtctaggsst aacgctgtaa taacgttgct  | 600 |
| tcataaaagg aaaaaatgtc                                              |     |

(2) INFORMATION FOR SEQ ID NO:3189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3189:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Phe Arg Asp Glu Arg Thr Val Gln Asn Pro Leu Leu Glu Thr Ala |  |
| 1 5 10 15                                                       |  |
| Ala Thr Gly Gln Ser Met Pro Met Thr Xaa Val Pro Arg Thr Gly Pro |  |
| 20 25 30                                                        |  |
| Gly Cys Leu Gly Ser Pro Pro Ala Gln Ala Leu Ser Ser Ser Leu Ala |  |
| 35 40 45                                                        |  |
| Gly Val Gln Gly Ala Pro Lys Arg Leu Gly Ala Ser Lys Pro Ser Trp |  |
| 50 55 60                                                        |  |
| Ile Val Arg Thr Glu Ser Asn Val Arg Arg Glu Arg Ala Lys Arg Pro |  |
| 65 70 75 80                                                     |  |
| Asp Pro Pro Cys Thr Ile Cys Lys Gly Thr Gly Arg Ile Asp Cys Arg |  |
| 85 90 95                                                        |  |
| Asn Cys Phe Gly Arg Gly Arg Thr Asn His Ala Asp Val Ala Met Leu |  |
| 100 105 110                                                     |  |
| Pro Asn Gly Glu Trp Pro Gln Trp Cys Arg Ile Cys Gly Gly Ser Gly |  |
| 115 120 125                                                     |  |
| Leu Asp Tyr Cys Leu Arg Cys His Gly Thr Gly Glu Tyr Arg Glu Pro |  |
| 130 135 140                                                     |  |
| Met Gly Phe His Phe Thr Val Gln Arg Lys                         |  |
| 145 150                                                         |  |

(2) INFORMATION FOR SEQ ID NO:3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..133  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575965  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3190:

Met Pro Met Thr Xaa Val Pro Arg Thr Gly Pro Gly Cys Leu Gly Ser  
1 5 10 15  
Pro Pro Ala Gln Ala Leu Ser Ser Ser Leu Ala Gly Val Gln Gly Ala  
20 25 30  
Pro Lys Arg Leu Gly Ala Ser Lys Pro Ser Trp Ile Val Arg Thr Glu  
35 40 45  
Ser Asn Val Arg Arg Glu Arg Ala Lys Arg Pro Asp Pro Pro Cys Thr  
50 55 60  
Ile Cys Lys Gly Thr Gly Arg Ile Asp Cys Arg Asn Cys Phe Gly Arg  
65 70 75 80  
Gly Arg Thr Asn His Ala Asp Val Ala Met Leu Pro Asn Gly Glu Trp  
85 90 95  
Pro Gln Trp Cys Arg Ile Cys Gly Gly Ser Gly Leu Asp Tyr Cys Leu  
100 105 110  
Arg Cys His Gly Thr Gly Glu Tyr Arg Glu Pro Met Gly Phe His Phe  
115 120 125  
Thr Val Gln Arg Lys  
130

(2) INFORMATION FOR SEQ ID NO:3191:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 131 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..131  
(D) OTHER INFORMATION: / Ceres Seq. ID 1575966  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3191:

Met Thr Xaa Val Pro Arg Thr Gly Pro Gly Cys Leu Gly Ser Pro Pro  
1 5 10 15  
Ala Gln Ala Leu Ser Ser Ser Leu Ala Gly Val Gln Gly Ala Pro Lys  
20 25 30  
Arg Leu Gly Ala Ser Lys Pro Ser Trp Ile Val Arg Thr Glu Ser Asn  
35 40 45  
Val Arg Arg Glu Arg Ala Lys Arg Pro Asp Pro Pro Cys Thr Ile Cys  
50 55 60  
Lys Gly Thr Gly Arg Ile Asp Cys Arg Asn Cys Phe Gly Arg Gly Arg  
65 70 75 80  
Thr Asn His Ala Asp Val Ala Met Leu Pro Asn Gly Glu Trp Pro Gln  
85 90 95  
Trp Cys Arg Ile Cys Gly Gly Ser Gly Leu Asp Tyr Cys Leu Arg Cys  
100 105 110  
His Gly Thr Gly Glu Tyr Arg Glu Pro Met Gly Phe His Phe Thr Val  
115 120 125  
Gln Arg Lys  
130

(2) INFORMATION FOR SEQ ID NO:3192:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 855 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..855
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3192:

|             |             |            |             |            |             |     |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| attaaaaaaaa | aaaggaaaag  | ggaggccagc | cggggtgggct | gctatcaggc | cttttggccg  | 60  |
| agctagccca  | ccggctagca  | cttccttatg | gcaccgagaa  | gccaaagcgt | vnnngtgaca  | 120 |
| gagaagggag  | tagcgaagag  | gaggttgcc  | tccctggcgg  | cggcgcttga | agccggttct  | 180 |
| ttcggcgctc  | gcaatcttct  | cgccggttcc | tgcgcaacct  | cctcaaggac | gcctccttaa  | 240 |
| gtatggagac  | aagctccctg  | ctaaggatca | ggcacaggac  | acagcctatg | agcaattaca  | 300 |
| atcatacccc  | tcataaaaagt | ttacaacaac | gactcaagct  | cttatggact | aaaaggacat  | 360 |
| tctatcttta  | agtcagtttg  | taattccgaa | gcttcatgaa  | cggcaccCtt | cggtatcacg  | 420 |
| tacagacagc  | ttcagccgaa  | gctgtttctt | cctgcaggac  | cttcagcgac | gaagcatggt  | 480 |
| cccaacagtg  | gttaactcca  | ccccagggga | tacagcagcg  | caccagtctt | gatgggaaat  | 540 |
| ggtgttccgg  | cagcagttcg  | aggtactgga | caggtctacc  | tgaagttaac | ttcaggaaaag | 600 |
| acgctcggtc  | tgaaggacat  | actctatgtg | ccatcgatga  | gccggaacct | catattagtg  | 660 |
| tcgctgctat  | gtcgacaggg  | tctcaaatta | gtgtttgagt  | ctaataaagt | ggtcctgtct  | 720 |
| aagtttggtg  | ctttgttggg  | aagtcatatg | agtcaggcgg  | tttgttccgt | ctttctgttt  | 780 |
| tgaataatca  | ttcttcttac  | catgttaatg | tggctctgtg  | taacgattcc | attaataata  | 840 |
| tatggcattc  | ccgtt       |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:3193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..50
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3193:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Arg | Ser | Gln | Ala | Xaa | Xaa | Thr | Glu | Lys | Gly | Val | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Arg | Arg | Leu | Pro | Ser | Leu | Ala | Ala | Ala | Leu | Glu | Ala | Gly | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     | Phe |
| Gly | Ala | Arg | Asn | Leu | Leu | Ala | Gly | Phe | Cys | Ala | Thr | Ser | Ser | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Thr |
| Pro | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 50  |

(2) INFORMATION FOR SEQ ID NO:3194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..100
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1575994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3194:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Gly | Thr | Leu | Arg | Tyr | His | Val | Gln | Thr | Ala | Ser | Ala | Glu | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Ser | Ser | Cys | Arg | Thr | Phe | Ser | Asp | Glu | Ala | Trp | Ser | Gln | Gln | Trp |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Leu | Thr | Pro | Pro | Gln | Gly | Ile | Gln | Gln | Arg | Thr | Ser | Leu | Asp | Gly | Lys |

35 40 45  
Trp Cys Ser Gly Ser Ser Ser Arg Tyr Trp Thr Gly Leu Pro Glu Val  
50 55 60  
Asn Phe Arg Lys Asp Ala Arg Ser Glu Gly His Thr Leu Cys Ala Ile  
65 70 75 80  
Asp Glu Pro Glu Pro His Ile Ser Val Ala Ala Met Ser Thr Gly Ser  
85 90 95  
Gln Ile Ser Val  
100

(2) INFORMATION FOR SEQ ID NO:3195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3195:

Met Gly Asn Gly Val Pro Ala Ala Val Arg Gly Thr Gly Gln Val Tyr  
1 5 10 15  
Leu Lys Leu Thr Ser Gly Lys Thr Leu Val Leu Lys Asp Ile Leu Tyr  
20 25 30  
Val Pro Ser Met Ser Arg Asn Leu Ile Leu Val Ser Leu Leu Cys Arg  
35 40 45  
Gln Gly Leu Lys Leu Val Phe Glu Ser Asn Lys Val Val Leu Ser Lys  
50 55 60  
Phe Gly Thr Leu Leu Glu Ser His Met Ser Gln Ala Val Cys Ser Val  
65 70 75 80  
Phe Leu Phe

(2) INFORMATION FOR SEQ ID NO:3196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3196:

cccaatcctc ccgcgcgrgc gacgccttcc cctccctcct tccctcgtcc catgctccgc 60  
cgctgacacg ttggcccgcac ttaacottac gatggccgcc gcctccgccca tcacgcgcgt 120  
ctccggcggt gtgcttcccc aaaccttccct atccccccgg tcgccgccgc cgcaggctcc 180  
agccgtggcc tcttcattcc gccggtcttc cttgtgcgct tcccctcgcc ggatcactca 240  
cataatcccc cgcgctgatg caagtgcga agctggagaa ccggagcctg tcaactgcttc 300  
agatgaatcc gaagaggagg tggccgaggg gtctgtcgct gtggcggagg gggaggaacc 360  
gacgcgcgcc agcaagccga agGttaagtt cggcgaaata attgggattc tgaataagca 420  
gttcattgag gaggctgaga aggtgaagac tgtaccggat ctgaggcctg gcgatatcat 480  
tgagcttagg atgcaacggc ccaacaaaag gagattgtcg ctctttaagg gcataatcat 540  
cgcaagcac aaagctggtg ttcacaccac aatccgtgtc agaaggatca ttgctggtgt 600  
aggagttgag attaccttcc cagtgtactc acccaggatc aaggaaatca cggttatcag 660  
gcacaagaaa gtgaggagag caaagttgta ctacctgaaa gacaagcttc cccgcttttc 720  
aacattcaag tgaaatcaga tatgctgaca gaacgacttt ttccaccacc atctcgattt 780  
ctcttaaac ttttttttct acttccctat cgatatcatc atatttcaact gtaatctctg 840  
ggtatcagat gtgtaatatc tacagcttta tatcatactt ggcttagtgc aatgttttgt 900  
ttgtgtcag tgtacaaaat tcatactagc accttggtat tatgaatttg caaataacaag 960

gttatgc

(2) INFORMATION FOR SEQ ID NO:3197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1576003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3197:

Pro Ile Leu Pro Pro Xaa Arg Arg Leu Pro Leu Pro Pro Ser Ser Val  
1 5 10 15  
Pro Cys Ser Ala Ala Asp Thr Leu Ala Arg Leu Asn Leu Thr Met Ala  
20 25 30  
Ala Ala Ser Ala Ile Thr Ala Val Ser Gly Val Val Leu Pro Gln Thr  
35 40 45  
Phe Leu Ser Pro Arg Ser Pro Pro Gln Val Leu Ala Val Ala Ser  
50 55 60  
Ser Phe Arg Arg Leu Ser Leu Cys Ala Ser Pro Arg Arg Ile Thr His  
65 70 75 80  
Ile Ile Pro Arg Ala Asp Ala Ser Ala Glu Ala Gly Glu Pro Glu Pro  
85 90 95  
Val Thr Ala Ser Asp Glu Ser Glu Glu Glu Val Ala Glu Gly Ser Val  
100 105 110  
Ala Val Ala Glu Gly Glu Glu Pro Thr Pro Pro Ser Lys Pro Lys Val  
115 120 125  
Lys Phe Gly Glu Ile Ile Gly Ile Leu Asn Lys Gln Phe Ile Glu Glu  
130 135 140  
Ala Glu Lys Val Lys Thr Val Pro Asp Leu Arg Pro Gly Asp Ile Ile  
145 150 155 160  
Glu Leu Arg Met Gln Arg Pro Asn Lys Arg Arg Leu Ser Leu Phe Lys  
165 170 175  
Gly Ile Ile Ile Ala Lys His Lys Ala Gly Val His Thr Thr Ile Arg  
180 185 190  
Val Arg Arg Ile Ile Ala Gly Val Gly Val Glu Ile Thr Phe Pro Val  
195 200 205  
Tyr Ser Pro Arg Ile Lys Glu Ile Thr Val Ile Arg His Lys Lys Val  
210 215 220  
Arg Arg Ala Lys Leu Tyr Tyr Leu Lys Asp Lys Leu Pro Arg Phe Ser  
225 230 235 240  
Thr Phe Lys

(2) INFORMATION FOR SEQ ID NO:3198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1576004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3198:

Met Ala Ala Ala Ser Ala Ile Thr Ala Val Ser Gly Val Val Leu Pro  
1 5 10 15  
Gln Thr Phe Leu Ser Pro Arg Ser Pro Pro Pro Gln Val Leu Ala Val  
20 25 30



Ala Ser Ser Phe Arg Arg Leu Ser Leu Cys Ala Ser Pro Arg Arg Ile  
35 40 45  
Thr His Ile Ile Pro Arg Ala Asp Ala Ser Ala Glu Ala Gly Glu Pro  
50 55 60  
Glu Pro Val Thr Ala Ser Asp Glu Ser Glu Glu Glu Val Ala Glu Gly  
65 70 75 80  
Ser Val Ala Val Ala Glu Gly Glu Glu Pro Thr Pro Pro Ser Lys Pro  
85 90 95  
Lys Val Lys Phe Gly Glu Ile Ile Gly Ile Leu Asn Lys Gln Phe Ile  
100 105 110  
Glu Glu Ala Glu Lys Val Lys Thr Val Pro Asp Leu Arg Pro Gly Asp  
115 120 125  
Ile Ile Glu Leu Arg Met Gln Arg Pro Asn Lys Arg Arg Leu Ser Leu  
130 135 140  
Phe Lys Gly Ile Ile Ile Ala Lys His Lys Ala Gly Val His Thr Thr  
145 150 155 160  
Ile Arg Val Arg Arg Ile Ile Ala Gly Val Gly Val Glu Ile Thr Phe  
165 170 175  
Pro Val Tyr Ser Pro Arg Ile Lys Glu Ile Thr Val Ile Arg His Lys  
180 185 190  
Lys Val Arg Arg Ala Lys Leu Tyr Tyr Leu Lys Asp Lys Leu Pro Arg  
195 200 205  
Phe Ser Thr Phe Lys  
210

(2) INFORMATION FOR SEQ ID NO:3199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3199:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| cttaaaaacc tctgctcggg cctaggggttt cctcccagtc gtcctcgctt ggcgtccgcc  | 60  |
| ttagcccgcc gccaggagag cgggctcggt cgggttcgtcg aagatcccgg atctgctctg  | 120 |
| tcacgaggtc tttcgggcggg tgttggtctcg cgaggtgtag cgagccaagg tctggtcgcc | 180 |
| ttttcaggag agtttcgaga agctgaaatg gctcctaaag ctgctcctgc caagaagggt   | 240 |
| gatgccaaag cccaggcctt gaagggttgc aaggctgtga agtctgggtc agtaaagaag   | 300 |
| accaagaaga tccgcacgtc cgtgacattt caccgcccc aagacctgaa gaaggctagg    | 360 |
| gaccccaagt acccaagaat cagcactacc ggaaggaaca agcttgatca gtaccaaatt   | 420 |
| ctcaagtatc ccctcaccac agaatcggcg atgaagaaga ttgaagataa caacactctt   | 480 |
| gttttcattg tgcacctcaa ggcagacaag ragaagatca Aggctgctgt caagaagatg   | 540 |
| tatgacattc aggccaagaa ggtcaacacc ctgatcaggc ctgatggaaa gaagaaggct   | 600 |
| tacgtgaagc ttatgcctga ctatgatgct cttgatgtgg ccaacaaaat cggcatcatc   | 660 |
| taaagttacc gcgtcaggca tctgctgtgc tctatttcca tgtgaaacca gagtttttgt   | 720 |
| agctatggct cagtggctcc atgaccatgt cttatgcaca cttacgaatt tgatatcatc   | 780 |
| caagtcacag gttgtgctca tcaatacttg gatactatca cttattcgta ttgggttggt   | 840 |
| ctttggctct cacatttctt tgtattgggt tgggtgtttg atctcacctt tcttcgcatt   | 900 |
| gggttggtct ttggaaattg gaactcggcc tgatagctgt tggagtatag tgtatggatc   | 960 |
| tgcgttc                                                             |     |

(2) INFORMATION FOR SEQ ID NO:3200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1576027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3200:

Leu Lys Asn Leu Cys Ser Gly Leu Gly Phe Pro Pro Ser Arg His Arg  
1 5 10 15  
Leu Ala Ser Ala Leu Ala Arg Arg Gln Glu Ser Arg Leu Gly Arg Phe  
20 25 30  
Val Glu Asp Pro Gly Ser Ala Leu Ser Arg Gly Leu Ser Ala Gly Val  
35 40 45  
Val Ser Arg Gly Val Ala Ser Gln Gly Leu Val Ala Phe Ser Gly Glu  
50 55 60  
Phe Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly  
65 70 75 80  
Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly  
85 90 95  
Ser Val Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg  
100 105 110  
Pro Lys Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser  
115 120 125  
Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro  
130 135 140  
Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu  
145 150 155 160  
Val Phe Ile Val Asp Leu Lys Ala Asp Lys Xaa Lys Ile Lys Ala Ala  
165 170 175  
Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile  
180 185 190  
Arg Pro Asp Gly Lys Lys Lys Ala Tyr Val Lys Leu Met Pro Asp Tyr  
195 200 205  
Asp Ala Leu Asp Val Ala Asn Lys Ile Gly Ile Ile  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1576028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3201:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln  
1 5 10 15  
Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ser Val Lys Lys Thr  
20 25 30  
Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Lys Thr Leu Lys  
35 40 45  
Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg Asn  
50 55 60  
Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu Ser  
65 70 75 80  
Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp  
85 90 95  
Leu Lys Ala Asp Lys Xaa Lys Ile Lys Ala Ala Val Lys Lys Met Tyr  
100 105 110  
Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Lys  
115 120 125  
Lys Lys Ala Tyr Val Lys Leu Met Pro Asp Tyr Asp Ala Leu Asp Val

130 135 140  
Ala Asn Lys Ile Gly Ile Ile  
145 150  
(2) INFORMATION FOR SEQ ID NO:3202:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..115  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576029  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3202:  
Met Met Leu Leu Met Trp Pro Thr Lys Ser Ala Ser Ser Lys Val Thr  
1 5 10 15  
Ala Ser Gly Ile Cys Cys Ala Leu Phe Pro Cys Glu Thr Arg Val Phe  
20 25 30  
Val Ala Met Ala Gln Trp Leu His Asp His Val Leu Cys Thr Leu Thr  
35 40 45  
Asn Leu Ile Ser Ser Lys Ser Gln Val Val Leu Ile Asn Thr Trp Ile  
50 55 60  
Leu Ser Leu Ile Arg Ile Gly Leu Val Phe Gly Ser His Ile Ser Leu  
65 70 75 80  
Tyr Trp Val Gly Val Leu Ile Ser Pro Phe Phe Ala Leu Gly Trp Ser  
85 90 95  
Leu Glu Ile Gly Thr Arg Pro Asp Ser Cys Trp Ser Ile Val Tyr Gly  
100 105 110  
Ser Ala Phe  
115

(2) INFORMATION FOR SEQ ID NO:3203:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1041 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1041  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576041  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3203:

atcacttgac ttgcgagcga ccgcggctca cgtcggctgc ataaattgct tcgtagacta 60  
gtaccacaca gtttgcgaga aggggagagg tagagggttc gaggtagaga gataganang 120  
mngagaagra gggcgaggcg gcggatccgt cactccgttc ttctccgctg atctggagga 180  
aggargcgar gggagttgca aatccatcaa tggecactcc aaccacctat tcagtcogca 240  
tatcctcgga gaccacaaag attgaagcct ggggtggtgtc tgacgaagct ttggccaggc 300  
aactgcagga dgaggagaac acgcgtgamg ctretgccga caccagagaa gtcrcggca 360  
atgtaccctt ggagtcacgc tcaccggctg ttgartacag gsctgcacag aatgcagctc 420  
aggttgcaag ggaagacaat gtgGacccag ataatatgGt catatgGagc aactacaagc 480  
attaggggaa gcagtaggaa ttcagtccag agggttatct gatgagctga tatcttattt 540  
ggagccattt aggaacaagt gcactttctt ctccaggaaa aagaacagtg aggaatgtgt 600  
gatctgcaag acaacatata gaagccggca gaaattgata agactaccct gcagccactg 660  
ttatcacgca gattgcataa ctcgttggct taagatcaac aaggcatgcc cagtctgcaa 720  
cgaggagggtg tttggatgaa ctgcaagggtt cctggcagat gctgcggttt catcgttact 780  
tgcttgccgc atgcttttga gaagacggtg gacgcataag gtccattgtt tgtgattatg 840  
ttgtgagcct agtttggtgc cctttgctta agaggactgg ctctgcccac gcatgggtcg 900  
gtctacacgt gtgctagtaa ctggaccagg tgcggttttg tgatgcgtct atccatcttg 960  
gttttatcac aaattgatag atctgttgtg tgggtagttt ggttgccggt ttctgaatat 1020  
aatggatggt gtttttgcgc c

(2) INFORMATION FOR SEQ ID NO:3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1576042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3204:

Met Ala Thr Pro Thr Thr Tyr Ser Val Arg Ile Ser Ser Glu Thr His  
1 5 10 15  
Lys Ile Glu Ala Trp Val Val Ser Asp Glu Ala Leu Ala Arg Gln Leu  
20 25 30  
Gln Xaa Glu Glu Asn Thr Arg Xaa Ala Xaa Ala Asp Thr Arg Glu Val  
35 40 45  
Xaa Gly Asn Val Pro Leu Glu Ser Ser Ser Pro Ala Val Xaa Tyr Arg  
50 55 60  
Xaa Ala Gln Asn Ala Ala Gln Val Ala Arg Glu Asp Asn Val Asp Pro  
65 70 75 80  
Asp Asn Met Val Ile Trp Ser Asn Tyr Lys His  
85 90

(2) INFORMATION FOR SEQ ID NO:3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1576043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3205:

Met Tyr Pro Trp Ser His Arg His Arg Leu Xaa Thr Xaa Leu His  
1 5 10 15  
Arg Met Gln Leu Arg Leu Gln Gly Lys Thr Met Trp Thr Gln Ile Ile  
20 25 30  
Trp Ser Tyr Gly Ala Thr Thr Ser Ile Arg Gly Ser Ser Arg Asn Ser  
35 40 45  
Val Gln Arg Val Ile  
50

(2) INFORMATION FOR SEQ ID NO:3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1576044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3206:

Met Glu Gln Leu Gln Ala Leu Gly Glu Ala Val Gly Ile Gln Ser Arg  
1 5 10 15  
Gly Leu Ser Asp Glu Leu Ile Ser Tyr Leu Glu Pro Phe Arg Asn Lys  
20 25 30  
Cys Thr Phe Phe Ser Arg Lys Lys Asn Ser Glu Glu Cys Val Ile Cys

(2) INFORMATION FOR SEQ ID NO:3207:

(A) LENGTH: 769 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..769  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576045

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| cccaaaacgc | ccaccacgcc  | gccactcgca | accgcacacc  | agccctcgca | accaccacc   | 60  |
| acgtccgaga | cgctccgagat | ggagttctct | gccgcgtacc  | tgctgccgtg | cctggggcgcc | 120 |
| ggcccgcccc | ccacgctccc  | gaccaaggac | gacgtgcgtc  | gcatactgag | atccgtcagc  | 180 |
| gccgaggttg | aggaggaccg  | cctcgacctg | Gtcttcgcc   | tcctagaggt | taaggacatc  | 240 |
| gccgagctga | tcGccacggg  | cggggagcat | ctcgctacg   | cgccgtcagg | agccgtgtgt  | 300 |
| gcgctgcttg | cgactcctgc  | cgctcgcgag | gtcgaggagg  | aggccaacga | ggaggaggat  | 360 |
| gaggacatcg | ccctcttcaa  | cctcttcgac | tgactcgtca  | acctacgtg  | cgctccggga  | 420 |
| ccgcgggcaa | ccaaggacga  | gtgcccatgc | taccgcgaca  | tgaccaccgg | acacggcaac  | 480 |
| cgcaccaggc | ccaagtgcc   | ctgatgatat | tcattccttc  | gctctgtctt | gcattgcgtat | 540 |
| gtaatgtata | ggctgtgcaa  | tgcatgcata | catgatacat  | gccgtgactc | tggtatcgcg  | 600 |
| gatgcctatg | catgcttttc  | actagctatt | attactacta  | ctactactct | tcctgtcttc  | 660 |
| ctactgtgtg | caccaaaagt  | agagggacga | catgcatggc  | gatgacatgt | cgtgttatgt  | 720 |
| gcactggcgg | ccgcttgccc  | aggtcataat | tcattgctctg | tgtattgtg  |             |     |

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..130  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576046

[illegible]

130

(2) INFORMATION FOR SEQ ID NO:3209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1576047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3209:

Gln Asn Ala His His Ala Ala Thr Arg Asn Arg Thr Pro Ala Leu Ala  
1 5 10 15  
Thr His His His Val Arg Asp Val Arg Asp Gly Val Pro Arg Arg Val  
20 25 30  
Pro Ala Ala Val Pro Gly Arg Arg Pro Gly Pro His Ala Pro Asp Gln  
35 40 45  
Gly Arg Arg Ala Ser His Pro Glu Ile Arg Gln Arg Arg Gly Gly Gly  
50 55 60  
Gly Pro Pro Arg Pro Gly Leu Arg Pro Pro Arg Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1576048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3210:

Met Glu Phe Leu Ala Ala Tyr Leu Leu Pro Cys Leu Gly Ala Gly Pro  
1 5 10 15  
Ala Pro Thr Leu Pro Thr Lys Asp Asp Val Arg Arg Ile Leu Arg Ser  
20 25 30  
Val Ser Ala Glu Val Glu Glu Asp Arg Leu Asp Leu Val Phe Ala Leu  
35 40 45  
Leu Glu Val Lys Asp Ile Ala Glu Leu Ile Ala Thr Gly Gly Glu His  
50 55 60  
Leu Ala Tyr Ala Pro Ser Gly Ala Ala Ala Val Val Ala Thr Pro  
65 70 75 80  
Ala Ala Ala Glu Val Glu Glu Ala Thr Lys Glu Glu Asp Glu Asp  
85 90 95  
Ile Ala Leu Phe Asn Leu Phe Asp  
100

(2) INFORMATION FOR SEQ ID NO:3211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..999

(D) OTHER INFORMATION: / Ceres Seq. ID 1576049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3211:

```

gagtagcaat cactgctgcg cccgataggw ggcagcgagc cagcdhmcca mccgactctg 60
ttccaacgag cctwcccwcc caaacttgca cgctgcccc gctctcgcc cggccccga 120
tccagatcca ggggtggaata gggaaaggcc atacaccatg gcggatttct ccaaggaatc 180
ttgcccttct gtgaagaaca ttttacttct ggattctgaa ggaaagcgtg ttgctgtaaa 240
gtattttctca gatgattggc cgactaatgc atcaaagtta gcctacgaaa agtctgtwtt 300
tactaaaact ctaaagacaa atgcacggac agaagctgag ataacattgt ttgatggtta 360
tattgwcgk tacaagtttg tacrtgacct tcacttkttt gtcaccgctg gagatgatga 420
gGaatgagct catcttagca agtgactac atgggttttc tgattctgtt ggtcttctac 480
tcaggggtga tgttgmgag cggactgcmc ttgagaactt ggatttgata cttctctgca 540
tcgatgaaat ttagatggg ggaatcatcc tggaaacaga tgcaaacc attgctggta 600
agggtgcaac caatgctgtt gatggttctg tgcctttttc tgagcagacg atatctcagg 660
cactagccac agctaggag caccttgcaa gatctctact gaaatgaaca accagcaata 720
tgtatgacgt attatatgac atatatgtgt gtaggttggg ctactgaatg ttgaggtct 780
ttgtagacgt tattcgtccc aaagtgtgc tgtgacagag cctagttgaa tatccgaggg 840
attggtcaca tgctcgtaa atttttttt tgaaccagtg agtttgtagc tgccatattt 900
caggtaaaac ataaaataaa gagttgtaat tgggtgtaat ataattttca ccatacaaaa 960
aaaaattcat ctcaactatc aaaccatggt aaaaggttc

```

(2) INFORMATION FOR SEQ ID NO:3212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1576050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3212:

```

Met Val Ile Leu Xaa Thr Ser Leu Tyr Xaa Thr Phe Thr Xaa Leu
1 5 10 15
Ser Pro Leu Glu Met Met Arg Asn Glu Leu Ile Leu Ala Ser Val Leu
 20 25 30
His Gly Phe Ser Asp Ser Val Gly Leu Leu Leu Arg Gly Asp Val Xaa
 35 40 45
Lys Arg Thr Ala Leu Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp
 50 55 60
Glu Ile Val Asp Gly Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile
65 70 75 80
Ala Gly Lys Val Ala Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser
 85 90 95
Glu Gln Thr Ile Ser Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala
 100 105 110
Arg Ser Leu Leu Lys
 115

```

(2) INFORMATION FOR SEQ ID NO:3213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1576051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3213:

```

Met Met Arg Asn Glu Leu Ile Leu Ala Ser Val Leu His Gly Phe Ser
1 5 10 15
Asp Ser Val Gly Leu Leu Leu Arg Gly Asp Val Xaa Lys Arg Thr Ala
 20 25 30

```

Leu Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp Glu Ile Val Asp  
35 40 45  
Gly Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile Ala Gly Lys Val  
50 55 60  
Ala Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser Glu Gln Thr Ile  
65 70 75 80  
Ser Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala Arg Ser Leu Leu  
85 90 95  
Lys

(2) INFORMATION FOR SEQ ID NO:3214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1576052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3214:

Met Arg Asn Glu Leu Ile Leu Ala Ser Val Leu His Gly Phe Ser Asp  
1 5 10 15  
Ser Val Gly Leu Leu Leu Arg Gly Asp Val Xaa Lys Arg Thr Ala Leu  
20 25 30  
Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp Glu Ile Val Asp Gly  
35 40 45  
Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile Ala Gly Lys Val Ala  
50 55 60  
Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser Glu Gln Thr Ile Ser  
65 70 75 80  
Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala Arg Ser Leu Leu Lys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:3215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 655 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..655

(D) OTHER INFORMATION: / Ceres Seq. ID 1576067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3215:

gccccgtcat tgcttgccct cagtctccag agaacgcgat ttgttctgtt gttcgggtccc 60  
caatcttcgc ctccgCtccg cccgccccga cccagatcag gagctgagag atggacgccca 120  
acaggcgcca aggtgggatt cagcagttgc tggctgcgga gCaggaggct cagcaaattg 180  
tgaatgcggc tagagctgct aagtcagcaa ggcttaggca agcgaaagag gaggcagaga 240  
gggaaatagc cgaataccgt gccagatgg aggctgagtt ccagaggaag gtcgcagaga 300  
gcagtgggtga ctctggtgcg aacgtcaagc gtctcgagga agagacaacg gcgaaaatcg 360  
aacagctcaa ccagcaggct gcaagcatct cccagatgt cattcagatg cttctgaggc 420  
atgtcaccac cgtgaagaac tgagaagtgc tgctccaaa ctatggtcat cggctctatt 480  
atttttgtca gagcaggtga ggaataataa tatggccctt gtaccagtaa ttcttttttt 540  
aactacggaa taagccgcag cagctttagc ggcaaccgtg actgttacta ccagaacttg 600  
ccattatttg gtataatcgg caaattaaat aatattgttt tatattggat ttttg

(2) INFORMATION FOR SEQ ID NO:3216:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..60  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576068  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3216:  
Ala Arg Ser Leu Leu Ala Ser Ser Leu Gln Arg Thr Arg Phe Val Leu  
1                  5                  10                  15  
Leu Phe Gly Pro Gln Ser Ser Pro Pro Leu Arg Pro Pro Arg Pro Arg  
                  20                  25                  30  
Ser Gly Ala Glu Arg Trp Thr Pro Thr Gly Ala Lys Val Gly Phe Ser  
                  35                  40                  45  
Ser Cys Trp Leu Arg Ser Arg Arg Leu Ser Lys Leu  
50                  55                  60

(2) INFORMATION FOR SEQ ID NO:3217:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 63 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..63  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576069  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3217:  
Pro Ala His Cys Leu Pro Pro Val Ser Arg Glu Arg Asp Leu Phe Cys  
1                  5                  10                  15  
Cys Ser Val Pro Asn Leu Arg Leu Arg Ser Ala Arg Pro Asp Pro Asp  
                  20                  25                  30  
Gln Glu Leu Arg Asp Gly Arg Gln Gln Ala Pro Arg Trp Asp Ser Ala  
                  35                  40                  45  
Val Ala Gly Cys Gly Ala Gly Gly Ser Ala Asn Cys Cys Glu Cys Gly  
50                  55                  60

(2) INFORMATION FOR SEQ ID NO:3218:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 110 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..110  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1576070  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3218:  
Met Asp Ala Asn Arg Arg Gln Gly Gly Ile Gln Gln Leu Leu Ala Ala  
1                  5                  10                  15  
Glu Gln Glu Ala Gln Gln Ile Val Asn Ala Ala Arg Ala Ala Lys Ser  
                  20                  25                  30  
Ala Arg Leu Arg Gln Ala Lys Glu Glu Ala Glu Arg Glu Ile Ala Glu  
                  35                  40                  45  
Tyr Arg Ala Gln Met Glu Ala Glu Phe Gln Arg Lys Val Ala Glu Ser  
50                  55                  60  
Ser Gly Asp Ser Gly Ala Asn Val Lys Arg Leu Glu Glu Glu Thr Thr  
65                  70                  75                  80  
Ala Lys Ile Glu Gln Leu Asn Gln Gln Ala Ala Ser Ile Ser Pro Asp

85 90 95  
Val Ile Gln Met Leu Leu Arg His Val Thr Thr Val Lys Asn  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..892
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3219:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| accgcagcca | caccccaaca  | tcaaaaccct | cccattctctt | cccctccgcc | gccgtctctg | 60  |
| ctctcaagat | cgccatggcg  | tcagaaaaga | agcagtcgaa  | cccgatgcgg | gagatcaagg | 120 |
| tgcagaagct | cgtgtctaat  | atctccgttg | gagagagtgg  | agatcgactc | acccgcgccg | 180 |
| ccaaggtgtt | ggagcagttg  | agtgggcagt | ctccggtttt  | ctccaaggca | aggtatactg | 240 |
| tgaggtcttt | cggatttcgt  | cgtaatgaga | agattgcatg  | ctatttcta  | cgtgctgtat | 300 |
| gcttcttgaa | attgggaaaa  | catgatgaga | ccattaaaAg  | aatgctcaaa | agcacttgag | 360 |
| ctcaatccaa | catacctgaa  | agccctgctt | cggagggcag  | aagcgcatga | aaagcttgaa | 420 |
| cattatgatg | aagctattgc  | cgatatgaaa | aaggttggtg  | aagtggatcc | ttcaaatcaa | 480 |
| caagccacga | ggtctctttt  | ccgacttgag | cccctggcag  | ctgagaagag | ggaaaagatg | 540 |
| aaggaagaaa | tgattgcaaa  | gctgaaagat | ctggggaact  | ctgtgctggg | ccgcttcggg | 600 |
| atgagtgttg | acaatttcaa  | agctgtcaaa | gatccaaaca  | ctggctctta | cagcattcaa | 660 |
| ttccaaaagt | aacacgacgt  | gaagaaagac | atggatgaat  | atggctgggc | ggcatatttc | 720 |
| agttgtaatt | gttcaaggaa  | cttgtgcgtc | acatacctgg  | acaatatcca | aacagatata | 780 |
| tgcaaatcga | tctgaagggtg | ggacatggaa | gaggaattgg  | agtattgcgt | cgcgtttgca | 840 |
| tttgtcgcac | gttagactgt  | tagagatgct | ttctcgagtg  | cgaacttgca | tg         |     |

(2) INFORMATION FOR SEQ ID NO:3220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | His | Thr | Pro | Thr | Ser | Lys | Pro | Ser | His | Leu | Phe | Pro | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Val | Ser | Ala | Leu | Lys | Ile | Ala | Met | Ala | Ser | Glu | Lys | Lys | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Pro | Met | Arg | Glu | Ile | Lys | Val | Gln | Lys | Leu | Val | Leu | Asn | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gly | Glu | Ser | Gly | Asp | Arg | Leu | Thr | Arg | Ala | Ala | Lys | Val | Leu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Leu | Ser | Gly | Gln | Ser | Pro | Val | Phe | Ser | Lys | Ala | Arg | Tyr | Thr | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Phe | Gly | Ile | Arg | Arg | Asn | Glu | Lys | Ile | Ala | Cys | Tyr | Ser | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Ala | Val | Cys | Phe | Leu | Lys | Leu | Gly | Lys | His | Asp | Glu | Thr | Ile | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Met | Leu | Lys | Ser | Thr |     |     |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3221:

Met Met Arg Pro Leu Lys Glu Cys Ser Lys Ala Leu Glu Leu Asn Pro  
1 5 10 15  
Thr Tyr Leu Lys Ala Leu Leu Arg Arg Ala Glu Ala His Glu Lys Leu  
20 25 30  
Glu His Tyr Asp Glu Ala Ile Ala Asp Met Lys Lys Val Val Glu Val  
35 40 45  
Asp Pro Ser Asn Gln Gln Ala Thr Arg Ser Leu Phe Arg Leu Glu Pro  
50 55 60  
Leu Ala Ala Glu Lys Arg Glu Lys Met Lys Glu Glu Met Ile Ala Lys  
65 70 75 80  
Leu Lys Asp Leu Gly Asn Ser Val Leu Gly Arg Phe Gly Met Ser Val  
85 90 95  
Asp Asn Phe Lys Ala Val Lys Asp Pro Asn Thr Gly Ser Tyr Ser Ile  
100 105 110  
Gln Phe Gln Lys  
115

(2) INFORMATION FOR SEQ ID NO:3222:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..115  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3222:

Met Arg Pro Leu Lys Glu Cys Ser Lys Ala Leu Glu Leu Asn Pro Thr  
1 5 10 15  
Tyr Leu Lys Ala Leu Leu Arg Arg Ala Glu Ala His Glu Lys Leu Glu  
20 25 30  
His Tyr Asp Glu Ala Ile Ala Asp Met Lys Lys Val Val Glu Val Asp  
35 40 45  
Pro Ser Asn Gln Gln Ala Thr Arg Ser Leu Phe Arg Leu Glu Pro Leu  
50 55 60  
Ala Ala Glu Lys Arg Glu Lys Met Lys Glu Glu Met Ile Ala Lys Leu  
65 70 75 80  
Lys Asp Leu Gly Asn Ser Val Leu Gly Arg Phe Gly Met Ser Val Asp  
85 90 95  
Asn Phe Lys Ala Val Lys Asp Pro Asn Thr Gly Ser Tyr Ser Ile Gln  
100 105 110  
Phe Gln Lys  
115

(2) INFORMATION FOR SEQ ID NO:3223:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3223:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaagararav  | ggggaggtcg  | acgagacaga  | gagagaaggc  | caagaggctt  | cctctcccca  | 60   |
| ttctctccctt | ccgtgcccta  | gccgagccag  | ccgcgaggaa  | ggaggcatcc  | cgccgtctcg  | 120  |
| cctggcgccc  | gcccgtoggc  | cgaccttctg  | ccgcagcttc  | caattgtaaa  | aagatcatag  | 180  |
| atTTTTgtgc  | aagagcgagt  | ggatatggaa  | ccatcccctc  | agcctatggg  | tgctcgtgcc  | 240  |
| ggtgggtcac  | aagtgtatcc  | tgctctctgc  | tatccgcctg  | cagcaacagt  | agctcctgct  | 300  |
| tctgttgtat  | ctgctggttt  | acagtcaggg  | cagccattcc  | cagccaatcc  | tggtcatatg  | 360  |
| agtgtcagc   | accagattgt  | ctaccaacaa  | gctcaacaat  | tccaccaaca  | gctccagcag  | 420  |
| caacaacaac  | agcagcttca  | gcagttctgg  | ggtgaacgca  | tgactgaaat  | tgaggcgacg  | 480  |
| actgatttca  | agaaccacaa  | cttgccactt  | gcgaggataa  | agaagatcat  | gaaggccgat  | 540  |
| gaagatgttc  | gcatgatctc  | agctgaagct  | cctgtagtct  | ttgcaaaaagc | ttgtgagata  | 600  |
| ttcatactgg  | agctgacact  | taVggctcgtg | gatgcmcaact | gaggwgwaca  | agcgccgcac  | 660  |
| yttgcwaamg  | aatgacattg  | cagcagcgat  | cactaggact  | gacattttatg | acttcttgggt | 720  |
| cgacattgtt  | cccagggwtg  | agatgaagga  | ggmcggaatt  | gggcttcccta | gggctgggtct | 780  |
| gccacccatg  | ggagccccag  | ctgatgcata  | tccatactac  | tacatgccac  | agcagcaggt  | 840  |
| gcctggttct  | ggaatggttt  | atgggtgccc  | gcaagggcac  | ccagtgaactt | atTTgtggca  | 900  |
| ggagcctcag  | caacagcagg  | agcaagctcc  | tgaagagcag  | caatctgcat  | gaaagtggct  | 960  |
| gagaatattg  | ctcagaagct  | atcacctgat  | tcagagttct  | catttttaggt | tgtccaaact  | 1020 |
| gcaggTTTTc  | ttagtaatat  | cgttggttat  | caaactgaaa  | caggcgattc  | taagtagggt  | 1080 |
| gtagcatcat  | ggtagtTTTca | tttctgcttg  | tgatgttagt  | tgaaaggata  | atgattagtg  | 1140 |
| gctagtggat  | taaagttacc  | ataccatttc  | cttctattcc  | gaaagtgdgy  | ttccwtgwgw  | 1200 |

cytctg

(2) INFORMATION FOR SEQ ID NO:3224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1576103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Xaa | Gly | Arg | Ser | Thr | Arg | Gln | Arg | Glu | Lys | Ala | Lys | Arg | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Leu | Pro | Ile | Pro | Pro | Phe | Arg | Ala | Leu | Ala | Glu | Pro | Ala | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Glu | Ala | Ser | Arg | Arg | Leu | Ala | Trp | Arg | Pro | Pro | Val | Gly | Arg | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Ser | Ala | Ala | Ala | Ser | Asn | Cys | Lys | Lys | Ile | Ile | Asp | Phe | Cys | Ala | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ala | Ser | Gly | Tyr | Gly | Thr | Ile | Pro | Ser | Ala | Tyr | Gly | Cys | Arg | Cys | Arg |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Trp | Val | Thr | Ser | Val | Ser | Cys | Leu | Cys | Leu | Ser | Ala | Cys | Ser | Asn | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Ser | Cys | Phe | Cys | Cys | Ile | Cys | Trp | Phe | Thr | Val | Arg | Ala | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Pro | Ser | Gln | Ser | Trp | Ser | Tyr | Glu | Cys | Ser | Ala | Pro | Asp | Cys | Leu | Pro |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Thr | Ser | Ser | Thr | Ile | Pro | Pro | Thr | Ala | Pro | Ala | Ala | Thr | Thr | Thr | Ala |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Ala | Ser | Ala | Val | Leu | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 145 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3225:

Met Glu Pro Ser Pro Gln Pro Met Gly Val Ala Ala Gly Gly Ser Gln  
1 5 10 15  
Val Tyr Pro Ala Ser Ala Tyr Pro Pro Ala Ala Thr Val Ala Pro Ala  
20 25 30  
Ser Val Val Ser Ala Gly Leu Gln Ser Gly Gln Pro Phe Pro Ala Asn  
35 40 45  
Pro Gly His Met Ser Ala Gln His Gln Ile Val Tyr Gln Gln Ala Gln  
50 55 60  
Gln Phe His Gln Gln Leu Gln Gln Gln Gln Gln Gln Leu Gln Gln  
65 70 75 80  
Phe Trp Val Glu Arg Met Thr Glu Ile Glu Ala Thr Thr Asp Phe Lys  
85 90 95  
Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp  
100 105 110  
Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe Ala Lys  
115 120 125  
Ala Cys Glu Ile Phe Ile Leu Glu Leu Thr Leu Xaa Val Val Asp Xaa  
130 135 140  
His  
145

(2) INFORMATION FOR SEQ ID NO:3226:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1576105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3226:

Met Gly Val Ala Ala Gly Gly Ser Gln Val Tyr Pro Ala Ser Ala Tyr  
1 5 10 15  
Pro Pro Ala Ala Thr Val Ala Pro Ala Ser Val Val Ser Ala Gly Leu  
20 25 30  
Gln Ser Gly Gln Pro Phe Pro Ala Asn Pro Gly His Met Ser Ala Gln  
35 40 45  
His Gln Ile Val Tyr Gln Gln Ala Gln Gln Phe His Gln Gln Leu Gln  
50 55 60  
Gln Gln Gln Gln Gln Gln Leu Gln Gln Phe Trp Val Glu Arg Met Thr  
65 70 75 80  
Glu Ile Glu Ala Thr Thr Asp Phe Lys Asn His Asn Leu Pro Leu Ala  
85 90 95  
Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser  
100 105 110  
Ala Glu Ala Pro Val Val Phe Ala Lys Ala Cys Glu Ile Phe Ile Leu  
115 120 125  
Glu Leu Thr Leu Xaa Val Val Asp Xaa His  
130 135

(2) INFORMATION FOR SEQ ID NO:3227:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 773 base pairs

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- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..773  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3227:

|              |            |            |            |            |            |     |
|--------------|------------|------------|------------|------------|------------|-----|
| arcgctcgtg   | gaaaggagac | gtctctgaac | cgaggctgcg | actgcgaggg | cagcgaggca | 60  |
| gacgagacca   | cgcttcttgt | cgctgaatc  | ccctcgagar | ccgccggcgw | ascatggcgc | 120 |
| gggtcccccagc | cgctctctcc | tcctctaca  | cggacagcac | gggatcctcc | tccgactcag | 180 |
| Gctccacctc   | ctcgggaatc | gaccgcccgc | gccacgagcg | ggagcggcgg | cggtccgcgt | 240 |
| cggacgacga   | cagctacagc | acaagctctt | atgacagtga | ccgtgaggtg | tctggcagat | 300 |
| ctcggaaaca   | taagaagagc | agcagatcaa | gaaagtctag | ggagagggag | cggagCaaag | 360 |
| atagacatca   | taaacgagac | aagagtaaac | acaaagagaa | gaaagagagt | gagcatgctg | 420 |
| atggccctgt   | ccagctttcc | aagtttcttg | gacgggacaa | agaaaaggaa | gaaggtactc | 480 |
| aacggagtgc   | aatatctggt | aaaaagataa | tgatgaagct | tgagaagaca | aaggaagaca | 540 |
| aggcagcaga   | gagcaagcga | aacgaactgt | tgaagtttct | gaatgccagt | tacgattgat | 600 |
| gtgttcgaat   | yGctgacgcg | gaaagtgcag | watgcccttt | tttatcgtct | ttgcactggt | 660 |
| gcttttggtg   | atacttaagt | tataaacgtt | ttgtttcttg | tctataactt | ggccacccaa | 720 |
| gttttgttat   | gctcaactag | cgactgagtg | aaggtctaca | tgcaattgat | ttg        |     |

(2) INFORMATION FOR SEQ ID NO:3228:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..198  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Trp | Lys | Gly | Asp | Val | Ser | Glu | Pro | Arg | Leu | Arg | Leu | Arg | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Arg | Gly | Arg | Ser | Ser | His | Ala | Ser | Cys | Arg | Val | Asn | Pro | Leu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Xaa | Arg | Arg | Xaa | Xaa | Met | Ala | Arg | Ser | Pro | Ala | Ala | Ser | Ser | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Thr | Asp | Ser | Thr | Gly | Ser | Ser | Ser | Asp | Ser | Gly | Ser | Thr | Ser | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ile | Asp | Arg | Arg | Arg | His | Glu | Arg | Glu | Arg | Arg | Arg | Ser | Ala | Ser |
| 65  |     |     |     |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Asp | Asp | Ser | Tyr | Ser | Thr | Ser | Ser | Tyr | Asp | Ser | Asp | Arg | Glu | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Arg | Ser | Arg | Lys | His | Lys | Lys | Ser | Ser | Arg | Ser | Arg | Lys | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Glu | Arg | Glu | Arg | Ser | Lys | Asp | Arg | His | His | Lys | Arg | Asp | Lys | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | His | Lys | Glu | Lys | Lys | Glu | Ser | Glu | His | Ala | Asp | Gly | Pro | Val | Gln |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Ser | Lys | Phe | Leu | Gly | Arg | Asp | Lys | Glu | Lys | Glu | Glu | Gly | Thr | Gln |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Arg | Ser | Ala | Ile | Ser | Gly | Lys | Lys | Ile | Met | Met | Lys | Leu | Glu | Lys | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Lys | Glu | Asp | Lys | Ala | Ala | Glu | Ser | Lys | Arg | Asn | Glu | Leu | Leu | Lys | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Leu | Asn | Ala | Ser | Tyr | Asp |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3229: